

# Inference and Characterization of Planar Trajectories

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*All knowledge is, in the final analysis, history.  
All sciences are, in the abstract, mathematics.  
All judgments are, in their rationale, statistics.*  
– C. Radhakrishna Rao.



## Abstract

Inference and characterization of planar trajectories have long been the focus of scientific and commercial research. Efficient algorithms for both precise and efficient trajectory reconstruction remain in high demand in a wide variety of applications.

Given time series GPS data of a moving object, trajectory reconstruction is the process of inferring the path between successive observation points. However, widely separated points and measurement errors can give rise to trajectories with sharp angles, which are not typical of a moving object. Smoothing spline methods can efficiently build up a more smooth trajectory. In conventional smoothing splines, the objective function is augmented with a penalty term, which has a single parameter that controls the smoothness of reconstruction. Adaptive smoothing splines extend the single parameter to a function that can vary, hence the degree of smoothness can be different regions. A new method named the V-spline is proposed, which incorporates both location and velocity information but penalizes excessive accelerations. In the application of interest, the penalty term is also dependent on a known operational state of the object. The V-spline includes a parameter that controls the degree to which the velocity information is used in the reconstruction. In addition, the smoothing penalty adapts the observations are irregular in time. An extended cross-validation technique is used to find all spline parameters.

It is known that a smoothing spline can be thought of as the posterior mean of a Gaussian process regression in a certain limit. By constructing a reproducing kernel Hilbert space with an appropriate inner product, the Bayesian form of the V-spline is derived when the penalty term is a fixed

constant instead of a function. An extension to the usual generalized cross-validation formula is utilized to find the optimal V-spline parameters.

In on-line trajectory reconstruction, smoothing methods give way to filtering methods. In most algorithms for combined state and parameter estimation in state-space models either estimate the states and parameters by incorporating the parameters in the state-space, or marginalize out the parameters through sufficient statistics. Instead of these approaches, an adaptive Markov chain Monte Carlo algorithm is proposed. In the case of a linear state-space model and starting with a joint distribution over states, observations, and parameters, an MCMC sampler is implemented with two phases. In the learning phase, a self-tuning sampler is used to learn the parameter mean and covariance structure. In the estimation phase, the parameter mean and covariance structure informs the proposed mechanism and is also used in a delayed-acceptance algorithm, which greatly improves sampling efficiency. Information on the resulting state of the system is indicated by a Gaussian mixture. In the on-line mode, the algorithm is adaptive and uses a sliding window approach by cutting off historical data to accelerate sampling speed and to maintain applicable acceptance rates. This algorithm is applied to the joint state and parameters estimation in the case of irregularly sampled GPS time series data.

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# Chapter 1

## Introduction

### 1.1 Background

The Global Positioning System (abbreviated as GPS) is a space-based navigation system consisting of a network of 24 satellites placed in space in six different 12-hour orbital paths (Agrawal and Zeng, 2015), so that at least five of them are in view from every point on the globe (Kaplan and Hegarty, 2005; Bajaj *et al.*, 2002). With these satellites, a GPS receiver sends geographic information to them and triangulate its location on the ground, such as longitude, latitude, and elevation. These receivers are using passive locating technology, by which they can receive signals without transmitting any data. It is perhaps the most widely publicized location-sensing system providing an excellent lateration framework for determining geographic positions (Hightower and Borriello, 2001). Offered free of charge and accessible worldwide, GPS is used in plenty applications in military and general public, including aircraft tracking, vehicle navigation, robot localization, surveying, astronomy, and so on.

For a moving vehicle, it is often mounted with a GPS unit that communicates with these satellites and records position, speed, and direction of traveling information. With this kind of information, a maneuvering target tracking system becomes available and useful. This tracking system can be used to reduce the cost by knowing in real-time the current location of a vehicle, such as a truck or a bus (Chadil *et al.*, 2008), and also be useful for Intelligent Transportation System (ITS) (McDonald, 2006). For instance, it can be used in probe cars to measure real-time traffic data to identify the congesting area. In particular, an orchardist is able to follow the trajectory and motion patterns of tractors, which are working on an orchard or vineyard, and monitor their working status with the tracking system.

It is suggested that the smoothing spline fitting through the measured values reflecting the movements is an excellent approach, see (Eubank, 2004; Durbin and Koopman, 2012) for details. This algorithm can approximate data points throughout the whole process.

## 1.2 Smoothing Spline Based Reconstruction

Starting from interpolation, the simplest way of connecting a set of sequences  $(t_1, y_1), \dots, (t_n, y_n)$  is by straight line segments. Known as piecewise linear interpolation. Apparently, sharp turnings occur at joint knots. A smooth path is expected and more common in real life application. A single polynomial function goes through the entire interval, such as Bézier curve, is not as flexible as a combination of several polynomials, each of which is defined on subintervals and joint at certain knots. This kind of piecewise polynomial interpolation is called a *spline*.

The core idea of splines is to augment the vector of inputs  $T$  with additional variables, then use linear models in this space of derived input features. Adding constraints to construct basis functions  $h_i(t), i = 1, 2, \dots, n$ , a linear basis expansion in  $T$  is represented as

$$f(t) = \sum_{i=1}^n \theta_i h_i(t).$$

The key step of a spline interpolation is the choice of basis functions. Once the  $h_i(t)$  have been determined, the models are linear in the variables space.

Several kinds of splines were introduced by Trevor Hastie (2009). One of them is B-spline, short for basis spline, which is constructed from polynomial pieces and joint at knots. B-spline has a closed-form expression of positions and allows continuity between the curve segments and goes through the points smoothly with ignoring the outliers, see e.g. (Komoriya and Tanie, 1989; Ben-Arieh *et al.*, 2004). It is flexible and has minimal support with respect to a given degree, smoothness, and domain partition. Once the knots are given, it is easy to compute B-spline recursively for any desired degree of the polynomial (De Boor *et al.*, 1978; Cox, 1982). Basic simplicity of the idea is explained in (Dierckx, 1995; Eilers and Marx, 1996). The attractive feature of B-spline is its flexibility for univariate regression. For example, Gasparetto and Zanotto (2007) is using a fifth-order B-spline to compose the overall trajectory with a set of paired data. Roughly speaking, every spline can be represented by B-spline basis.

Another widely used spline is piecewise cubic spline, which is continuous on interval

$[a, b]$  and its first and second derivatives are continuous as well (Wolberg, 1988). For example, consider the model in the following form

$$f(t) = d_i(t - t_i)^3 + c_i(t - t_i)^2 + b_i(t - t_i) + a_i,$$

for given coefficients  $d_i, c_i, b_i$  and  $a_i$ , where  $t_i \leq t \leq t_{i+1}$ ,  $i = 1, 2, \dots, n$ .  $f$  is a cubic spline on  $[a, b]$  if (i) on each intervals  $f$  is a polynomial; (ii) the polynomial pieces fit together at knots  $t_i$  in such a way that  $f$  itself, its first and second derivatives are continuous at each  $t_i$ . If the second and third derivatives of  $f$  are zero at  $a$  and  $b$ ,  $f$  is said to be a natural cubic spline and these conditions are called the *natural boundary conditions*, (Green and Silverman, 1993).

To find the best estimation  $\hat{f}(t)$  going through observation  $y_i$ ,  $i = 1, \dots, n$ , one can use regression methods returning the least residual sum of squares among all the sequences. Consider a model  $y_i = f(t_i) + \varepsilon_i$  with random errors  $\{\varepsilon_i\}_{i=1}^n \sim N(0, \sigma^2)$  in space  $C^{(m)}[a, b]$ , the classical parametric regression assumes that  $f$  has the form of  $f(t, \beta)$ , which is known up to the data estimated parameters  $\beta$  (Kim and Gu, 2004). When  $f(t, \beta)$  is linear in  $\beta$ , we will have a standard linear model.

However, a parametric approach only captures features contained in the preconceived class of functions and increases model bias (Yao *et al.*, 2005). To avoid this, nonparametric methods have been developed. Rather than giving specified parameters, it is desired to reconstruct  $f$  from the data  $y(t_i) \equiv y_i$  itself (Craven and Wahba, 1978). The estimates of polynomial smoothing splines appear as a solution to the following minimization problem: find  $\hat{f} \in C^{(m)}[a, b]$  that minimizes the penalized residual sum of squares:

$$\text{RSS} = \sum_{i=1}^n (y_i - f(t_i))^2 + \lambda \int_a^b (f^{(m)})^2 dt \quad (1.1)$$

for pre-specified value  $\lambda (> 0)$  (Aydin and Tuzemen, 2012). In the above equation, the first term is the residual sum squares controlling the lack of fit. The second term is the roughness penalty weighted by a smoothing parameter  $\lambda$ , which varies from 0 to  $+\infty$  and establishes a trade-off between interpolation and straight line in the following way:

$$\begin{cases} \lambda = 0 & f \text{ can be any function that interpolates the data} \\ \lambda = +\infty & \text{the simple least squares line fit since no second derivative can be tolerated} \end{cases}$$

(Trevor Hastie, 2009).

Hence, the cost of the equation (1.1) is determined not only by its goodness-of-fit to the data quantified by the residual sum of squares but also by its roughness

(Schwarz, 2012). The motivation of the roughness penalty term is from a formalization of a mechanical device: if a thin piece of flexible wood, called a spline, is bent to the shape of the curve  $g$ , then the leading term in the strain energy is proportional to  $\int f''^2$  (Green and Silverman, 1993).

## 1.3 Parameter Selection

As discussed in the previous section, the determination of an optimal smoothing parameter  $\lambda$  in the interval  $(0, +\infty)$  was found to be an underlying complication and the fundamental idea of nonparametric smoothing is to let the data choose the amount of smoothness, which consequently decides the model complexity (Gu, 1998). Various studies for selecting an appropriate smoothing parameter are developed and compared in literatures. Most of these methods are focusing on data driven criteria, such as cross-validation (CV), generalized cross-validation (GCV) (Craven and Wahba, 1978) and generalized maximum likelihood (GML) (Wahba, 1985) and recently developed methods, such as improved Akaike information criterion (AIC) (Hurvich *et al.*, 1998), exact risk approaches (Wand and Gutierrez, 1997) and so on. See e.g. (Craven and Wahba, 1978; Härdle *et al.*, 1988; Härdle, 1990; Wahba, 1990; Green and Silverman, 1993; Cantoni and Ronchetti, 2001; Aydin *et al.*, 2013).

A classical parameter selection method is *cross-validation* (CV). The idea behind this method can be traced back to 1930s (Larson, 1931). Because in most applications, only a limited amount of data is available. Thus, an idea is to split this dataset into two subgroups, one of which is used for training the model and the other one is used to evaluate its statistical performance. The sample used in evaluation is considered as "new data" as long as data are i.i.d..

A single data split yields a validation estimate of the risk and averaging over several splits yields a cross-validation estimate (Arlot *et al.*, 2010). Because of the assumption that data are identically distributed, and training and validation samples are independent, CV methods are widely used in parameter selection and model evaluation.

For example, a  $k$ -fold CV splits the data into  $k$  roughly equal-sized parts. For the  $k$ th part, we fit the model to the other  $k - 1$  parts of the data, and calculate the prediction error of the fitted model when predicting the  $k$ th part of the data. A detailed procedure is given by (Wahba and Wold, 1975): suppose we have  $n$  paired data  $(t_1, y_1), \dots, (t_n, y_n)$ . Run a  $k$ -fold CV according to the following Algorithm 1.1. Mathematically, we denote the CV score as

---

**Algorithm 1.1:** *k*-fold Cross-Validation

---

```

1 Initialization: Remove the first data  $t_1$  and last date  $t_n$  from the dataset.
2 Split the rest data  $t_2, \dots, t_{n-1}$  into  $k$  groups by: Group  $k : t_{k+1}, t_{2k+1}, \dots$ 
3 Guess a value  $\lambda^*$ .
4 while CV score is not optimized do
5   for  $i = 1, \dots, k$  do
6     Delete the  $i$ th group of data. Fit a smoothing spline to the first data
       $(t_1, y_1)$ , the rest  $k - 1$  groups of dataset and the last data  $(t_n, y_n)$  with  $\lambda^*$ .
7     Compute the sum of squared deviations  $s_i$  of this smoothing spline from
      the deleted  $i$ th group data points.
8   end
9   Add the sums of squared deviations from steps 5 to 8 and divide it by  $k$  to
      achieve a cross-validation score of  $\lambda^*$ , that is  $s = \frac{1}{k} \sum_{i=1}^k s_i$ .
10  Vary  $\lambda$  systematically and repeat steps 5 to 9 until CV shows a minimum.
11 end

```

---

$$\text{CV}(\hat{f}, \lambda) = \frac{1}{n} \sum_i^n \left( y_i - \hat{f}^{(-k(i))}(t_i, \lambda) \right)^2,$$

where  $\hat{f}^{(-k)}(t)$  denotes the fitted function computed with the  $k$ th part of the data removed. Typical choices for  $k$  are 5 and 10 (Trevor Hastie, 2009). The function  $\text{CV}(\hat{f}, \lambda)$  provides an estimate of the test error curve, and the tuning parameter  $\lambda$  that minimizes it will be the optimal solution.

A special case of  $k$ -fold CV is setting  $k = n$ , which is known as *leave-one-out cross-validation*. In this scenario, the CV function takes each of the data out and calculate the errors of  $\hat{f}^{(-i)}$  from the remaining  $n - 1$  points. In fact, with the property that taking one point out does not affect the estimation, the fitting of a smoothing spline allows us to implement CV methods without hesitation.

As an improvement of CV, the GCV algorithm was proposed to calculate the trace of the estimation matrix  $A(\lambda)$  instead of calculating individual elements for linear fitting under squared error loss, in which way it provides further computational savings. Suppose we have a solution  $\hat{f} = A(\lambda)y$  with a given  $\lambda$ , for many linear fittings, the CV score is

$$\text{CV} = \frac{1}{n} \sum_{i=1}^n \left( y_i - \hat{f}^{(-i)}(t_i) \right)^2 = \frac{1}{n} \sum_{i=1}^n \left( \frac{y_i - \hat{f}(t_i)}{1 - A_{ii}} \right)^2,$$

where  $A_{ii}$  is the  $i$ th diagonal element of  $A(\lambda)$ . Then, the GCV approximation score is

$$\text{GCV} = \frac{1}{n} \sum_{i=1}^n \left( \frac{y_i - \hat{f}(t_i)}{1 - \text{tr}(A)/n} \right)^2.$$

In smoothing problems, GCV can also alleviate the tendency of cross-validation to under-smooth (Trevor Hastie, 2009).

Rather than  $\lambda$  being constant, a new challenge is posed that the smoothing parameter becomes a function  $\lambda(t)$  and is varying in domains. The structure of this penalty function controls the complexity of each domain and the whole final model. Donoho *et al.* (1995) introduced adaptive splines and a method to calculate piecewise parameters and Liu and Guo (2010) give an improved formula for this method. They proposed an approximation to the penalty function with an indicator and extended the generalized likelihood to the adaptive smoothing spline. This will be another interesting research topic.

Overall, almost every technique found in the scientific literatures on the reconstruction and trajectory planning problem is based on the optimization of objective functions or parameter selections, such as the objective function (1.1) and cross-validation approaches (Gasparotto and Zanotto, 2007).

## 1.4 Bayesian Filtering

Smoothing spline algorithms have several advantages in inferring and characterizing planar trajectories, particularly in reconstruction. However, subject to the property that smoothing splines require the solution of a global problem that involves the entire set of points to be interpolated, it might not be suitable for on-line estimation or instant updating (Biagiotti and Melchiorri, 2013). Therefore, it is time to use Bayesian filtering to implement on-line/instant estimation and prediction.

The word *filtering* refers to the methods for estimating the state of a time-varying system, which is indirectly observed through noisy measurements. A Bayes filter is a general probabilistic approach to infer an unknown probability density function recursively over time using incoming measurements and a mathematical process model. The concept *optimal estimation* refers to some criteria that measure the optimality in specific sense (Anderson and Moore, 1979). For example, a posterior estimation of  $\hat{x}_t \sim p(x_t | y_{1:t})$  that minimizes the loss function  $J_t = E[x_t - \hat{x}_t]^2$  for incorrect estimates, or least mean squared errors, maximum likelihood approximation and so on.

See e.g. (Chen *et al.*, 2003; Särkkä, 2013). Hence, an optimal *Bayesian filtering* is using Bayesian way of formulating optimal filtering by meeting some statistical criteria.

It is no doubt that in a conventional target tracking system, the most common method is the standard Kalman filter, which is a recursive solution to the discrete data linear filtering problem.

## Kalman Filter

In a discrete-time linear system, the optimal Bayesian solution coincides with the least squares solution. The successful optimal one was given by Kalman *et al.* (1960), the celebrated *Kalman filter*. It is a set of mathematical equations that provides an efficient computational means to estimate the state of a process in a recursive way by minimizing the mean of the squared errors (Bishop and Welch, 2001).

The Kalman filter recursively updates the estimated state by computing from the previous estimation and a new observation. In addition to eliminating the need for storing the entire past observed data, it is computationally more efficient than computing the estimate directly from the entire past observed data at each step of the filtering process (Haykin *et al.*, 2001).

A detailed Kalman filter and its may variants can be found in (Chen *et al.*, 2003; Rhodes, 1971; Kailath, 1981; Sorenson, 1985). Tusell *et al.* (2011) gives a review of some *R* packages, which are used to fit data with Kalman filter methods. Besides, it is also shown that the Kalman filter can be derived within a Bayesian framework and reduces to a maximum posterior probability (MAP) solution, and can be easily extended to ML solution. See e.g. (Haykin *et al.*, 2001; Guzzi, 2016).

Consider the following model

$$\begin{array}{ccccccc} \cdots & \rightarrow & x_{t-1} & \rightarrow & x_t & \rightarrow & x_{t+1} \rightarrow \cdots & \text{truth} \\ & & \downarrow & & \downarrow & & \downarrow \\ & & y_{t-1} & & y_t & & y_{t+1} & \cdots \text{observation} \end{array} \quad (1.2)$$

in which  $x_t = F(x_{t-1}) + \varepsilon_x$  is the true hidden state propagating through the transition matrix  $F$  and  $y_t = G(x_t) + \varepsilon_y$  is the observation measured by the measurement matrix  $G$  of the system, where  $\varepsilon$  indicates i.i.d.noise in the model.

To estimate the filtering state  $x_t$  from  $y_{1:t} = \{y_1, \dots, y_t\}$ , Bayesian wants to maximize the posterior  $p(x_t | y_{1:t})$  by marginalizing out all the previous measurements. Given the joint distribution of  $p(x_t, x_{t-1}, y_{1:t})$ , Kalman filter supposes the expectation  $\hat{x}_{t-1}$  and its variance  $S_{t-1}$  are known and passing through the system by  $\hat{x}_t = F\hat{x}_{t-1}$

and  $S_t = FS_{t-1}F^\top + Q_t$ . Because of the log-likelihood function is written in such a way that  $\ln p(x_t | y_{1:t}) \propto \frac{1}{2}(y_t - Gx_t)^2 - \frac{1}{2}(x_t - \hat{x}_{t-1})^2$ , as a result, the solution is

$$\hat{x}_t = (G^\top R_t^{-1}G + S_{t-1}^{-1})^{-1} (G^\top R_t^{-1}y_t + S_{t-1}^{-1}\hat{x}_{t-1}).$$

Additionally, by setting  $S_t^{-1} = G^\top R_t^{-1}G + S_{t-1}^{-1}$ , the recursive estimation of covariance matrix is  $S_t = S_{t-1} - K_t GS_{t-1}$ , and  $K_t = S_{t-1}G^\top(R_t + GS_{t-1}G^\top)^{-1}$  is named Kalman gain matrix. Consequently, the recursive estimation is

$$\hat{x}_t = \hat{x}_{t-1} + K_t(y_t - G\hat{x}_{t-1}). \quad (1.3)$$

Further, compared with the filtering distribution  $p(x_t | y_{1:t})$ , the prediction distribution is trying to find an  $n$ -steps later distribution  $p(x_{t+n} | y_{1:t})$  from the current state, and the smoothing distribution is to find the distribution  $p(x_k | y_{1:t})$  of a specific state  $x_k$  in the past for any  $k$ , where  $1 < k < t$ .

However, Kalman filter has a limitation that it does not apply to general non-linear model and non-Gaussian distributions. For a non-linear system, one can use the extended Kalman filter (EKF), which is widely used for solving nonlinear state estimation applications (Gelb, 1974; Bar-Shalom and Li, 1993). The EKF uses Taylor expansion to construct linear approximations of nonlinear functions, therefore, the state transition  $f$  and observation  $g$  do not have to be linear but to be differentiable. However, in the EKF process, these approximations can introduce large errors in the true posterior mean and covariance of the transformed (Gaussian) random variable (Wan and Van Der Merwe, 2000).

Alternatively, the unscented Kalman filter (UKF) is a derivative-free method (Julier and Uhlmann, 1997; Wan and Van Der Merwe, 2000; György *et al.*, 2014). It is using the Kalman filter to create a normal distribution that approximates the result of a non-linear transformation numerically by seeing what happens to a few deliberately chosen points. The unscented transform is used to recursively estimating the equation (1.3), where the state random variable is redefined as the concatenation of the original state and noise variables. By contrast, Kalman filter does not require numerical approximations.

The performances of EKF and UKF are compared in a few references regarding to different kinds of aspects, such as (Chandrasekar *et al.*, 2007; LaViola, 2003; St-Pierre and Gingras, 2004). There is not an overall conclusion that which one performs better.

Limited to its property, Kalman filter is tied up for a dynamic system, where the parameters and noise variances are unknown. In some dynamic systems, the variances

are obtained based on the system identification algorithm, correlation method, and least squares fusion criterion. To solve this issue, a self-tuning weighted measurement fusion Kalman filter is proposed by Ran and Deng (2010). Likewise, a new adaptive Kalman filter will be another choice (Oussalah and De Schutter, 2001).

However, when the target maneuver occurs, Kalman filtering accuracy will be reduced or even diverged due to the model mismatch and noise characteristics that cannot be known exactly (Liu *et al.*, 2014). Additionally, Kalman filter based methods require the state vector contains pre-specified coefficients during the whole approximation procedure and are within the bounded definition range determined at the beginning (Jauch *et al.*, 2017).

A more generic algorithm is introduced in the following section.

## Monte Carlo Filter

*Monte Carlo filter, chen2003bayesian*, is a class of Monte Carlo approaches. The power of these approaches is that they can numerically and efficiently handle integration and optimization problems.

The important advantage of Monte Carlo is that a large number of posterior moments can be estimated at a reasonable computational effort and that estimates of the numerical accuracy of these results are obtained in a simple way (Kloek and Van Dijk, 1978). *Sequential Monte Carlo* method is using Monte Carlo approaches to estimate and to compute recursively. One of the attractive merits is in the fact that they allow on-line estimation by combining the powerful Monte Carlo sampling methods with Bayesian inference at an expense of reasonable computational cost (Chen *et al.*, 2003).

For example, consider the model (1.2) with parameter  $\theta$ . The likelihood approximation is  $p(y_t | y_{1:t-1}, \theta)$  and can be written by

$$p(y_t | y_{1:t-1}, \theta) = \int p(y_t | x_t, \theta)p(x_t | y_{1:t-1}, \theta)dx_t = E[p(y_t | x_t, \theta)].$$

The standard Monte Carlo algorithm is trying to compute the integration by drawing  $N$  independent samples  $x_t^{(i)}$  from  $p(x_t | y_{1:t-1}, \theta)$  at first and then, by adding them up, to approximate the integration for large  $N$  in the following way

$$E[p(y_t | x_t, \theta)] \approx \frac{1}{N} \sum_i p(y_t | x_t^{(i)}, \theta),$$

(Kalos and Whitlock, 2008).

In terms of getting good samples of  $x_t^{(i)}$ , which can be used for representing  $p(y_t | x_t^{(i)}, \theta)$ , an importance sampling method was devised. The idea of this method is by

assigning weights  $W_t^{(i)}$  to samples, the most important ones are evaluated for computing the integral. Further, sequential importance sampling (SIS) allows a sequential update of the importance weights by

$$W_t^{(i)} \propto W_{t-1}^{(i)} \frac{p(y_t | x_t^{(i)}) p(x_t^{(i)} | x_{t-1}^{(i)})}{q(x_t^{(i)} | x_{t-1}^{(i)}, y_t)}$$

with an appropriate chosen *proposal distribution*  $q(x_t | x_{t-1}, y_t)$ . It is also called *importance density* or *important function*, Chen *et al.* (2003).

Nevertheless, the SIS makes samples skewed that only a few samples have proper weights as time increases and most of them have small but positive weights. This phenomenon is often called *weight degeneracy* or *sample impoverishment*, (Green, 1995; Berzuini *et al.*, 1997).

Besides the SIS processes, a resampling step, also known as a selection step, is trying to eliminate the samples with small weights and duplicate the samples with large weights in a principled way (Rubin, 2004; Tanner and Wong, 1987). This method is named *sampling and importance resampling* (SIR). Suppose samples with associated weights are  $\{x_t^{(i)}, W_t^{(i)}\}$ , a resampling step is executed by generating new samples  $\tilde{x}_t^{(i)}$  according to normalized weights  $\tilde{W}_t^{(i)}$ . It is pointed out that the resampling step does not prevent weights degeneracy but improve further calculation.

The common feature of SIS and SIR is that both of these methods are based on importance sampling and updating samples weights recursively. The difference is that in SIR, the resampling step is always performed. Whereas, in SIS, resampling is only taken when needed.

*Particle filter* (PF) is the most successful application of importance sampling with resampling algorithm. It randomly generates a cloud of points and push these points through the computation process. It is a recursive implementation of the Monte Carlo approaches (Doucet and Johansen, 2009).

A generic PF firstly generates  $N$  uniformly weighted random measurements  $\{x_{t-1}^{(i)}, \frac{1}{N}\}$  at time  $t - 1$ . Once a new observation  $y_t$  comes into the system, the weights will be updated recursively by involving the likelihood function  $p(y_t | x_t^{(i)})$  and propagation function  $p(x_t^{(i)} | x_{t-1}^{(i)})$ . In fact, it is the SIS step. To monitor how bad is the weight degeneracy, a suggested measurement *effective sample size* was introduced in (Kong *et al.*, 1994). It is the reciprocal of the sum of squared weights in the form of

$$N_{\text{eff}} = \frac{1}{\sum_{i=1}^N (W_t^{(i)})^2}.$$

If the  $N_{\text{eff}}$  is less than a predefined threshold, the resampling procedure is executed and the set of particles remains the same size  $N$ .

However, the PF sampling and resampling methods may cause practical problems. Such as high weighted particles have been selected many times and lead to the loss of diversity. This problem is known as sample impoverishment, in which way the particles are not representative. The improvements of particle filter's performance have been devoted by (Carpenter *et al.*, 1999; Godsill *et al.*, 2001; Stavropoulos and Titterington, 2001; Arnaud Doucet, 2011).

Apparently, Bayesian filtering has become a broad topic involving many scientific areas that a comprehensive survey and detailed treatment seems crucial to cater the ever growing demands of understanding this important field for many novices, though it is noticed by the author that in the literature there exist a number of excellent tutorial papers on particle filters and Monte Carlo filters (Chen *et al.*, 2003; Doucet *et al.*, 2000; Chen *et al.*, 2012; Doucet *et al.*, 2000).

## 1.5 Markov Chain Monte Carlo Methods

Schemes exist to counteract sample impoverishment, which incurs in particle filter (Ristic *et al.*, 2004). One approach is to consider the states for the particles to be predetermined by the forward filter and then to obtain the smoothed estimates by recalculating the particles' weights via a recursion from the final to the first time step (Godsill *et al.*, 2000). Another approach is to use a *Markov chain Monte Carlo* (MCMC) move step (Carlin *et al.*, 1992). MCMC refers to constructing Markov chains that move in the space of the unobserved quantity of interest and produces a sequence of dependent samples from the posterior distribution. After the chain has been run long enough, the sequence of visited states may be used as an approximation to the posterior distribution (Kokkala *et al.*, 2016).

MCMC methods are a set of powerful stochastic algorithms that allow us to solve most of these Bayesian computational problems when the data are available in batches (Andrieu *et al.*, 1999; Green, 1995; Andrieu *et al.*, 2001). They are based on sampling from probability distributions based on a Markov chain. If samples are unable to be drawn directly from a distribution  $\pi(x)$ , we can construct a Markov chain of samples from another distribution  $\hat{\pi}(x)$  that is equilibrium to  $\pi(x)$ . If the chain is long enough, these samples of the chain can be used as a basis for summarizing features of  $\pi(x)$  of interest (Smith and Roberts, 1993). This is a crucial property. See e.g. (Cappé *et al.*,

2009; Liu, 2008) for details.

## Metropolis-Hastings Algorithm

The *Metropolis-Hastings* (MH) algorithm is an important class of MCMC algorithms (Smith and Roberts, 1993; Tierney, 1994; Gilks *et al.*, 1995). Given essentially a probability distribution  $\pi(\cdot)$  (the "target distribution"), MH algorithm provides a way to generate a Markov chain  $x_1, x_2, \dots, x_t$ , who has the target distribution as a stationary distribution, for the uncertain parameters  $x$  requiring only that this density can be calculated at  $x$ . Suppose that we can evaluate  $\pi(x)$  for any  $x$ . The transition probabilities should satisfy the detailed balance condition

$$\pi(x^{(t)}) q(x', x^{(t)}) = \pi(x') q(x^{(t)}, x'),$$

which means that the transition from the current state  $\pi(x^{(t)})$  to the new state  $\pi(x')$  has the same probability as that from  $\pi(x')$  to  $\pi(x^{(t)})$ . In sampling method, drawing  $x_i$  first and then drawing  $x_j$  should have the same probability as drawing  $x_j$  and then drawing  $x_i$ . However, in most situations, the details balance condition is not satisfied. Therefore, a function  $\alpha(x, y)$  is introduced for satisfying

$$\pi(x') q(x', x^{(t)}) \alpha(x', x^{(t)}) = \pi(x^{(t)}) q(x^{(t)}, x') \alpha(x^{(t)}, x').$$

In this way, a tentative new state  $x'$  is generated from the proposal density  $q(x'; x^{(t)})$  and it is then accepted or rejected according to acceptance probability

$$\alpha = \frac{\pi(x')}{\pi(x^{(t)})} \frac{q(x^{(t)}, x')}{q(x', x^{(t)})}. \quad (1.4)$$

If  $\alpha \geq 1$ , then the new state is accepted. Otherwise, the new state is accepted with probability  $\alpha$ .

A simple mechanic proposing algorithm is *Random Walk Metropolis-Hastings* (RM MH). It is easy to implement and symmetric under the exchange of the initial and proposed points.

Besides, modified Metropolis-Hastings algorithms, such as the delayed-rejection MH, multiple-try MH and reversible-jump MH algorithms have been studied by Tierney and Mira (1999); Liu *et al.* (2000); Green (1995).

## Adaptive MCMC Algorithm

Metropolis-Hastings algorithm is widely used in statistical inference, to sample from complicated high-dimensional distributions. Typically, this algorithm has parameters

that must be tuned in each new situation to obtain reasonable mixing times, such as the step size in a random walk Metropolis (Mahendran *et al.*, 2012). Tuning of associated parameters such as proposal variances is crucial to achieving efficient mixing, but can also be difficult.

*Adaptive MCMC* methods have been developed to automatically adjust these parameters. See e.g. (Andrieu and Thoms, 2008; Atchade *et al.*, 2009; Roberts and Rosenthal, 2009). One of the most successful adaptive MCMC algorithms was introduced by Haario *et al.* (2001), where, based on the random walk Metropolis algorithm, the covariance of the proposal distribution is calculated using all of the previous states. For instance, with an adaptive MCMC chain  $x_0, x_1, \dots, x_t$ , the proposal  $x'$  is from  $N(\cdot | x_t, R_t)$ , where  $R_t$  is the covariance matrix determined by the spatial distribution of the state  $x_0, x_1, \dots, x_t$ .

Even though the adaptive Metropolis algorithm is non-Markovian, the establishment was verified that the adaptive MCMC algorithm indeed has the correct ergodic properties.

A Bayesian optimization for adaptive MCMC was proposed by Mahendran *et al.* (2012). The author proposed adaptive strategy consists of two phases: adaptation and sampling. In the first phase, Bayesian optimization is used to construct a randomized policy. After that, in the second phase, a mixture of MCMC kernels selected according to the learned randomized policy is used to explore the target distribution.

Further investigation in the use of adaptive MCMC algorithms to automatically tune the Markov chain parameters can be found at (Roberts and Rosenthal, 2009).

## Other Monte Carlo Algorithms

The *Hamiltonian Monte Carlo* (HMC), devised by Duane *et al.* (1987) as hybrid Monte Carlo, is using Hamiltonian dynamics to produce distant proposals for the Metropolis algorithm in order to avoid slow exploration of the state-space that results from the diffusive behavior of simple random walk proposals (Neal *et al.*, 2011). In practice, the HMC sampler is more efficient for sampling in high-dimensional distributions than MH.

The key feature of HMC is the Hamiltonian system equation as follows:

$$H(x, v) = U(x) + K(v),$$

which is consisting of potential energy  $U(x)$  with a  $d$ -dimensional momentum vector (position)  $x$  and kinetic energy function  $K(v) = \frac{v^\top M^{-1} v}{2}$  with a  $d$ -dimensional momen-

tum vector (velocity)  $v$ . To propose  $\{x', v'\}$ , HMC is using leapfrog method, which is based on Euler's method and modified Euler's method, to increase the proposing accuracy (Betancourt, 2017). It is accepted with the probability

$$\alpha = \min \{\exp[H(x, v) - H(x', v')], 1\}.$$

Compared with MH sampler, the HMC has a higher efficiency in most of the high-dimensional cases. It is incorporating not only with energy  $U(x)$  but also with a gradient. In this way, HMC explores a larger area and converges to balance faster.

The *Zig-Zag Monte Carlo* is using a continuous-time piecewise zig-zag process to increase the sampling efficiency (Bierkens *et al.*, 2016b). It is an application of the Curie-Weiss model, (Turitsyn *et al.*, 2011), in high dimension and provides a practically efficient sampling scheme for sampling in the big data regime with some remarkable properties (Bierkens and Duncan, 2017).

Given a target density  $\pi(\cdot)$ , the Zig-Zag process  $f(x, \theta)$  is defined in a  $d \otimes 2$  space  $\mathcal{E}$ .  $x$  is in the  $d$ -dimensional topological subspace and  $\theta$  is in a binary discrete  $\{-1, 1\}_d$  subspace denoting the flipping statuses. The switching rate  $\lambda(x, \theta)$  agrees with the target distribution  $\pi(\cdot)$  in a certain way and is defined as  $\lambda(x, \theta) = \max \{0, \theta U'(x)\} + \gamma(x)$ , where  $U'(x) = \lambda(x, \theta) - \lambda(x, -\theta)$ . Then, the Zig-Zag operator  $L$  is

$$Lf(x, \theta) = \theta \partial f_x + \lambda(x, \theta)[f(x, -\theta) - f(x, \theta)],$$

for all  $(x, \theta) \in \mathcal{E}$ .

Thereafter, the obtained sequence of the Zig-Zag process is used to approximate expectations with respect to  $\pi(\cdot)$  according to the law of large numbers. The application of Zig-Zag process in big data scheme and some properties are given in (Bierkens and Duncan, 2017; Bierkens *et al.*, 2016a).

The *t-walk* given by Christen *et al.* (2010) is a self-adjusting MCMC algorithm that requires no tuning and has been shown to provide good results in many cases of up to 400 dimensions. Because of the t-walk is not adaptive, it does not require new restricting conditions but only the log of the posterior and two initial points (Blaauw *et al.*, 2011).

Given a posterior distribution  $\pi(\cdot)$ , the new objective function  $f(x, x')$  is the product of  $\pi(x)\pi(x')$  from  $X \otimes X$ . The new proposal  $(y, y')$  is given by

$$(y, y') = \begin{cases} (x, h(x', x)) & \text{with probability 0.5} \\ (h(x', x), x') & \text{with probability 0.5} \end{cases}$$

where  $h(x, x')$  is a preselected proposing strategy. In each iteration, only one of the two chains  $x$  and  $x'$  moves according to a random walk. For example, suppose in the first step the  $x$  stays the same but  $y'$  is proposed from  $q(\cdot | x, x')$ , then the acceptance ratio is

$$\frac{\pi(y') q(x' | y', x)}{\pi(x') q(y' | x', x)}.$$

After a few iterations, there are two dual and coupled chains obtained. Hence, the t-walk is a kind of multiple chain approach.

Four recommendations for the choices of  $h(x, x')$  including a scaled random walk, referred to *the walk move*, *traverse move*, *hop moves* and *blow moves* are given in (Christen *et al.*, 2010). The t-walk is now available in a complete set of computer packages, including *R*, *Python*. It is convenient for researchers to go a deeper implementation.

## 1.6 Thesis Outline

In Chapter 2, an adaptive smoothing V-spline method, which is based on *Hermite spline* basis functions, is proposed to obtain a reconstruction of  $f$  and  $f'$  from noisy data  $y_{1:n}$  and  $v_{1:n}$ . Instead of minimizing the residuals of  $f(t_i) - y_i$  only, the residuals of  $f'(t_i) - v_i$  with a new parameter  $\gamma$  are consisted in the new objective function. A modified leave-one-out cross-validation algorithm is used for find the optimal parameters. Numerical simulation and real data implementation are given after theoretical methodology.

In Chapter 3, the Bayesian estimation form of the V-spline is given. It is proved that the Bayesian estimate is corresponding to a trivial V-spline in the reproducing kernel Hilbert space  $C_{\text{p.w.}}^{(2)}[0, 1]$ , where the second-derivative is piecewise-continuous. An extended GCV is used to find the optimal parameters for the Bayesian estimate.

In Chapter 4, it is to give a comprehensive overview of existing methods for sequential state and parameter inference. Basic concepts and popular algorithms on sequential state estimation are introduced firstly. Furthermore, the algorithms that can estimate combined unknown state and parameter are brought into a separate section. A numerical comparison of different methods is given at the end of this chapter.

In Chapter 5, it is using a random walk Metropolis-Hastings algorithm in a learning phase to learn the mean of covariance of the parameters space. After that, the information is implemented in the estimation phase, where an adaptive Delayed-Acceptance Metropolis-Hastings algorithm is proposed for estimating the posterior distribution of combined state and parameter. To remain a high running efficiency, a sliding window

approach, in which way historical data is cut off when new observations come into the data stream, is used to improve the sampling speed. This algorithm is applied to irregularly sampled time series data and implemented in real GPS data set.

The proof of theorems, details of equation calculations, and results of simulation studies are all presented in appendices. For details, the Appendix A includes V-spline related theorems, lemmas, calculations and figures. In Appendix B, the proposed adaptive sequential MCMC related works and outcomes are illustrated, including details of the recursive form calculation, tables and figures of parameters comparison and so on.

A spin-off outcome is presented in Appendix C. It is a data simplification method used for reducing the size of a dataset and saving storage costs without losing important information.

Finally, the list of references is at the end of this thesis.

# Chapter 2

## Adaptive Smoothing V-Spline for Trajectory Reconstruction

### 2.1 Introduction

GPS devices are widely used for tracking individuals and vehicles. The position and velocity of moving objects are determined by GPS units and can be used in batch and on-line estimation of trajectories.

The TracMap company, located in New Zealand and USA, uses GPS display units for precision farming in agriculture, horticulture, viticulture and aviation. The GPS units guide the drivers to the right paddock, orchard or specific row that require maintenance, showing them where the hazards are on the way. Besides, the operation data is collected and sent back to a remote server by the these units.

Given a sequence of position vectors in a tracking system, the simplest way of constructing the complete trajectory of a moving object is by connecting positions with a sequence of lines, known as line-based trajectory representation (Agarwal *et al.*, 2003). Vehicles with an omnidirectional drive or a differential drive can actually follow such a path in a drive-and-turn fashion, though it is highly inefficient (Gloderer and Hertle, 2010) and this kind of non-smooth motion can cause slippage and over-actuation (Magid *et al.*, 2006). By contrast, most vehicles typically return smooth trajectories without sharp turns.

Several methods have been investigated to solve this issue. One of them uses the minimal length path that is continuously differentiable and consists of line segments or arcs of circles, with no more than three segments or arcs between successive positions (Dubins, 1957). This method is called Dubins curve and has been extended to other

more complex vehicle models but is still limited to line segments and arcs of circles (Yang and Sukkarieh, 2010). However, there are still curvature discontinuities at the junctions between lines and arcs, leading to yaw angle errors (Wang *et al.*, 2017).

Spline methods have been developed to overcome these issues and to construct smooth trajectories. Magid *et al.* (2006) proposed a path-planning algorithm based on splines. The main objective of the method is the smoothness of the path, not a shortest or minimum-time path. A curve-based method uses a parametric cubic function  $P(t) = a_0 + a_1t + a_2t^2 + a_3t^3$  to obtain a spline that passes through any given sequence of joint position-velocity paired points  $(y_1, v_1), (y_2, v_2), \dots, (y_n, v_n)$  (Yu *et al.*, 2004). More generally, a B-spline gives a closed-form expression for the trajectory with continuous second derivatives and goes through the points smoothly while ignoring outliers, see e.g. (Komoriya and Tanie, 1989; Ben-Arieh *et al.*, 2004). It is flexible and has minimal support with respect to a given degree, smoothness, and domain partition. Gasparetto and Zanotto (2007) use fifth-order B-splines to compose the overall trajectory, allowing one to set kinematic constraints on the motion, expressed as the velocity, acceleration, and jerk. In computer (or computerized) numerical control (CNC), Erkorkmaz and Altintas (2001) presented a quintic spline trajectory generation algorithm connecting a series of reference knots that produces continuous position, velocity, and acceleration profiles. Yang and Sukkarieh (2010) proposed an efficient and analytical continuous curvature path-smoothing algorithm based on parametric cubic Bézier curves. Their method can fit ordered sequential points smoothly.

However, a parametric approach only captures features contained in the preconceived class of functions (Yao *et al.*, 2005) and increases model bias. To avoid this, nonparametric methods have been developed. Rather than giving specified parameters, it is desired to reconstruct the trajectory  $f(t)$  from the data  $y(t_i) \equiv y_i$ ,  $i = 1, \dots, n$ , (Craven and Wahba, 1978). Smoothing spline estimates of  $f(t)$  appear as a solution to the following minimization problem: find  $\hat{f} \in \mathcal{C}^{(2)}[a, b]$  that minimizes the penalized residual sum of squares:

$$\text{RSS} = \sum_{i=1}^n (y_i - f(t_i))^2 + \lambda \int_a^b (f''(t))^2 dt \quad (2.1)$$

for a pre-specified value  $\lambda > 0$  (Aydin and Tuzemen, 2012). In equation (2.1), the first term is a residual sum of squares and penalizes lack of fit. The second term is a roughness penalty term weighted by a smoothing parameter  $\lambda$ , which varies from 0 to  $+\infty$  and establishes a trade-off between interpolation and a straight line. The roughness penalty term is a formalization of a mechanical device: if a thin piece of

flexible wood, called a spline, is bent to the shape of the curve  $f$ , then the leading term in the strain energy is proportional to  $\int f''^2$ ; see e.g. (Green and Silverman, 1993). The reconstruction cost, equation (2.1), is determined not only by its goodness-of-fit to the data quantified by the residual sum of squares but also by its roughness (Schwarz, 2012). For a given  $\lambda$ , minimizing equation (2.1) will give the best compromise between smoothness and goodness-of-fit. Notice that the first term in equation (2.1) depends only on the values of  $f$  at  $t_i, i = 1, \dots, n$ . Green and Silverman (1993) show that the function that minimizes the objective function for fixed values of  $f(t_i)$  is a cubic spline: an interpolation of points via a continuous piecewise cubic function, with continuous first and second derivatives. The continuity requirements uniquely determine the interpolating spline, except at the boundaries (Sealfon *et al.*, 2005).

Zhang *et al.* (2013) propose Hermite interpolation on each interval to fit position, velocity and acceleration with kinematic constraints. Their trajectory formulation is a combination of several cubic splines on every interval or, alternatively, is a single function found by minimizing

$$p \sum_{i=1}^n |y_i - f(t_i)|^2 + (1-p) \int |f''(t)|^2 dt, \quad (2.2)$$

where  $p$  is a smoothing parameter (Castro *et al.*, 2006).

A conventional smoothing spline is controlled by one single parameter, which controls the smoothness of the spline on the whole domain. A natural extension is to allow the smoothing parameter to vary as a function of the independent variable, adapting to the change of roughness in different domains (Silverman, 1985; Donoho *et al.*, 1995). The objective function is now of the form

$$\sum_{i=1}^n (y_i - f(t_i))^2 + \int \lambda(t) (f''(t))^2 dt. \quad (2.3)$$

Similar to the conventional smoothing spline problem, one has to choose the penalty function  $\lambda(t)$ . The fundamental idea of nonparametric smoothing is to let the data choose the amount of smoothness, which consequently decides the model complexity (Gu, 1998). When  $\lambda$  is constant, most methods focus on data-driven criteria, such as cross-validation (CV), generalized cross-validation (GCV) (Craven and Wahba, 1978) and generalized maximum likelihood (GML) (Wahba, 1985). Allowing the smoothing parameter to be a function poses additional challenges, though Liu and Guo (2010) were able to extend GML to adaptive smoothing splines.

In this chapter, an adaptive smoothing spline called the V-spline is proposed that uses modified Hermite spline basis functions to obtain a reconstruction of  $f$  and  $f'$  from

noisy paired position data  $\mathbf{y} = \{y_1, \dots, y_n\}$  and velocity data  $\mathbf{v} = \{v_1, \dots, v_n\}$ . Rather than only using residuals  $f(t_i) - y_i$ , extra residuals  $f'(t_i) - v_i$  and a new parameter  $\gamma$  are included in the objective function. The parameter  $\gamma$  controls the degree to which the velocity information is used in the reconstruction. In this way, the spline keeps a balance between position and velocity. An advanced cross-validation formula is given for the V-spline parameters. It is shown that the new spline performs well on simulated signal data *Blocks*, *Bumps*, *HeaviSine* and *Doppler* (Donoho and Johnstone, 1994). Finally, an application of the V-spline to a set of 2-dimensional real data is given.

## 2.2 V-Spline

In the nonparametric regression, consider  $n$  paired time series points  $\{t_1, y_1, v_1\}, \dots, \{t_n, y_n, v_n\}$ , such that  $a \leq t_1 < t_2 < \dots < t_n \leq b$ ,  $y$  is the position information and  $v$  indicates its velocity. We define a positive piecewise constant function  $\lambda(t)$  :

$$\lambda(t) = \lambda_i \geq 0, \quad (2.4)$$

where  $t_i \leq t < t_{i+1}$ ,  $t_0 = a$ ,  $t_{n+1} = b$ , that will control the curvature penalty in each interval. For a function  $f : [a, b] \mapsto \mathbb{R}$  and  $\gamma > 0$ , define the objective function

$$J[f] = \frac{1}{n} \sum_{i=1}^n (f(t_i) - y_i)^2 + \frac{\gamma}{n} \sum_{i=1}^n (f'(t_i) - v_i)^2 + \sum_{i=0}^n \lambda_i \int_{t_i}^{t_{i+1}} (f''(t))^2 dt, \quad (2.5)$$

where  $\gamma$  is the parameter that weights the residuals between  $\mathbf{f}'$  and  $\mathbf{v}$ , and  $\lambda(t)$  is the smoothing parameter function.

**Theorem 1.** *For  $n \geq 2$ , the objective function  $J[f]$  is minimized by a cubic spline that is linear outside the knots.*

The solution to the objective function (2.5) is named *V-spline*, coming from the incorporation with velocity information and applications on vehicle and vessel tracking. The proof of Theorem 1 is in Appendix A.2.

### 2.2.1 Basis Functions

Suppose there is a time series sequence of observed dataset  $a \leq t_1 < t_2 < \dots < t_n \leq b$ . The function  $f(t)$  defined on this interval  $[t_1, t_n]$  is called V-spline, if it is the

solution to the objective function (2.5). Then, it has the following property: on each interior interval  $(t_i, t_{i+1})$ ,  $i = 1, \dots, n - 1$ ,  $f(t)$  is a cubic polynomial, but on interval  $(a, t_0)$  and  $(t_n, b)$  is linear;  $f(t)$  fits together at each point  $t_i$  in such a way that  $f(t)$  itself and its first derivatives are continuous at each  $t_i$ ,  $i = 1, \dots, n - 1$ .

Using Hermite interpolation on an arbitrary interval  $[t_i, t_{i+1}]$ , the cubic spline basis functions can be constructed as follows

$$h_{00}^{(i)}(t) = \begin{cases} 2\left(\frac{t-t_i}{t_{i+1}-t_i}\right)^3 - 3\left(\frac{t-t_i}{t_{i+1}-t_i}\right)^2 + 1 & t_i \leq t < t_{i+1} \\ 0 & \text{otherwise} \end{cases}, \quad (2.6)$$

$$h_{10}^{(i)}(t) = \begin{cases} \frac{(t-t_i)^3}{(t_{i+1}-t_i)^2} - 2\frac{(t-t_i)^2}{t_{i+1}-t_i} + (t-t_i) & t_i \leq t < t_{i+1} \\ 0 & \text{otherwise} \end{cases}, \quad (2.7)$$

$$h_{01}^{(i)}(t) = \begin{cases} -2\left(\frac{t-t_i}{t_{i+1}-t_i}\right)^3 + 3\left(\frac{t-t_i}{t_{i+1}-t_i}\right)^2 & t_i \leq t < t_{i+1} \\ 0 & \text{otherwise} \end{cases}, \quad (2.8)$$

$$h_{11}^{(i)}(t) = \begin{cases} \frac{(t-t_i)^3}{(t_{i+1}-t_i)^2} - \frac{(t-t_i)^2}{t_{i+1}-t_i} & t_i \leq t < t_{i+1} \\ 0 & \text{otherwise} \end{cases}. \quad (2.9)$$

Then a Hermite spline  $f^{(i)}(t)$  on interval  $[t_i, t_{i+1}]$  with points  $p_i = \{y_i, v_i\}$  and  $p_{i+1} = \{y_{i+1}, v_{i+1}\}$  can be expressed as

$$f^{(i)}(t) = h_{00}^{(i)}(t)y_i + h_{10}^{(i)}(t)v_i + h_{01}^{(i)}(t)y_{i+1} + h_{11}^{(i)}(t)v_{i+1}. \quad (2.10)$$

To construct a V-spline on the entire interval  $[t_1, t_n]$ , the new basis functions are defined in such way, that  $N_1 = h_{00}^{(1)}$ ,  $N_2 = h_{10}^{(1)}$ , and for all  $i = 1, 2, \dots, n - 2$ ,

$$N_{2i+1} = \begin{cases} h_{01}^{(i)} + h_{00}^{(i+1)} & \text{if } t < t_n \\ 0 & \text{if } t = t_n \end{cases},$$

$$N_{2i+2} = \begin{cases} h_{11}^{(i)} + h_{10}^{(i+1)} & \text{if } t < t_n \\ 0 & \text{if } t = t_n \end{cases},$$

and

$$N_{2n-1} = \begin{cases} h_{01}^{(n-1)} & \text{if } t < t_n \\ 1 & \text{if } t = t_n \end{cases},$$

$$N_{2n} = \begin{cases} h_{11}^{(n-1)} & \text{if } t < t_n \\ 0 & \text{if } t = t_n \end{cases}.$$

**Theorem 2.** On  $[t_1, t_n]$ , the functions  $N_1, \dots, N_{2n}$  provide a set of basis functions for the set of functions which are cubic on each interval  $[t_i, t_{i+1}]$ ,  $i = 1, \dots, n - 1$ , and continuous at joint knots, thus it is continuous on the entire interval  $[t_1, t_n]$ .

The proof of Theorem 2 is in Appendix A.3. As independent basis functions,  $N_1(t), \dots, N_{2n}(t)$  span a  $2n$  dimensional function space  $\mathcal{H}$ . For any  $f \in \mathcal{H}$ , it can be represented in the form of

$$f = \sum_{k=1}^{2n} \theta_k N_k(t), \quad (2.11)$$

where  $\{\theta_k\}_{k=1}^{2n}$  are parameters.

Figure 2.1 presents two basis functions on an arbitrary interval  $[t_i, t_{i+2})$  where they are continuous and differential. At the interior joint knot  $t_i$ , basis functions in the previous and following interval share the same position  $y_i$  and velocity  $v_i$ .

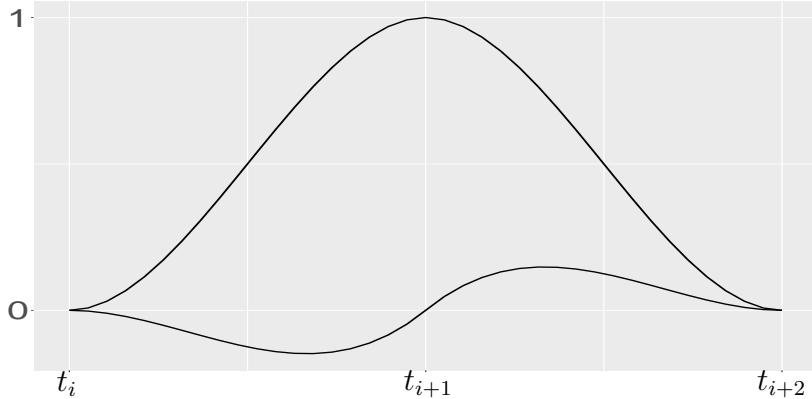


Figure 2.1: The two basis functions  $N_{2i+1}$  (upper) and  $N_{2i+2}$  (lower) on an arbitrary interval  $[t_i, t_{i+2})$ . Apparently, the basis functions are continuous on the interval and have continuous first derivatives.

From the definition of basis functions, it can be seen that at a joint knot of two neighbor intervals, Hermite spline basis functions share the same  $y_i$  and  $v_i$ . With this property, we construct V-spline basis functions. There are two parameters at each joint knots and 4 at the start and end knots. Hence, the degrees of freedom for parameters is  $2n - 4 + 4 = 2n$ . However  $2(n - 2)$  constraints are added to the joint knots, at which the spline have continuous first and second derivatives. Additional two constraints are added to the starting and ending knots to keep their first derivatives continuous. Consequently, parameters' the degrees of freedom is 2.

## 2.2.2 Solution to The Objective Function

Basis functions have been defined in the previous subsection, therefore the V-spline  $f(t)$  on  $[a, b]$ , where  $a \leq t_1 < t_2 < \dots < t_{n-1} < t_n \leq b$ , can be found by minimizing objective function (2.5), which reduces to

$$\text{MSE}(\theta, \lambda, \gamma) = (\mathbf{y} - \mathbf{B}\theta)^\top (\mathbf{y} - \mathbf{B}\theta) + \gamma (\mathbf{v} - \mathbf{C}\theta)^\top (\mathbf{v} - \mathbf{C}\theta) + n\theta^\top \boldsymbol{\Omega}_\lambda \theta, \quad (2.12)$$

where  $\{\mathbf{B}\}_{ij} = N_j(t_i)$ ,  $\{\mathbf{C}\}_{ij} = N'_j(t_i)$  and  $\left\{\Omega_{2n}^{(i)}\right\}_{jk} = \int_{t_i}^{t_{i+1}} \lambda_i N''_j(t) N''_k(t) dt$ . After substituting the series observation  $t_1, \dots, t_n$  into basis functions, we get  $N_1(t_1) = 1, N_1(t_2) = 0, \dots, N_{2i-1}(t_i) = 1, N_{2i}(t_i) = 0, \dots, N_{2n-1}(t_n) = 1, N_{2n}(t_n) = 0$ ; and into first derivative of basis functions, we get  $N'_1(t_1) = 0, N'_1(t_2) = 1, \dots, N'_{2i-1}(t_i) = 0, N'_{2i}(t_i) = 1, \dots, N'_{2n-1}(t_n) = 0, N'_{2n}(t_n) = 1$ . That means the matrices  $\mathbf{B}$  and  $\mathbf{C}$  in MSE equation (2.12) are  $n \times 2n$  dimensional and the elements are

$$\mathbf{B} = \{B\}_{ij} = \begin{cases} 1, & j = 2i - 1 \\ 0, & \text{otherwise} \end{cases} \quad (2.13)$$

$$\mathbf{C} = \{C\}_{ij} = \begin{cases} 1, & j = 2i \\ 0, & \text{otherwise} \end{cases} \quad (2.14)$$

where  $i = 1, \dots, n$ ,  $j = 1, \dots, 2n$  and  $k = 1, \dots, 2n$ . The  $i$ -th  $\Omega^{(i)}$  on the interval  $[t_i, t_{i+1}]$  is a  $2n \times 2n$  matrix and  $\Omega^{(n)}$  does not exist. Its detail is in Appendix A.1. As a result, the penalty term is a bandwidth four matrix written in such a way:

$$\boldsymbol{\Omega}_\lambda = \sum_{i=1}^{n-1} \lambda_i \Omega^{(i)}. \quad (2.15)$$

The solution to (2.12) is easily seen to be

$$\hat{\theta} = (\mathbf{B}^\top \mathbf{B} + \gamma \mathbf{C}^\top \mathbf{C} + n\boldsymbol{\Omega}_\lambda)^{-1} (\mathbf{B}^\top \mathbf{y} + \gamma \mathbf{C}^\top \mathbf{v}) \quad (2.16)$$

a generalized ridge regression. Therefore, the fitted smoothing spline is given by

$$\hat{f}(t) = \sum_{k=1}^{2n} N_k(t) \hat{\theta}_k \quad (2.17)$$

A smoothing spline with parameters  $\lambda(t)$  and  $\gamma$  is an example of a linear smoother (Trevor Hastie, 2009). This is because the estimated parameters in equation (2.16) are a linear combination of  $y_i$  and  $v_i$ . Denote by  $\hat{\mathbf{f}}$  and  $\hat{\mathbf{f}}'$  the  $2n$  vector of fitted values  $\hat{f}(t_i)$  and  $\hat{f}'(t_i)$  at the training points  $t_i$ . Then

$$\begin{aligned} \hat{\mathbf{f}} &= \mathbf{B} (\mathbf{B}^\top \mathbf{B} + \gamma \mathbf{C}^\top \mathbf{C} + n\boldsymbol{\Omega}_\lambda)^{-1} (\mathbf{B}^\top \mathbf{y} + \gamma \mathbf{C}^\top \mathbf{v}) \\ &\triangleq \mathbf{S}_{\lambda, \gamma} \mathbf{y} + \gamma \mathbf{T}_{\lambda, \gamma} \mathbf{v} \end{aligned} \quad (2.18)$$

$$\begin{aligned}\hat{\mathbf{f}}' &= \mathbf{C} (\mathbf{B}^\top \mathbf{B} + \gamma \mathbf{C}^\top \mathbf{C} + n \boldsymbol{\Omega}_\lambda)^{-1} (\mathbf{B}^\top \mathbf{y} + \gamma \mathbf{C}^\top \mathbf{v}) \\ &\triangleq \mathbf{U}_{\lambda, \gamma} \mathbf{y} + \gamma \mathbf{V}_{\lambda, \gamma} \mathbf{v}\end{aligned}\tag{2.19}$$

The fitted  $\hat{\mathbf{f}}$  and  $\hat{\mathbf{f}}'$  are linear in  $\mathbf{y}$  and  $\mathbf{v}$ , and the finite linear operators  $\mathbf{S}_{\lambda, \gamma}$ ,  $\mathbf{T}_{\lambda, \gamma}$ ,  $\mathbf{U}_{\lambda, \gamma}$  and  $\mathbf{V}_{\lambda, \gamma}$  are known as the smoother matrices. One consequence of this linearity is that the recipe for producing  $\hat{\mathbf{f}}$  and  $\hat{\mathbf{f}}'$  from  $\mathbf{y}$  and  $\mathbf{v}$ , do not depend on  $\mathbf{y}$  and  $\mathbf{v}$  themselves;  $\mathbf{S}_{\lambda, \gamma}$ ,  $\mathbf{T}_{\lambda, \gamma}$ ,  $\mathbf{U}_{\lambda, \gamma}$  and  $\mathbf{V}_{\lambda, \gamma}$  depend only on  $t_i$ ,  $\lambda(t)$  and  $\gamma$ .

Suppose in a traditional least squares fitting,  $\mathbf{B}_\xi$  is  $N \times M$  matrix of  $M$  cubic-spline basis functions evaluated at the  $N$  training points  $x_i$ , with knot sequence  $\xi$  and  $M \ll N$ . Thus the vector of fitted spline values is given by

$$\hat{\mathbf{f}} = \mathbf{B}_\xi (\mathbf{B}_\xi^\top \mathbf{B}_\xi)^{-1} \mathbf{B}_\xi \mathbf{y} = \mathbf{H}_\xi \mathbf{y}\tag{2.20}$$

Here the linear operator  $\mathbf{H}_\xi$  is a symmetric, positive semidefinite matrices, and  $\mathbf{H}_\xi \mathbf{H}_\xi = \mathbf{H}_\xi$  (idempotent) (Trevor Hastie, 2009). In our case, it is easily seen that  $\mathbf{S}_{\lambda, \gamma}$ ,  $\mathbf{T}_{\lambda, \gamma}$ ,  $\mathbf{U}_{\lambda, \gamma}$  and  $\mathbf{V}_{\lambda, \gamma}$  are symmetric, positive semidefinite matrices as well. Additionally, by Cholesky decomposition

$$(\mathbf{B}^\top \mathbf{B} + \gamma \mathbf{C}^\top \mathbf{C} + n \boldsymbol{\Omega}_\lambda)^{-1} = \mathbf{R} \mathbf{R}^\top,\tag{2.21}$$

it is easily to prove that  $\mathbf{T}_{\lambda, \gamma} = \mathbf{B} \mathbf{R} \mathbf{R}^\top \mathbf{C}^\top$  and  $\mathbf{U}_{\lambda, \gamma} = \mathbf{C} \mathbf{R} \mathbf{R}^\top \mathbf{B}^\top$ , then we will have  $\mathbf{T}_{\lambda, \gamma} = \mathbf{U}_{\lambda, \gamma}^\top$ . When  $\lambda = \gamma = 0$ , the matrix  $\mathbf{S}_{\lambda_0, \gamma_0} = \mathbf{B} (\mathbf{B}^\top \mathbf{B})^{-1} \mathbf{B}^\top$  is idempotent.

**Corollary 1.** *If  $f(t)$  is the V-spline on the entire interval  $[t_1, t_n]$ , for sufficient cases of  $\lambda(t)$  and  $\gamma$ ,  $f(t)$  has the following property:*

- (i) if  $\lambda(t)$  is piecewise constant and  $\gamma \neq 0$ , then  $f$  and  $f'$  are continuous,  $f''$  is piecewise linear but not continuous at knots;
- (ii) if  $\lambda(t)$  is piecewise constant and  $\gamma = 0$ , the same as above;
- (iii) if  $\lambda(t) = \lambda$  is constant on the entire interval and  $\gamma \neq 0$ , the same as above;
- (iv) if  $\lambda(t) = \lambda$  is constant on the entire interval and  $\gamma = 0$ , then  $f$ ,  $f'$  are continuous,  $f''$  is piecewise linear and continuous at knots.

The proof of Corollary 1 is in Appendix A.4.

### 2.2.3 Adjusted Penalty Term and Parameter Function

To get the reconstructed trajectory in a multi-dimensional space, one can use the V-spline to find the trajectory in each dimension separately and then combine them

together for a higher dimension, such as 2D and 3D. Typically, the data are not regularly sampled in time. Due to the property of Hermite spline, the combination of a multi-dimensional reconstruction for irregular time difference dataset will bring some issues. Image the situation that a vehicle is moving along the  $x$ -axis, but stays unchanged on its  $y$  position. By fitting  $\mathbf{x}$  and  $\mathbf{u}$ , the V-spline  $f_x(t)$  will give us the best fit which returns smallest errors to the objective function. While with the same parameter  $\lambda(t)$  and  $\gamma$ ,  $f_y(t)$  returns a cubic curve, where it should give us a straight line as we expected. Moreover, in some circumstances, with time increasing  $\mathbf{f}$  and  $\mathbf{f}'$  remain the same, or change slightly. In this situation, the Hermite spline will return wiggles in each dimension and curves in combined two dimensions.

To get a reliable reconstruction, we introduce an adjusted penalty term  $\frac{(\Delta t_i)^\alpha}{(\Delta d_i)^\beta}$ , where  $\alpha \geq 0$  and  $\beta \geq 0$ , to the penalty function  $\lambda(t)$ , in which the V-spline is penalized by its real difference of  $\Delta d_i$  and  $\Delta t_i$  for each interval  $[t_i, t_{i+1}]$ . With this term, when either  $\mathbf{u}$  for  $x$  or  $\mathbf{v}$  for  $y$  goes down or equals to 0, it will make sure that the penalty function will be large enough and returns a straight line rather than a curve on this domain. Because of the unit of the penalty term is  $m^2/t^3$ , to keep the same scale,  $\alpha$  and  $\beta$  in the adjusted penalty term are chosen as 3 and 2 respectively. From the physical point of view, the term is the reciprocal of the product of velocity and acceleration. Either velocity or acceleration goes to zero, the moving object should either stop, which returns a straight line through time on  $x$  or  $y$  axes and a dot on the higher dimension or keep moving with the same speed, which returns a linear instead of a curved path.

Thus, the final form of the penalty function is

$$\lambda(t) = \frac{(\Delta t_i)^3}{(\Delta d_i)^2} \lambda, \quad (2.22)$$

where  $t_i \leq t < t_{i+1}$ . Eventually, in the objective function, there is one parameter  $\lambda$  controlling the curvature of V-spline on different domains, and another one  $\gamma$  controlling the residuals of velocity.

## 2.3 Parameter Selection and Cross-Validation

The problem of choosing the smoothing parameter is ubiquitous in curve estimation, and there are two different philosophical approaches to this question. The first one is to regard the free choice of smoothing parameter as an advantageous feature of the procedure. The other one is to find the parameter automatically by the data (Green

and Silverman, 1993). We prefer the latter one, use data to train our model and find the best parameters. The most well-known method is cross-validation.

Assuming that mean of the random errors is zero, the true regression curve  $f(t)$  has the property that, if an observation  $y$  is taken away at a point  $t$ , the value  $f(t)$  is the best predictor of  $y$  in terms of returning a least value of  $(y - f(t))^2$ .

Now, focus on an observation  $y_i$  at point  $t_i$  as being a new observation by omitting it from the set of data, which are used to estimate  $\hat{f}$ . Denote by  $\hat{f}^{(-i)}(t, \lambda)$  the estimated function from the remaining data, where  $\lambda$  is the smoothing parameter. Then  $\hat{f}^{(-i)}(t, \lambda)$  is the minimizer of

$$\frac{1}{n} \sum_{j \neq i} (y_j - f(t_j))^2 + \lambda \int (f'')^2 dt, \quad (2.23)$$

and can be quantified by the cross-validation score function

$$CV(\lambda) = \frac{1}{n} \sum_{i=1}^n \left( y_i - \hat{f}^{(-i)}(t_i, \lambda) \right)^2.$$

The basis idea of the cross-validation is to choose the value of  $\lambda$  that minimizes  $CV(\lambda)$  (Green and Silverman, 1993).

An efficient way to calculate the cross-validation score is introduced by (Green and Silverman, 1993). Through the equation (2.20), it is known that the value of the smoothing spline  $\hat{f}$  depend linearly on the data  $y_i$ . Define the matrix  $A(\lambda)$ , which is a map vector of observed values  $y_i$  to predicted values  $\hat{f}(t_i)$ . Then we have

$$\hat{\mathbf{f}} = A(\lambda)\mathbf{y}$$

and the following lemma.

**Lemma 1.** *The cross-validation score satisfies*

$$CV(\lambda) = \frac{1}{n} \sum_{i=1}^n \left( \frac{y_i - \hat{f}(t_i)}{1 - A_{ii}(\lambda)} \right)^2$$

where  $\hat{f}$  is the spline smoother calculated from the full data set  $\{(t_i, y_i)\}$  with smoothing parameter  $\lambda$ .

For a V-spline and its MSE function, there are two parameters  $\lambda(t)$  and  $\gamma$  to be estimated for. Therefore,  $\hat{f}^{(-i)}(t, \lambda)$  is the minimizer of

$$\frac{1}{n} \sum_{j \neq i} (y_j - f(t_j))^2 + \frac{\gamma}{n} \sum_{j \neq i} (v_j - f'(t_j))^2 + \int \lambda(t) (f'')^2 dt, \quad (2.24)$$

and the cross-validation score function is

$$CV(\lambda(t), \gamma) = \frac{1}{n} \sum_{i=1}^n \left( y_i - \hat{f}^{(-i)}(t_i, \lambda(t), \gamma) \right)^2. \quad (2.25)$$

Additionally, it is known that the parameter  $\hat{\theta} = (B^\top B + \gamma C^\top C + n\Omega_\lambda)^{-1} (B^\top \mathbf{y} + \gamma C^\top \mathbf{v})$  and will give us the following form

$$\begin{aligned} \hat{\mathbf{f}} &= B\hat{\theta} = B \left( B^\top B + \gamma C^\top C + n\Omega_\lambda \right)^{-1} B^\top \mathbf{y} + B \left( B^\top B + \gamma C^\top C + n\Omega_\lambda \right)^{-1} C^\top \mathbf{v} \\ &= S\mathbf{y} + \gamma T\mathbf{v}, \end{aligned} \quad (2.26)$$

$$\begin{aligned} \hat{\mathbf{f}}' &= C\hat{\theta} = C \left( B^\top B + \gamma C^\top C + n\Omega_\lambda \right)^{-1} B^\top \mathbf{y} + C \left( B^\top B + \gamma C^\top C + n\Omega_\lambda \right)^{-1} C^\top \mathbf{v} \\ &= U\mathbf{y} + \gamma V\mathbf{v}. \end{aligned} \quad (2.27)$$

From Lemma 1, we can prove the following theorem:

**Theorem 3.** *The cross-validation score of a V-spline satisfies*

$$CV(\lambda(t), \gamma) = \frac{1}{n} \sum_{i=1}^n \left( \frac{\hat{f}(t_i) - y_i + \gamma \frac{T_{ii}}{1-\gamma V_{ii}} (\hat{f}'(t_i) - v_i)}{1 - S_{ii} - \gamma \frac{T_{ii}}{1-\gamma V_{ii}} U_{ii}} \right)^2 \quad (2.28)$$

where  $\hat{f}$  is the V-spline smoother calculated from the full data set  $\{(t_i, y_i, v_i)\}$  with smoothing parameter  $\lambda(t)$  and  $\gamma$ .

The proof of Theorem 3 follows immediately from a lemma, and gives an expression for the deleted residuals  $y_i - \hat{f}^{(-i)}(t_i)$  and  $v_i - \hat{f}'^{(-i)}(t_i)$  in terms of  $y_i - \hat{f}(t_i)$  and  $v_i - \hat{f}'(t_i)$  respectively.

**Lemma 2.** *For fixed  $\lambda(t), \gamma$  and  $i$ , denote  $\mathbf{f}^{(-i)}$  by the vector with components  $f_j^{(-i)} = \hat{f}^{(-i)}(t_j, \lambda(t), \gamma)$ ,  $\mathbf{f}'^{(-i)}$  by the vector with components  $f_j'^{(-i)} = \hat{f}'^{(-i)}(t_j, \lambda(t), \gamma)$ , and define vectors  $\mathbf{y}^*$  and  $\mathbf{v}^*$  by*

$$\begin{cases} y_j^* = y_j & j \neq i \\ y_i^* = \hat{f}^{(-i)}(t_i) & \text{otherwise} \end{cases} \quad (2.29)$$

$$\begin{cases} v_j^* = v_j & j \neq i \\ v_i^* = \hat{f}'^{(-i)}(t_i) & \text{otherwise} \end{cases} \quad (2.30)$$

Then

$$\hat{\mathbf{f}}^{(-i)} = S\mathbf{y}^* + \gamma T\mathbf{v}^* \quad (2.31)$$

$$\hat{\mathbf{f}}'^{(-i)} = U\mathbf{y}^* + \gamma V\mathbf{v}^* \quad (2.32)$$

## 2.4 Simulation Study

### 2.4.1 Numerical Examples

In this section, we examine the visual quality of the proposed method with four functions: *Blocks*, *Bumps*, *HeaviSine* and *Doppler*, which have been used in (Donoho and Johnstone, 1994, 1995; Abramovich *et al.*, 1998) because of their caricature features in imaging, spectroscopy and other scientific signal processing. However it is unfair for V-spline fitting "jump" position in *Blocks* and *Bumps* function because it fits position and velocity simultaneously and these points imply infinite first derivative in original functions, which are impossible for vehicles or individuals. In terms of this issue, we treat these functions as velocity, and use noise free points to generate accurate position data, then add noises back to them.

For calculating consideration, we use  $n = 1024$  (Nason, 2010). Because of all noises are randomly generated, for the convenience of reinitialization and repeatable comparison, we set random seed at 2016. The noises are i.i.d.zero-mean Gaussian distributed with standard deviation regarding to signal-to-noise ratio (SNR), which specifies the ratio of the standard deviation of the function to the standard deviation of the simulated errors. Explicitly, if the standard deviation of the true signal  $f$  is  $\sigma_f$ , the simulated data will be  $f + \varepsilon$ , where the simulated error  $\varepsilon \sim N(0, \sigma_f/SNR)$ .

Therefore, if the original function  $g(t)$  is treated as velocity function  $f'(t) = g(t)$ , thus by setting initial position  $y_0 = 0$ , acceleration  $a_0 = 0$  and using the following formula

$$f(t_{i+1}) = f(t_i) + (g(t_i) + g(t_{i+1})) \frac{t_{i+1} - t_i}{2} \quad (2.33)$$

for calculating position information, we can easily generate simulated data. Further, we add some i.i.d.zero-mean  $\varepsilon$  noises with SNR to them to get the measurements by

$$\begin{aligned} y_i &= f(t_i) + \varepsilon_f, \\ v_i &= g(t_i) + \varepsilon_g, \end{aligned} \quad (2.34)$$

where  $\varepsilon_f \sim N(0, \sigma_f/SNR)$  and  $\varepsilon_g \sim N(0, \sigma_g/SNR)$ . The value of SNR can be chosen 7 or 3. For wavelet transform reconstructions, we use the threshold policy of *sure* and *BayesThresh* with levels  $l = 4, \dots, 9$ , see (Donoho and Johnstone, 1995; Abramovich *et al.*, 1998). A semi-parametric regression model with spatially adaptive penalized splines (*P-spline*) is added in comparison, see (Krivobokova *et al.*, 2008; Ruppert *et al.*, 2003).

For V-spline, we have two parameters  $\lambda$  and  $\gamma$  to optimize. To evaluate the performance of the velocity term in objective function (2.5) and the adjusted penalty term in (2.22), the parameter  $\gamma$  is set as 0 in one reconstruction of V-spline, whose objective function and solution become

$$J[f]_{\gamma=0} = \frac{1}{n} \sum_{i=1}^n (f(t_i) - y_i)^2 + \sum_{i=1}^{n-1} \lambda_i \int_{t_i}^{t_{i+1}} (f'')^2 dt, \quad (2.35)$$

and

$$\hat{\theta}_{\gamma=0} = (\mathbf{B}^\top \mathbf{B} + n\Omega_\lambda)^{-1} \mathbf{B}^\top \mathbf{y} \quad (2.36)$$

and the adjusted penalty term in (2.22) was removed from another reconstruction, noted as "V-spline without APT". Figure 2.2 to 2.5 display the original (velocity), generated position, wavelet with two different threshold methods, P-spline and three kinds of V-spline fitted functions. The parameters  $\lambda$  and  $\gamma$  of a V-spline are automatically selected with the formula (2.28) by `optim` function in *R* (Nelder and Mead, 1965).

By comparing, we can see that all these methods can rebuild up the skeleton of generated trajectory. *Wavelet(sure)* method has more wiggles in interior interval than *Wavelet(BayesThresh)* does, and the latter one becomes fluctuation near boundary knots. *P-spline* gives a smoother fitting than wavelets, but the drawback is lack of specific details. V-spline without velocity loses some information, as can be seen from *Blocks* and *Bumps* where there should be a straight line. V-spline without adjusted penalty term gets over-fitting when the direction changes more frequently than normal, although it catches specific feature in *HeaviSine*. The proposed V-spline performs much better than other methods and returns the near-true trajectory reconstructions.

Figure 2.6 shows the estimated penalty values  $\lambda(t) = \frac{(\Delta t)^3}{(\Delta d)^2} \lambda$  at SNR=7. The figures in the left column illustrate the values of the penalty term at different intervals, the figures in the right column are the observations and reconstructed trajectory. Bigger black dots present larger penalty values. It can be seen that  $\lambda(t)$  adapts to the smoothness pattern of position and will be large where a long time gap may occur. The details of how this penalty function works will be explained in next subsection. Figure A.1 illustrates the reconstructions of V-spline at SNR=3.

Figure 2.7 demonstrates the estimated velocity functions. By taking the first derivative of fitted V-spline, it is simple to get the original four velocity functions. The fittings of velocity are not as smooth as that of position, because we only care about the smoothness of position rather than velocity in our cross-validation formula (2.28). However, velocity information does help us in reconstructing the trajectory.

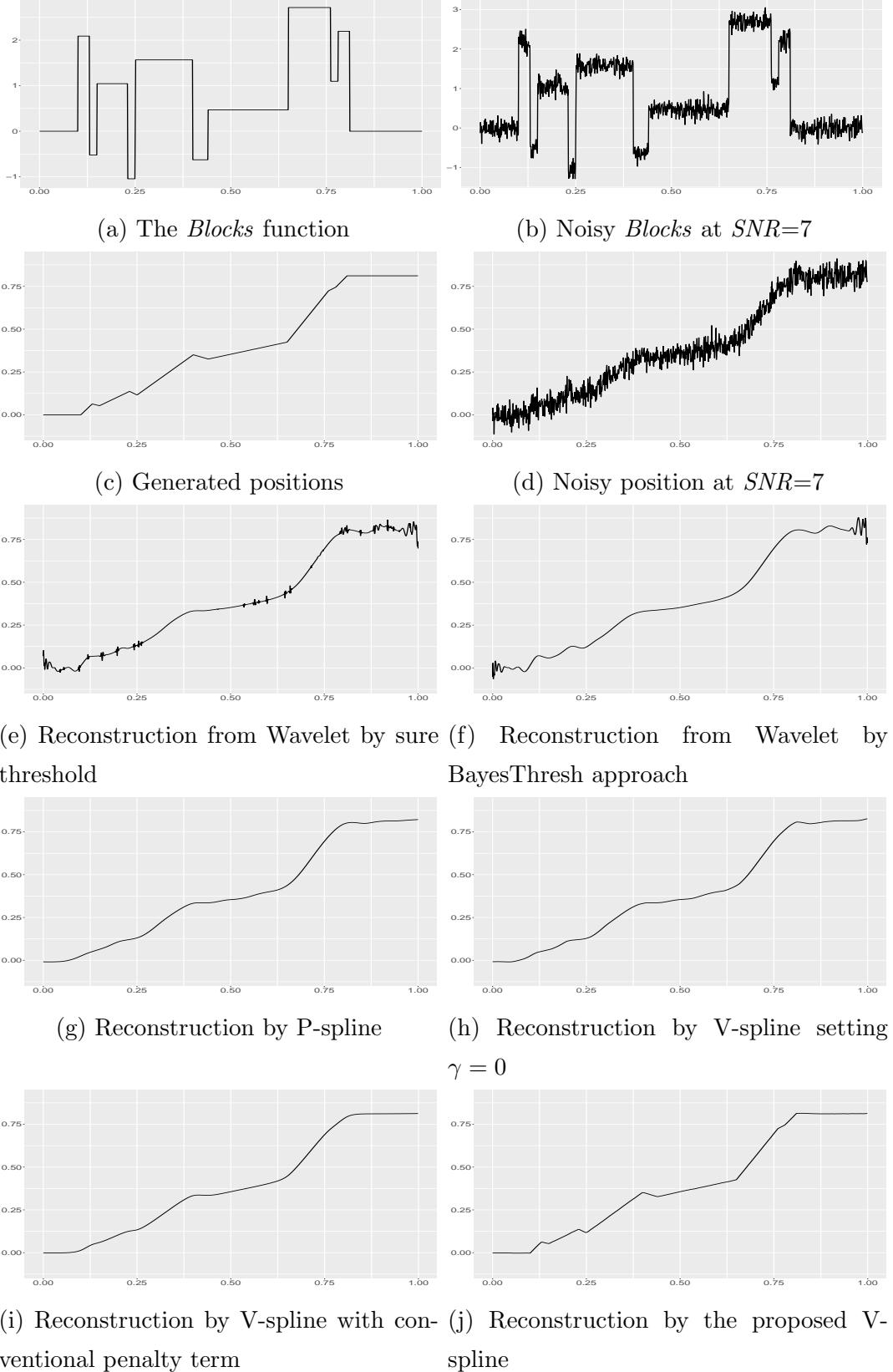


Figure 2.2: Numerical example: *Blocks*. Comparison of different reconstruction methods with simulated data.

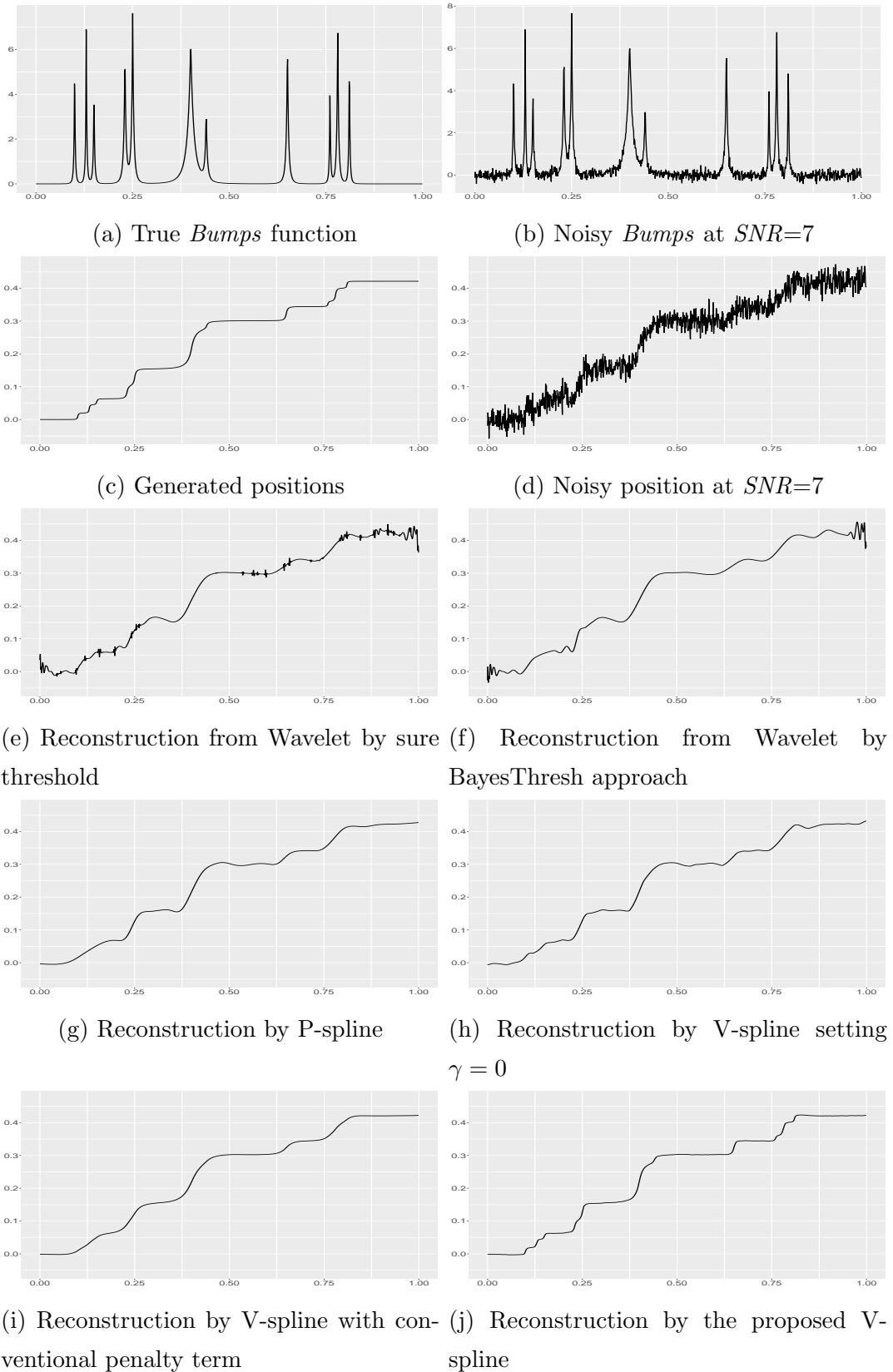


Figure 2.3: Numerical example: *Bumps*. Comparison of different reconstruction methods with simulated data.

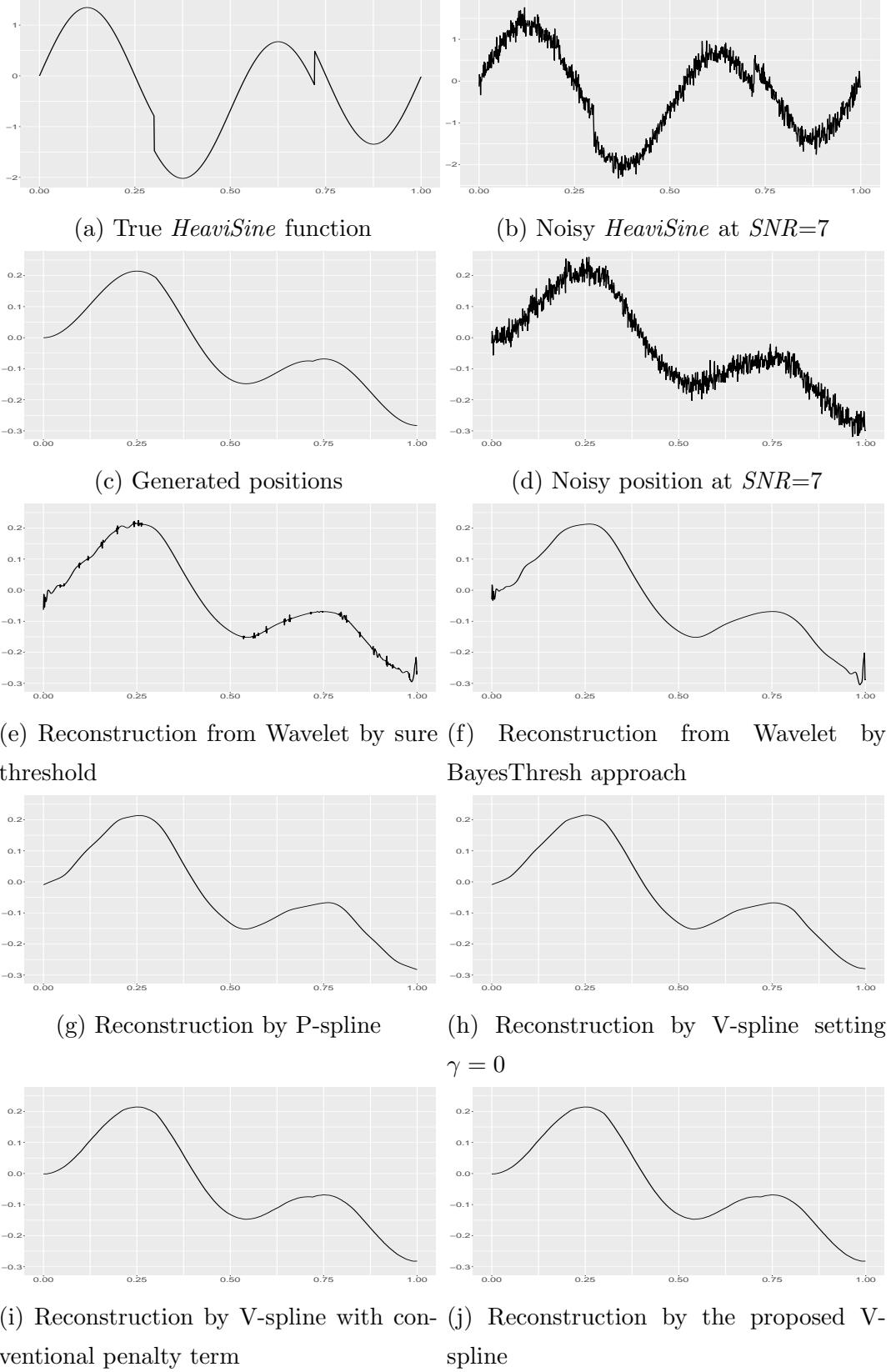


Figure 2.4: Numerical example: *HeaviSine*. Comparison of different reconstruction methods with simulated data.

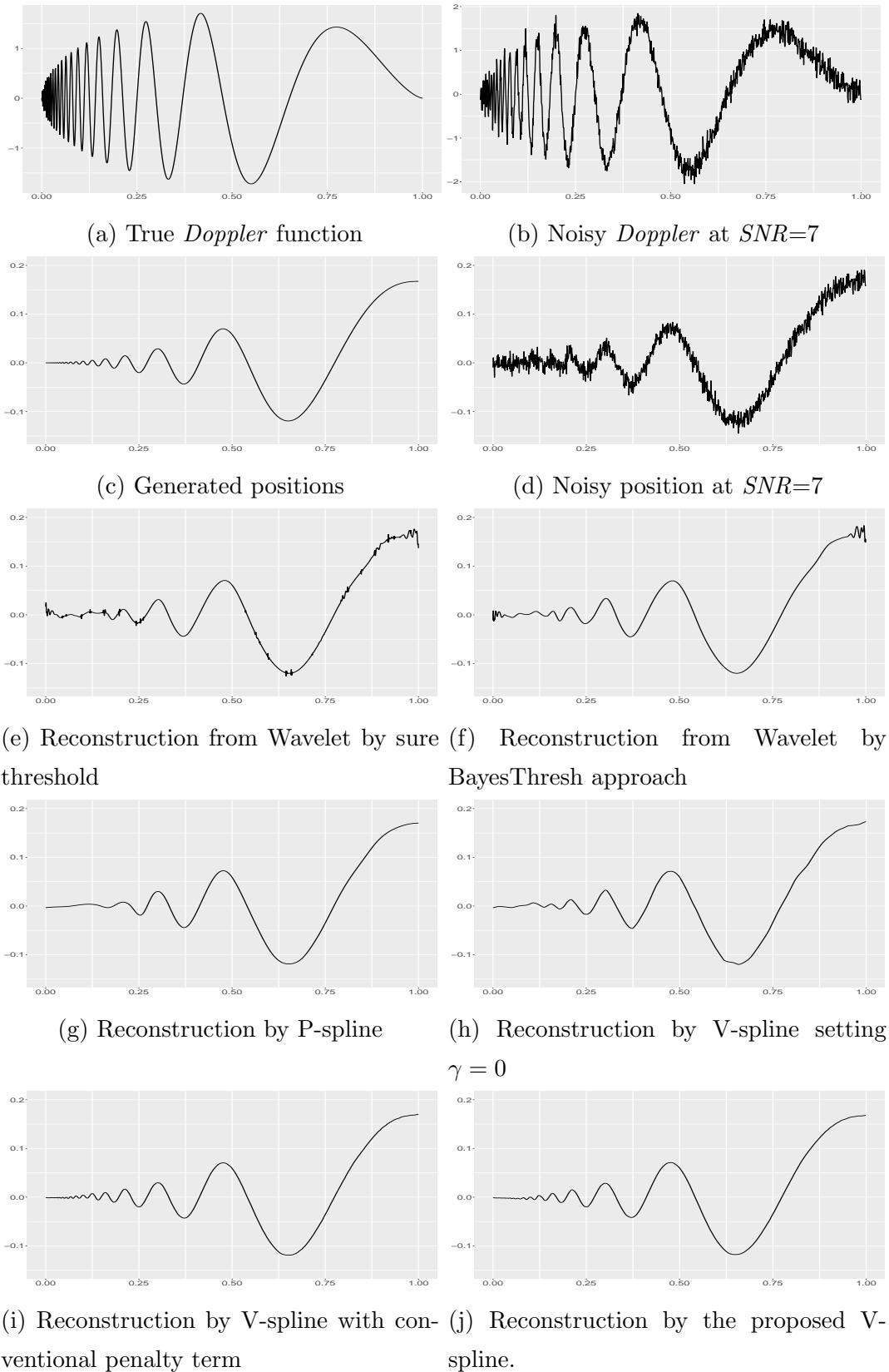
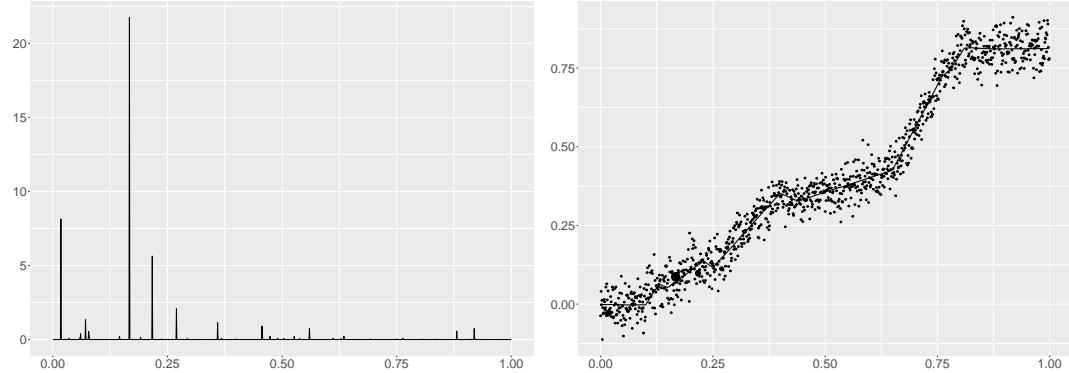
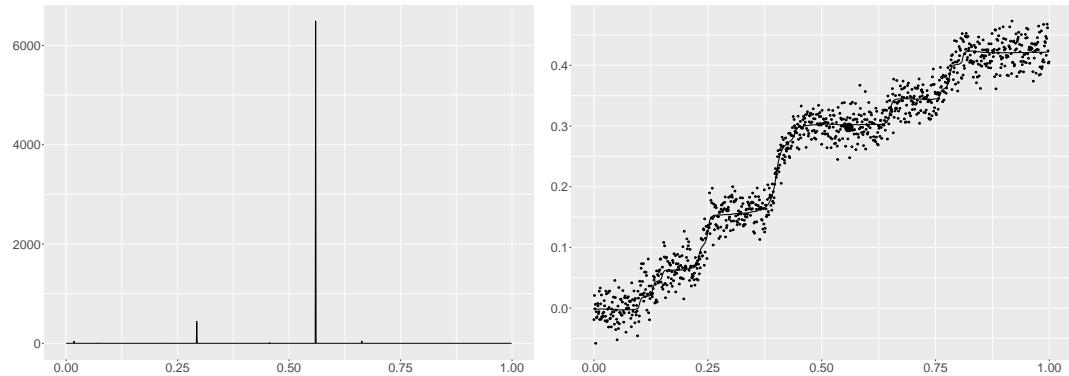


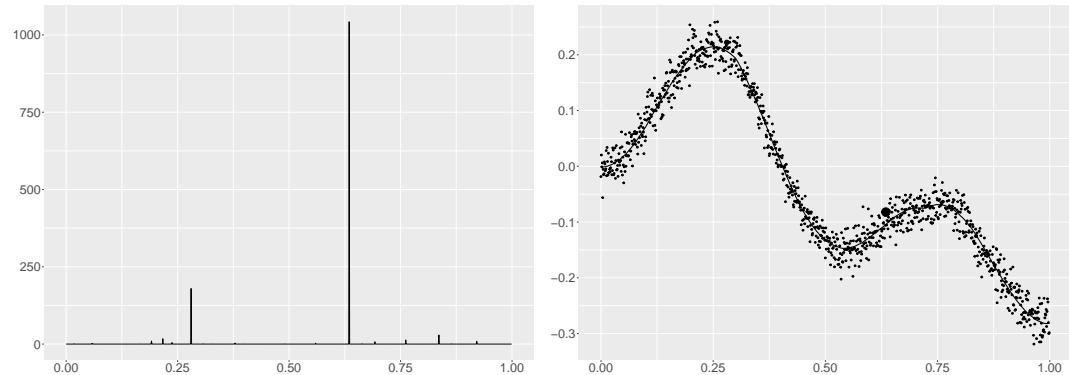
Figure 2.5: Numerical example: *Doppler*. Comparison of different reconstruction methods with simulated data



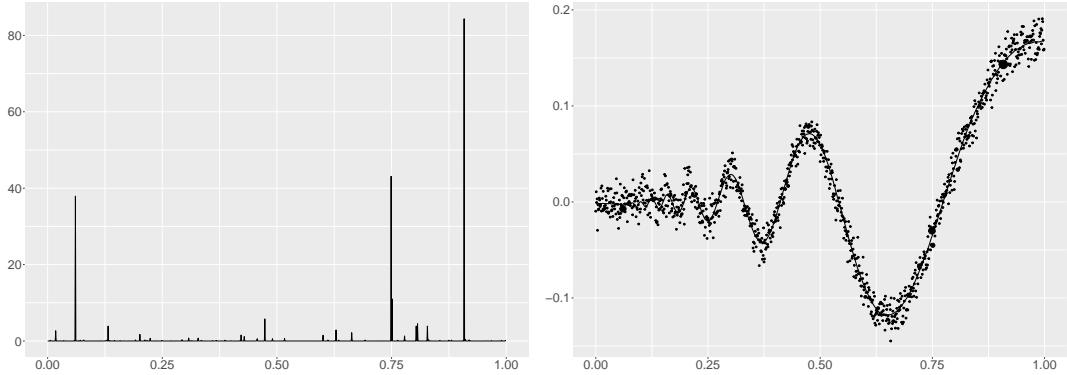
(a) Distribution of the penalty values in reconstructed *Blocks*



(b) Distribution of the penalty values in reconstructed *Bumps*



(c) Distribution of the penalty values in reconstructed *HeaviSine*



(d) Distribution of the penalty values in reconstructed *Doppler*

Figure 2.6: Distribution of the penalty values  $\lambda(t)$  in V-spline. Figures on the left side indicate the values varying in intervals. On the right side, these values are projected into reconstructions. The bigger the blacks dots present, the larger the penalty values are.

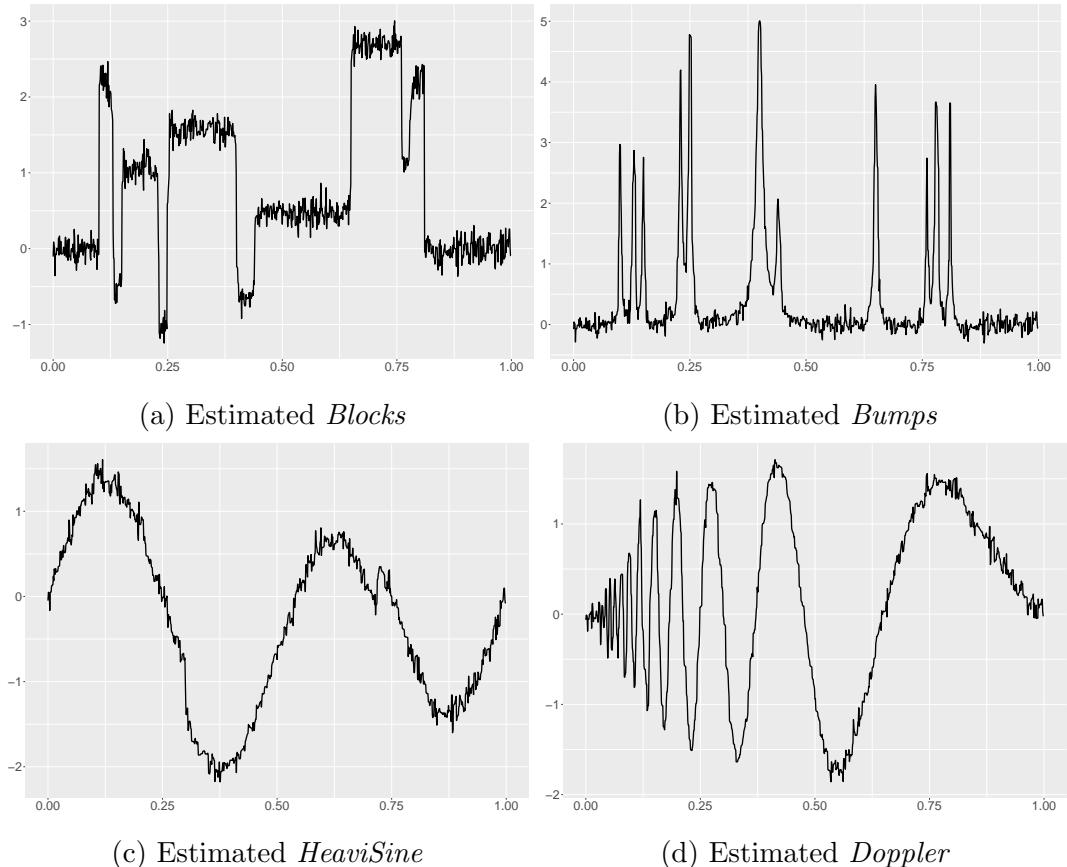


Figure 2.7: Estimated velocity functions by V-spline. The velocity is generated from the original simulation functions by equation (2.33)

Table 2.1: MSE. Mean squared errors of different methods. The numbers in bold indicate the least error among these methods under the same level. The difference is not significant.

MSE ( $10^{-4}$ )	SNR	V-spline	$VS_{\gamma=0}$	$VS_{APT=0}$	P-spline	W(sure)	W(Bayes)
<i>Blocks</i>	7	16.53	15.99	16.69	16.14	<b>15.39</b>	16.68
	3	89.79	<b>87.64</b>	89.94	88.27	98.35	90.24
<i>Bumps</i>	7	4.40	4.19	4.55	4.33	<b>4.18</b>	4.59
	3	23.93	<b>23.19</b>	24.10	23.55	26.23	23.74
<i>HeaviSine</i>	7	4.16	4.01	4.16	4.02	<b>3.79</b>	4.19
	3	22.63	<b>22.19</b>	22.65	22.02	23.53	22.07
<i>Doppler</i>	7	1.15	<b>1.07</b>	1.10	1.15	<b>1.07</b>	1.13
	3	6.27	<b>5.94</b>	6.28	6.05	6.85	6.29

### 2.4.2 Evaluation

To examine the performance of the V-spline, we conduct a evaluation by comparing the mean squared errors and true mean squared errors, which are respectively calculated with the following formulas:

$$MSE = \frac{1}{n} \sum_{i=1}^n \left( y_i - \hat{f}_{\lambda,\gamma}(t_i) \right)^2, \quad (2.37)$$

$$TMSE = \frac{1}{n} \sum_{i=1}^n \left( f(t_i) - \hat{f}_{\lambda,\gamma}(t_i) \right)^2. \quad (2.38)$$

The results are shown in table 2.1 and 2.2. All of these methods have good performances in fitting noisy data. The differences of mean squared error between these methods are not significant, as can be seen from table 2.1. The proposed method is not the best among these simulations according to MSE. However, from table 2.2, V-spline returns the smallest true mean squared errors. The difference is significant, that means the reconstruction from V-spline is closer to the true trajectory.

### 2.4.3 Residual Analysis

The simulated data is generated by equations (2.34) and the SNRs are set at 7 and 3 separately to compare the performances of different algorithms. All of the algorithms can reconstruct the true trajectory from noisy data and return acceptable MSE values, though V-spline returns the least TMSE in most of the circumstances.

Table 2.2: TMSE. True mean squared errors of different methods. The numbers in bold indicate the least error among these methods under the same level. The proposed V-spline returns the smallest TMSE among all the methods under the same level except for *Doppler* with SNR=7. The differences are significant.

TMSE ( $10^{-6}$ )	SNR	V-spline	$VS_{\gamma=0}$	$VS_{APT=0}$	P-spline	W(sure)	W(Bayes)
<i>Blocks</i>	7	<b>1.75</b>	54.25	28.68	54.76	201.02	182.12
	3	<b>16.44</b>	152.5	30.76	171.59	1138.08	712.36
<i>Bumps</i>	7	<b>1.64</b>	23.44	21.10	24.21	71.71	69.26
	3	<b>8.51</b>	77.78	37.12	77.52	330.77	238.79
<i>HeaviSine</i>	7	<b>1.53</b>	7.80	1.56	9.54	55.37	44.88
	3	<b>8.21</b>	33.56	8.49	34.26	240.72	110.49
<i>Doppler</i>	7	1.51	6.67	<b>1.08</b>	8.26	14.87	12.01
	3	<b>8.10</b>	22.14	8.25	19.95	81.48	50.33

Table 2.3 is comparing the capability of V-spline in retrieving the true SNR. The measurements are generated from  $f$  and  $g$  with predefined SNR. The V-spline reconstructs the true trajectory and retrieves the SNR value, both of which are close to the truth.

Further analysis in figures A.2 and A.3 shows that the residuals from V-splines are independent.

## 2.5 Application on Real Dataset

In this section, we apply the proposed V-spline to real dataset, which is recorded by a GPS unit mounted on a tractor. The original dataset contains the information about time marks, longitude, latitude, velocity, bearing (in degrees, heading to North) and boom status.

In a two or higher  $d$ -dimensional curve nonparametric regression, consider the general form of a length  $n$  time series data points  $\{t_1, p_1, s_1\}, \dots, \{t_n, p_n, s_n\}$ , such that  $a \leq t_1 < t_2 < \dots < t_n \leq b$ ,  $p_i$  and  $s_i$  are  $d$ -dimensional vectors contain position and velocity information at time  $i$  respectively. The positive piecewise constant function  $\lambda(t) = \lambda_i$  on each interval  $t_i \leq t < t_{i+1}$ ,  $t_0 = a$ ,  $t_{n+1} = b$ . Then the function  $f : [a, b] \mapsto \mathbb{R}^d$  with  $\gamma > 0$  is a V-spline in the  $d$ -dimensional space if it is the solution

Table 2.3: Retrieved SNR. V-spline effectively retrieves the SNR, which is calculated by  $\sigma_{\hat{f}}/\sigma_{(\hat{f}-y)}$ .

SNR	predefined value	generated $f$	V-spline $\hat{f}$
<i>Blocks</i>	7	6.9442	6.9485
	3	2.9761	2.9817
<i>Bumps</i>	7	6.9442	6.9548
	3	2.9761	2.9953
<i>HeaviSine</i>	7	6.9442	6.9207
	3	2.9761	2.9706
<i>Doppler</i>	7	6.9442	6.8757
	3	2.9761	2.9625

to the generic form of the objective function:

$$J[f] = \frac{1}{n} \sum_{i=1}^n \|f(t_i) - p_i\|_d^2 + \frac{\gamma}{n} \sum_{i=1}^n \|f'(t_i) - s_i\|_d^2 + \sum_{i=0}^n \lambda_i \int_{t_i}^{t_{i+1}} \|f''(t)\|_d^2 dt. \quad (2.39)$$

Particularly, the GPS data is recorded in a 2-dimensional form, in which scenario  $d = 2$ . Hence, in the following application, we split the 2-dimensional function  $f(x, y)$  into two sub functions  $f_x(t)$  on  $x$ -axis and  $f_y(t)$  on  $y$ -axis with respect to time  $t$ . Compared with other parameters, choosing time  $t$  to be the parameter has some advantages: (i) the expressions of all the constraints are simpler (Zhang *et al.*, 2013); (ii) it can be simply applied from 2-dimension to 3-dimension by adding an extra  $z$ -axis. Without loss of generality, a dataset in a higher dimensional space can be projected into several sub-spaces, such as  $p = \{x, y, z, \dots\}$  and  $s = \{u, v, w, \dots\}$ .

Thereafter, at first, we convert the longitude and latitude information from a 3D sphere to 2D surface by Universal Transverse Mercator coordinate system (UTM) and then project the speed  $s$  into  $u$  and  $v$  on  $x$ -axis and  $y$ -axis respectively by

$$u = s \cdot \sin\left(\omega \frac{\pi}{180}\right), \quad (2.40)$$

$$v = s \cdot \cos\left(\omega \frac{\pi}{180}\right), \quad (2.41)$$

where  $\omega$  is the bearing in degrees. Boom status is tagged as 0 if it is not operating and 1 if it is. Time marks are transformed by subtracting the first mark, in which way the time starts from 0. Time duplicated data, caused by errors, had been removed from the dataset. In the convenience of comparing with wavelet algorithm, we choose the first 512 out of 928 rows of data. The original data is plotted in figure 2.8.

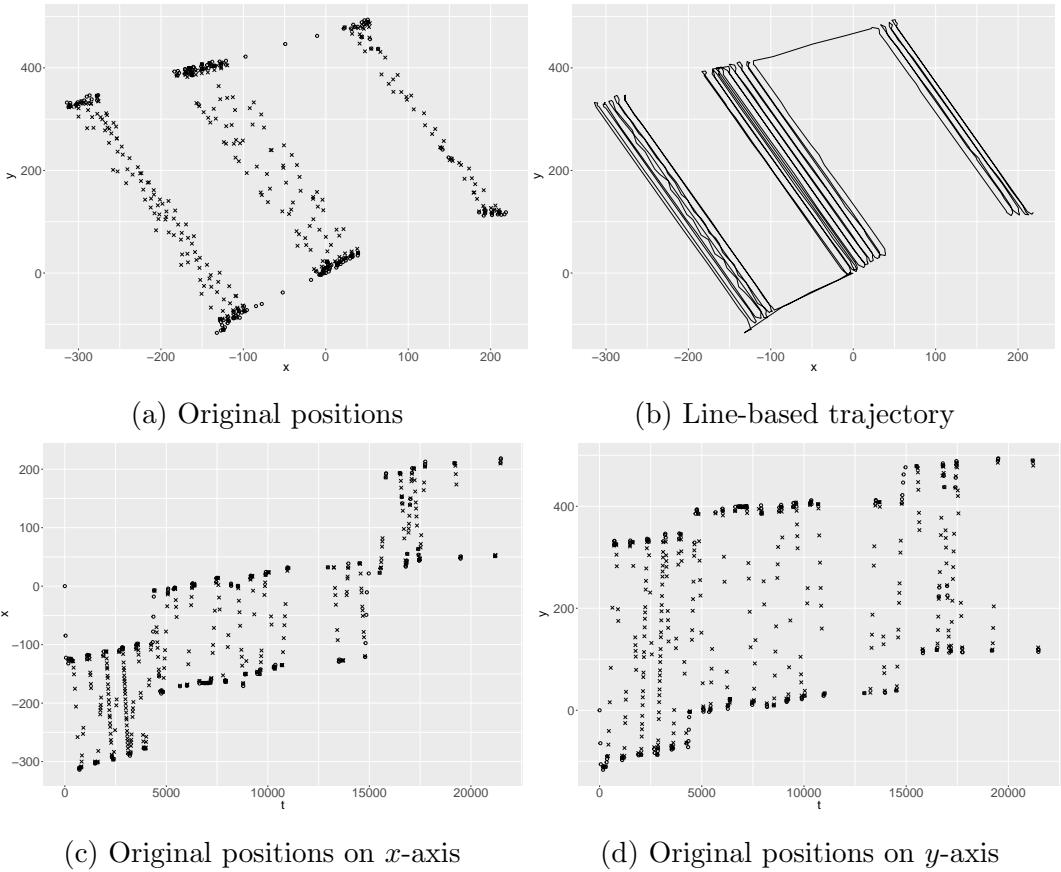


Figure 2.8: Original data points. Figure 2.8a is the original positions recorded by GPS units. Circle points mean the boom is not operating; cross points mean it is operating. Figure 2.8b is the line-based trajectory by simply connecting all points sequentially with straight lines. Figure 2.8c is the original  $x$  position. Figure 2.8d is the original  $y$  positions.

Table 2.4: Mean squared error. V-spline returns smallest errors among all these methods. P-spline was unable to reconstruct the  $y$  trajectory as the original dataset contains 0  $\Delta_y$ .

MSE	V-spline	$VS_{\gamma=0}$	$VS_{APT=0}$	P-spline	W(sure)	W(Bayes)
$x$	<b>0.2046</b>	0.2830	0.3298	2860.5480	256.0494	6.2959
$y$	<b>0.0020</b>	0.3062	0.3115	NA	1960.2220	19.3330

To fit the real data, we bring the parameter  $\lambda_d$  to our model. Then, we are now having three parameters  $\lambda_d$  and  $\lambda_u$  regarding boom status and  $\gamma$  controlling velocity residuals. The criteria of a good fitting are that it can catch more information, recognize time gaps between two points where tractor stops and return a smaller MSE.

### 2.5.1 1-Dimensional Trajectory

We treat  $x$  and  $y$  position separately and compare how the velocity information and the adjusted penalty term of equation (2.22) work in our model. All parameters in fitted V-spline are automatically selected by cross-validation by equation (2.28). Figure 2.9 and figure 2.10 compare the results of fitted methods on  $x$  and  $y$  axes. P-spline gives over-fitting on  $x$  axis reconstruction and not applicable on  $y$  axis due to errors. Wavelet(sure) misses some key points at corners when a tractor tries to turn around. V-spline without adjusted penalty term presents less fitting at time gap knots, where time marks keep increasing while position stays the same and velocity is 0. If we take the last knot  $p_k$  before and the first knot  $p_{k+1}$  after the time gap, Hermite spline basis will use  $y_k, v_k, y_{k+1}$  and  $v_{k+1}$  to build up a cubic spline, even though the velocity information is not useful. That is why we got a curve rather than a straight line. Wavelet(BayesThresh), V-spline without velocity and proposed V-spline give acceptable results.

Table 2.4 illustrates the MSE of all methods on both  $x$  and  $y$  axes. The proposed V-spline returns the least errors among all methods.

The penalty function of the proposed V-spline is

$$\lambda(t) = b \frac{(\Delta t)^3}{(\Delta d)^2} \lambda_d + (1 - b) \frac{(\Delta t)^3}{(\Delta d)^2} \lambda_u, \text{ where } \begin{cases} b = 1 & \text{if boom is operating} \\ b = 0 & \text{if boom is not operating} \end{cases} \quad (2.42)$$

To tell the differences more clearly, we take  $\lambda(t)$  in our demonstration. Figure 2.11

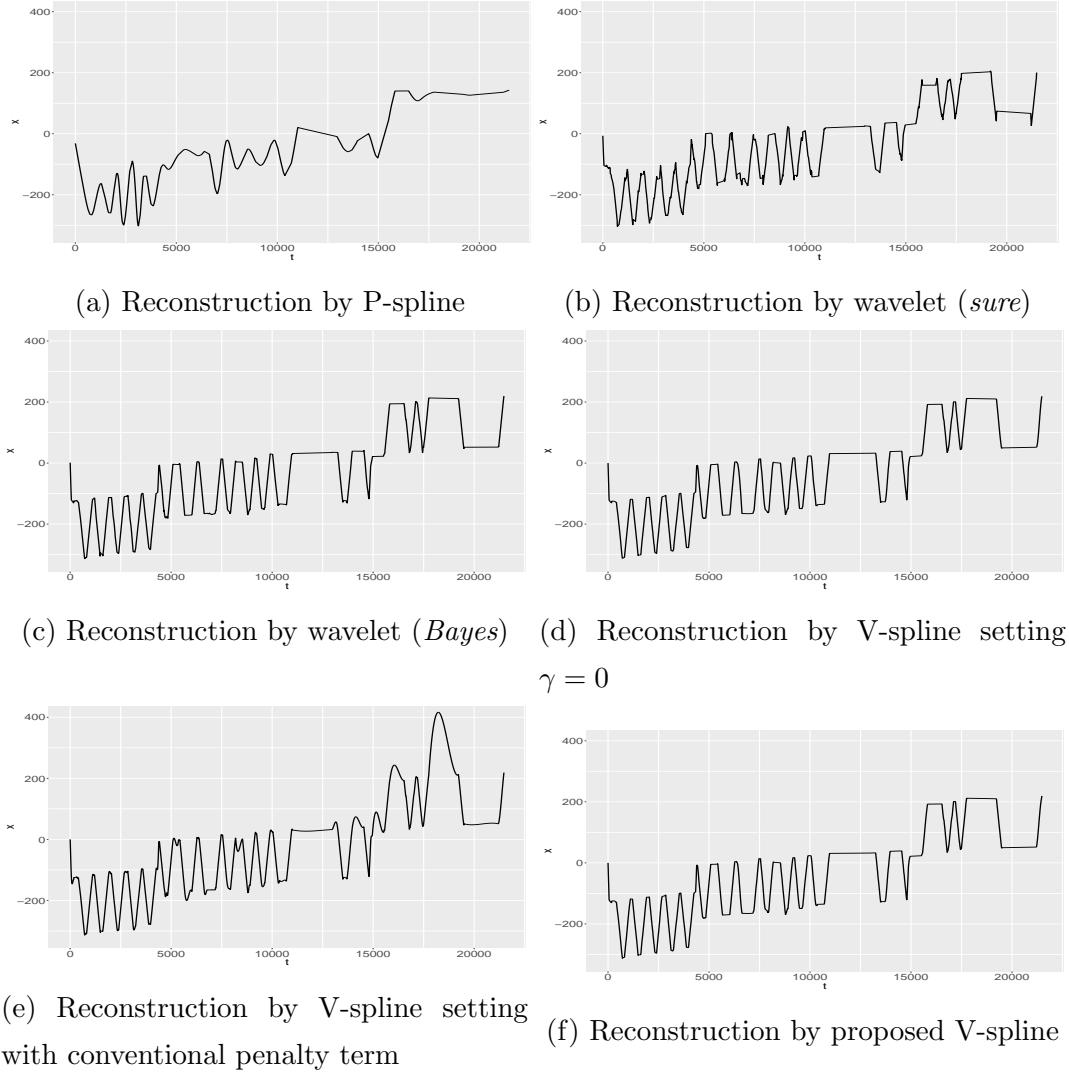


Figure 2.9: Fitted data points on  $x$  axis. Figure 2.9a Fitted by P-spline, which gives over-fitting on these points and misses some information. Figure 2.9b Fitted by wavelet (*sure*) algorithm. At some turning points, it gives over-fitting. Figure 2.9c Fitted by wavelet (*BayesThresh*) algorithm. It fits better than (*sure*) and the result is close to the proposed method. Figure 2.9d Fitted by V-spline without velocity information. The reconstruction is good to get the original trajectory. Figure 2.9e Fitted by V-spline without adjusted penalty term. It gives less fitting at boom-not-operating points because of a large time gap. Figure 2.9f Fitted by proposed method. It fits all data points in a good way.

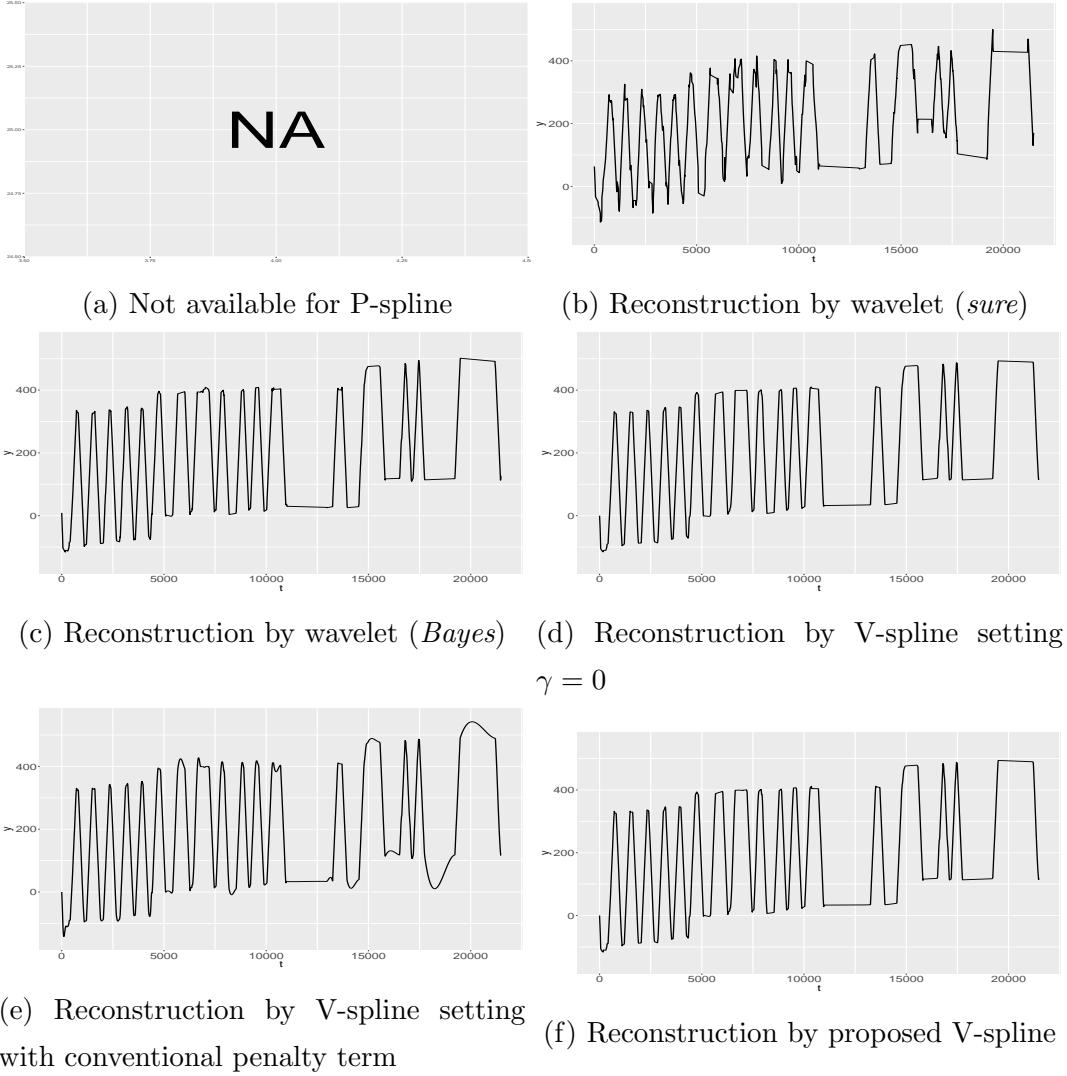
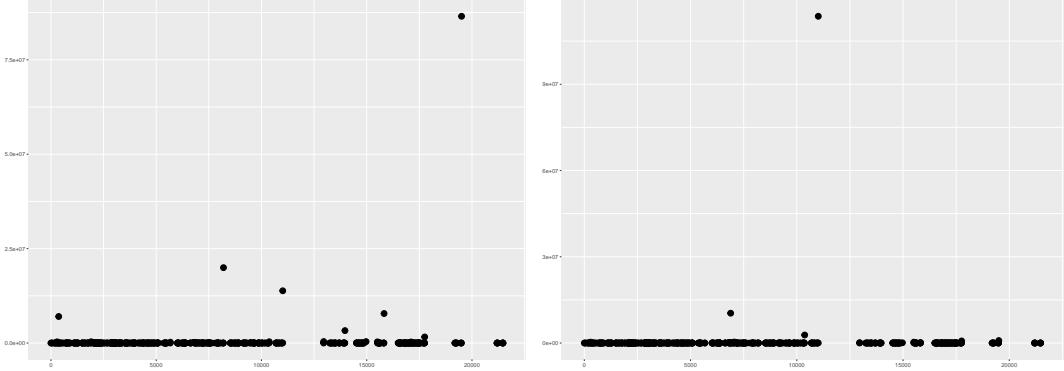
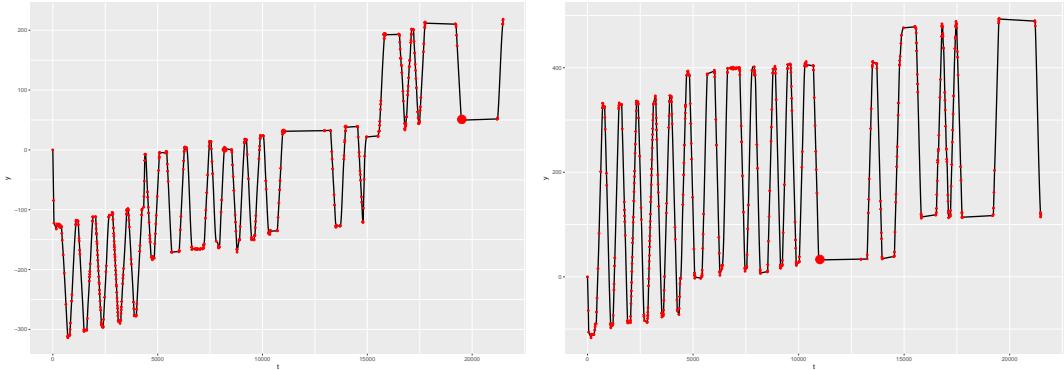


Figure 2.10: Fitted data points on  $y$  axis. Figure 2.10a Fitted P-spline is not applicable on  $y$  axis as the matrix is not invertible. Figure 2.10b Fitted by wavelet (*sure*) algorithm. At some turning points, it gives over-fitting. Figure 2.10c Fitted by wavelet (*BayesThresh*) algorithm is much better than wavelet (*sure*). Figure 2.10d Fitted by V-spline without velocity information. The reconstruction is good to get the original trajectory. Figure 2.10e Fitted by V-spline without adjusted penalty term. It gives less fitting at boom-not-operating. Figure 2.10f Fitted by proposed method. It fits all data points in a good way.



(a) Distribution of the penalty term on  $x$  and  $y$



(b) Reconstruction on  $x$  and  $y$

Figure 2.11: The penalty value  $\lambda(t)$  of the V-spline on  $x$  and  $y$  axes. Red dots are the measurements  $\mathbf{y}$ . The bigger red dots in figure 2.11b indicate larger penalty values. It can be seen that most of large penalty values occur at turnings, where the tractor likely slows down and takes breaks.

indicates that at turning points and long time gap knots, the adjusted penalty term will lead  $\lambda(t)$  to large values, which forces the spline to be a straight line between two knots. It can be seen in figure 2.11b clearly. Histogram plots of  $\lambda(t)$  show that most of the penalty values are small, which allows the V-spline to go as closer as possible to the observed points. Only a few of penalty values are large, so that V-spline gives a straight line at tricky points.

The 1-dimensional reconstruction gets the best fittings  $\hat{f}_x$  and  $\hat{f}_y$  on  $x$  and  $y$  axes separately using different penalty values, denoted as  $\lambda_{d,x}$ ,  $\lambda_{u,x}$ ,  $\lambda_{d,y}$ ,  $\lambda_{u,y}$ ,  $\gamma_x$  and  $\gamma_y$ . The final reconstruction is the combination of  $\hat{f}_x$  and  $\hat{f}_y$ . It is shown in figure 2.12.

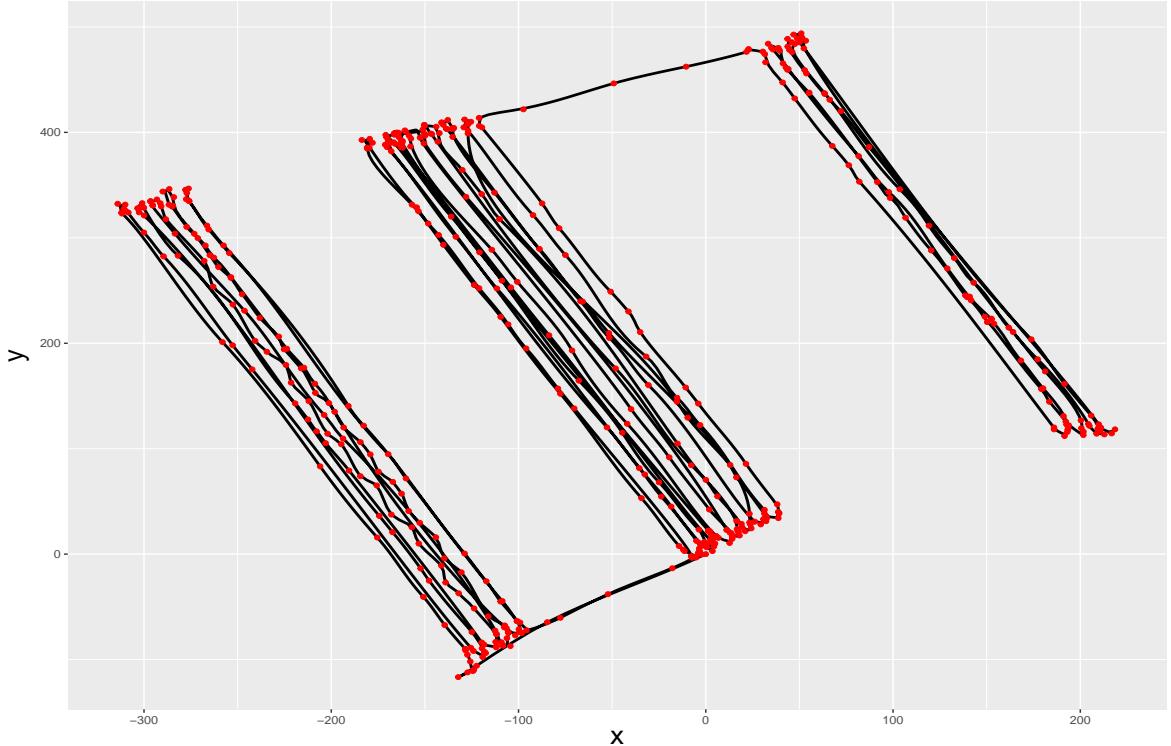


Figure 2.12: Combined reconstruction on  $x$  and  $y$ . Red dots are the measurements  $\mathbf{y}$ . The bigger size it is, the larger penalty value it indicates.

### 2.5.2 2-Dimensional Trajectory

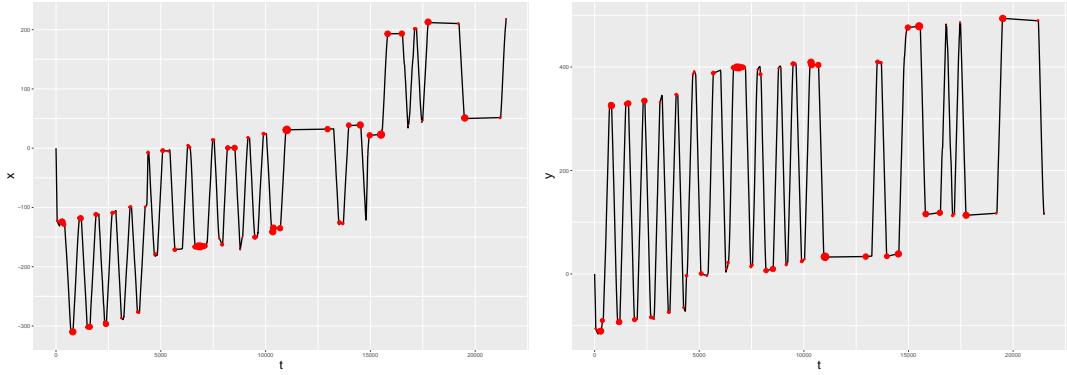
In a 2-dimensional trajectory reconstruction, different from combined 1-dimensional reconstruction, we are using the same parameters  $\lambda_d$ ,  $\lambda_u$  and  $\gamma$  for both  $x$  and  $y$  axes. The overall best parameters return the least cross-validation score on all axes. Explicitly, it is calculated by the following formula

$$CV = CV_x + CV_y. \quad (2.43)$$

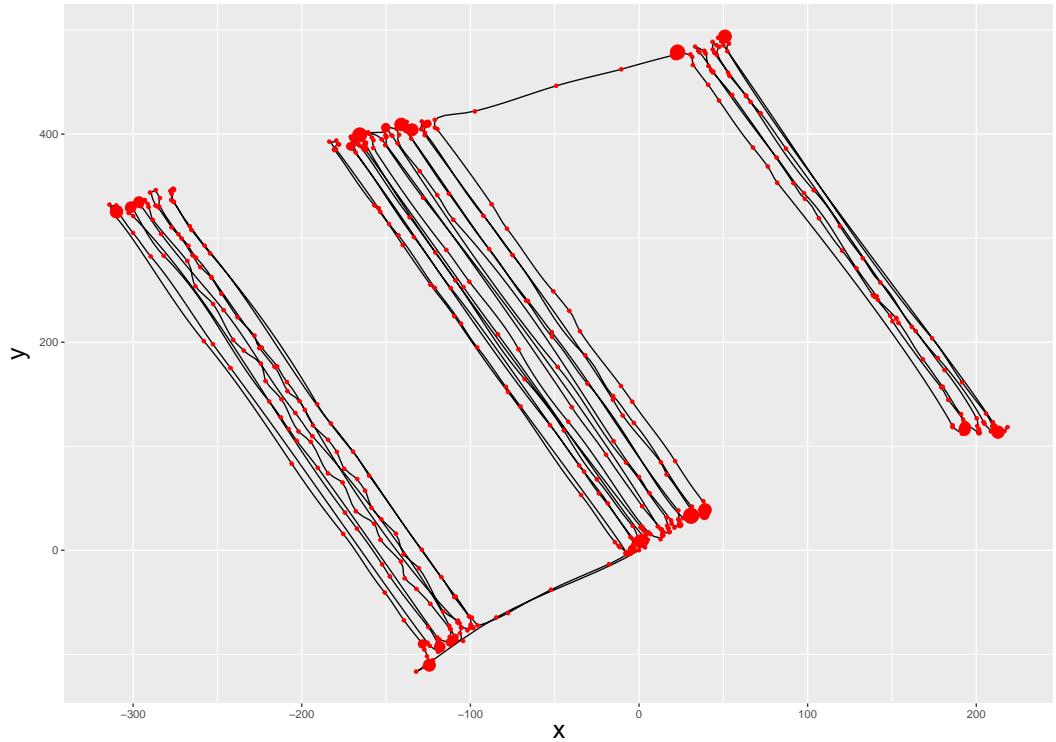
In the adjusted penalty term,  $\Delta d$  is the Euclidean distance  $\Delta_d(p_1, p_2) = \sqrt{(\Delta x)^2 + (\Delta y)^2}$  between two positions on the 2D surface. Similarly in 1-dimensional reconstruction, the velocity information keeps trajectory in the right direction and the penalty term makes sure that the crazy curve will disappear between long-time-gap points. Figure 2.13 demonstrates the complete 2D reconstruction of the whole dataset.

The penalty function  $\lambda(t)$  of a 2-dimensional reconstruction is shared by  $x$  and  $y$  axes and presented in figure 2.14. The complete penalty term is

$$n\theta_x^\top \Omega_{\lambda_d, \lambda_u} \theta_x + n\theta_y^\top \Omega_{\lambda_d, \lambda_u} \theta_y.$$



(a) 2-dimensional reconstruction on separate  $x$  and  $y$



(b) 2-dimensional reconstruction

Figure 2.13: 2-dimensional reconstruction. Larger dots indicate bigger values of penalty function  $\lambda(t)$ .

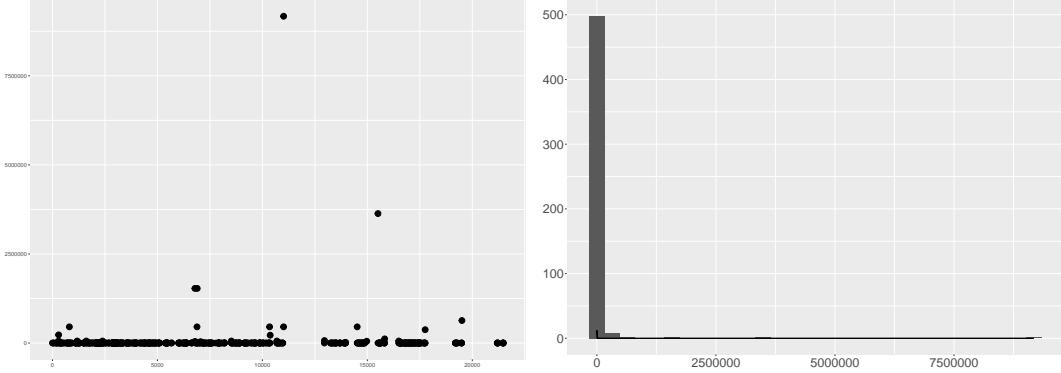


Figure 2.14: Penalty value of  $\lambda(t)$  in 2-dimensional reconstruction.

Similarly, most of the large penalty values appear at long-time-gap knots and turning points. A histogram plot of penalty function shows that most of the values are small and only a couple of them are large.

The following figure 2.15 is a complete reconstruction from the whole observed dataset  $\{x, u, y, v\}$ . The overall reconstruction gives a smoothing path that goes through each measurement and avoids curvatures at turning points.

## 2.6 Conclusion and Discussion

In this chapter, a V-spline model is proposed to solve the objective function, which is consisting of both position and velocity information. The adjusted penalty function adapts to complicated curvatures. In a high  $d$ -dimensional space, V-spline can be projected into sub-spaces with respect to  $t$  and combined each solution together as a final. This method performs better when we know  $p$  and  $s$  information than other methods.

Additionally, the reconstruction of a V-spline contains  $4 \times (n - 1)$  parameters if we have  $n$  knots. By adding  $2 \times (n - 2)$  constraints, the original function, and its first derivative are continuous at each interior knots, the degrees of freedom will be  $4 \times (n - 1) - 2 \times (n - 2) = 2n$ . Because there are  $n$  position and  $n$  velocity points, thus we do not need to specify more parameters or add more constraints to the model.

Even though the mean squared errors of a V-spline is not the least comparing with other methods, the true mean squared errors are the least of among all the methods. That means the reconstruction is closer to the true path.

In parameter selection, the cross-validation only focuses on the errors of  $f$  ignoring that in  $f'$ . So the reconstruction of  $f'$  is not as smooth as that of  $f$ , which does not

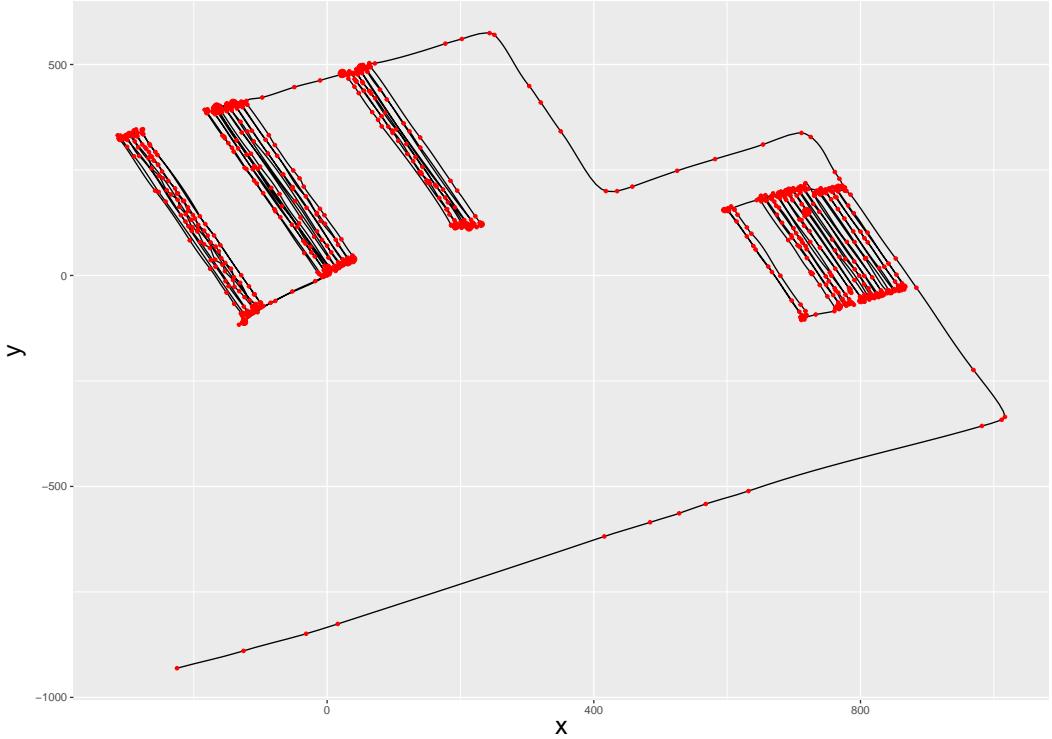


Figure 2.15: 2-dimensional reconstruction. Larger dots indicate bigger values of penalty function  $\lambda(t)$ .

affect trajectory reconstruction. A drawback of V-spline is that the computing time in finding local minimal CV score is higher than using B-spline. If there is an efficient way to compute matrix inverse, the calculation speed will be much faster. So in the simulation and application studies, we try to optimize our coding to make it run as faster as possible.

Another potential application of V-spline is to vessel monitoring system. The system is a fisheries surveillance that allows environmental and fisheries regulatory organization to track and monitor the activities of fishing vessels. The system calculates the position of the moving object and sends a data report to shore-side users. This information includes time, latitude and longitude positions. However, due to weak signals, the tracking system may lose useful information. The V-spline can help to reconstruct the whole trajectory for a fishery vessel and to analyze its behavior. For example, a larger penalty value indicates stops on the sea inferring that the vessel is casting nets; a smaller penalty value indicates the vessel is moving normally.

After all, there is a wide range of applications for V-spline in real life. A future work is to implement V-spline on-line for instant estimation and to make it run faster.



# Chapter 3

## V-Spline as Bayes Estimate

### 3.1 Introduction

A Hilbert space is a real or complex inner product space with respect to the distance function induced by the inner product (Dieudonné, 2013). Particularly, the Hilbert space  $\mathcal{L}_2[0, 1]$  is a set of square integrable functions  $f(t) : [0, 1] \mapsto \mathbb{R}$ , where all functions satisfy

$$\mathcal{L}_2[0, 1] = \left\{ f : \int_0^1 f^2 dt < \infty \right\}$$

with an inner product  $\langle f, g \rangle = \int_0^1 fg dt$ .

Consider a regression problem with observations  $y_i = f(t_i) + \varepsilon_i$ ,  $i = 1, \dots, n$ , consisting i.i.d. Gaussian noises  $\varepsilon_i \sim N(0, \sigma^2)$  in the space  $\mathcal{C}^{(m)}[0, 1] = \{f : f^{(m)} \in L_2[0, 1]\}$ . The classic nonparametric or semi-parametric regression is a function that minimizes the following penalized least square functional

$$\frac{1}{n} \sum_{i=1}^n (y_i - f(t_i))^2 + \lambda \int_0^1 (f^{(m)})^2 dt, \quad (3.1)$$

where the first term is the lack of fit of  $f$  to the data. In the second term, generally,  $\lambda$  is a fixed smoothing parameter controlling the trade-off between over-fitting and bias (Trevor Hastie, 2009). The minimizer  $f_\lambda$  of the above equation resides in an  $n$ -dimensional space and the computation in multivariate settings is generally of the order  $O(n^3)$  (Kim and Gu, 2004). It is shown that a piecewise polynomial smoothing spline of degree  $2m - 1$  is well known to provide an aesthetically satisfying method for estimating  $f$  if  $\mathbf{y}$  cannot be interpolated exactly by some polynomial of degree less than  $m$  (Schoenberg, 1964). For instance, when  $m = 2$ , a piecewise cubic smoothing

spline provides a powerful tool to estimate the above nonparametric function, in which the penalty term is  $\int f''^2 dt$  (Hastie and Tibshirani, 1990).

Further, Wahba (1978) shows that a Bayesian version of this problem is to take a Gaussian process prior  $f(t_i) = a_0 + a_1 t_i + \dots + a_{m-1} t_i^{m-1} + x_i$  on  $f$  with  $x_i = X(t_i)$  being a zero-mean Gaussian process whose  $m$ th derivative is scaled white noise,  $i = 1, \dots, n$  (Speckman and Sun, 2003). The extended Bayes estimates  $f_\lambda$  with a "partially diffuse" prior is as exactly the same as spline solution. Some works have been done on discovering the relationship between nonparametric regression and Bayesian estimation. Heckman and Woodroffe (1991) show that if  $f$  the regression function  $E(y | f)$  has unknown prior distribution  $\mathbf{f} = (f(t_1), \dots, f(t_n))^\top$  lying in a known class of  $\Omega$ , then the maximum is taken over all priors in  $\Omega$  and the minimum is taken over linear estimator of  $\mathbf{f}$ . Branson *et al.* (2017) propose a Gaussian process regression method that acts as a Bayesian analog to local linear regression for sharp regression discontinuity designs. It is no doubt that one of the attractive features of the Bayesian approach is that, in principle, one can solve virtually any statistical decision or inference problem. Particularly, one can provide an accuracy assessment for  $\hat{f} = E(f | \mathbf{y})$  using posterior probability regions (Cox, 1993).

Based on the correspondence, Craven and Wahba (1978) propose an generalized cross-validation estimate for the minimizer  $f_\lambda$ . The estimate  $\hat{\lambda}$  is the minimizer of the function where the trace of matrix  $A(\lambda)$  in (2.3) is incorporated. It is also able to establish an optimal convergence property for their estimator when the number of observations in a fixed interval tends to infinity (Wecker and Ansley, 1983). A high efficient algorithm to optimize generalized cross-validation and generalized maximum likelihood scores with multiple smoothing parameters via the Newton method was proposed by Gu and Wahba (1991). This algorithm can also be applied to the maximum likelihood and the restricted maximum likelihood estimation. The behavior of the optimal regularization parameter in the method of regularization was investigated by Wahba and Wang (1990).

In this chapter, it is proved that the V-spline can be estimated by a Bayesian approach in second-derivative-piecewise-continuous reproducing kernel Hilbert space. The GCV is used to find the optimal parameters for V-spline.

## 3.2 Polynomial Smoothing Splines on $[0, 1]$ as Bayes Estimates

A polynomial smoothing spline of degree  $2m - 1$  is a piecewise polynomial of the same degree on each intervals  $[t_i, t_{i+1}]$ ,  $i = 1, \dots, n - 1$ , and the first  $2m - 2$  derivatives are continuous at joint knots. For instance, when  $m = 2$ , a piecewise cubic smoothing spline is a special case of the polynomial smoothing spline providing a powerful tool to estimate the above nonparametric function (3.1) in the space  $\mathcal{C}^{(2)}[0, 1]$ , where the penalty term is  $\int f''^2 dt$  (Hastie and Tibshirani, 1990; Wang, 1998). If a general space  $\mathcal{C}^{(m)}[0, 1]$  is equipped with an appropriate inner product, it can be made a reproducing kernel Hilbert space.

### 3.2.1 Polynomial Smoothing Spline

A spline is a numeric function that is piecewise-defined by polynomial functions, and which possesses a high degree of smoothness at the places where the polynomial pieces connect (known as knots) (Judd, 1998; Chen, 2009). Suppose we are given observed data  $(t_1, y_1), (t_2, y_2), \dots, (t_n, y_n)$  in the interval  $[0, 1]$ , satisfying  $0 \leq t_1 < t_2 < \dots < t_n \leq 1$ , a piecewise polynomial function  $f(t)$  can be obtained by dividing the interval into contiguous intervals  $(t_1, t_2), \dots, (t_{n-1}, t_n)$  and represented by a separate polynomial on each interval. For any continuous  $f \in \mathcal{C}^{(m)}[0, 1]$ , it can be represented in a linear combination of basis functions  $h_m(t)$  as  $f(t) = \sum_{m=1}^M \beta_m h_m(t)$ , where  $\beta_m$  are coefficients (Ellis *et al.*, 2009). It is just like every vector in a vector space can be represented as a linear combination of basis vectors.

A smoothing polynomial spline is uniquely the smoothest function that achieves a given degree of fidelity to a particular data set (Whittaker, 1922). In deed, the minimizer of function (3.1) is the curve estimate  $\hat{f}(t)$  over all spline functions  $f(t)$  with  $m - 1$  continuous derivatives fitting observed data in the space  $\mathcal{C}^{(m)}[0, 1]$ . In fact, Kimeldorf and Wahba (1971, 1970) prove that the minimizer  $f_\lambda$  of function (3.1) has the following form

$$f(t) = \sum_{\nu=1}^m d_\nu \phi_\nu(t) + \sum_{i=1}^n c_i R_1(t, t_i). \quad (3.2)$$

where  $\{\phi_\nu(t)\}$  is a set of basis functions of space  $\mathcal{H}_0$  and  $R(\cdot, \cdot)$  is the reproducing kernel in  $\mathcal{H}_1$ .

Additionally, the coefficients  $c_i$  and  $d_\nu$  might be changed when different  $\phi_\nu$  and  $R_1$  are used, but the function estimate remains the same regardless of the choices of  $\phi_\nu$

and  $R_1$  (Gu, 2013).

### 3.2.2 Reproducing Kernel Hilbert Space on $[0, 1]$

For any  $f \in \mathcal{C}^{(m)}[0, 1]$ , its standard Taylor expansion is

$$f(t) = \sum_{\nu=0}^{m-1} \frac{t^\nu}{\nu!} f^{(\nu)}(0) + \int_0^1 \frac{(t-u)_+^{m-1}}{(m-1)!} f^{(m)}(t) dt, \quad (3.3)$$

where  $(\cdot)_+ = \max(0, \cdot)$ . With an inner product

$$\langle f, g \rangle = \sum_{\nu=0}^{m-1} f^{(\nu)}(0)g^{(\nu)}(0) + \int_0^1 f^{(m)}g^{(m)} dt, \quad (3.4)$$

the representer is

$$R_s(t) = \sum_{\nu=0}^{m-1} \frac{s^\nu}{\nu!} \frac{t^\nu}{\nu!} + \int_0^1 \frac{(s-u)_+^{m-1}}{(m-1)!} \frac{(t-u)_+^{m-1}}{(m-1)!} du \triangleq R_0(s, t) + R_1(s, t). \quad (3.5)$$

It is easily to prove that  $R(s, t)$  is non-negative and is reproducing kernel, by which  $\langle R(s, t), f(t) \rangle = \langle R_s(t), f(t) \rangle = f(s)$ . Additionally,  $R_s^{(\nu)}(0) = s^\nu / \nu!$  for  $\nu = 0, \dots, m-1$ .

Before moving on to further steps, we are now introducing the following two theorems.

**Theorem 4.** (Aronszajn, 1950) Suppose  $R$  is a symmetric, positive definite kernel on a set  $X$ . Then, there is a unique Hilbert space of functions on  $X$  for which  $R$  is a reproducing kernel.

**Theorem 5.** (Gu, 2013) If the reproducing kernel  $R$  of a space  $\mathcal{H}$  on domain  $X$  can be decomposed into  $R = R_0 + R_1$ , where  $R_0$  and  $R_1$  are both non-negative definite,  $R_0(x, \cdot), R_1(x, \cdot) \in \mathcal{H}$ , for  $\forall x \in X$ , and  $\langle R_0(x, \cdot), R_1(y, \cdot) \rangle = 0$ , for  $\forall x, y \in X$ , then the spaces  $\mathcal{H}_0$  and  $\mathcal{H}_1$  corresponding respectively to  $R_0$  and  $R_1$  form a tensor sum decomposition of  $\mathcal{H}$ . Conversely, if  $R_0$  and  $R_1$  are both nonnegative definite and  $\mathcal{H}_0 \cap \mathcal{H}_1 = \{0\}$ , then  $\mathcal{H} = \mathcal{H}_0 \oplus \mathcal{H}_1$  has a reproducing kernel  $R = R_0 + R_1$ .

According to Theorem 4, the Hilbert space associated with  $R(\cdot)$  can be constructed as containing all finite linear combinations of the form  $\sum a_i R(t_i, \cdot)$ , and their limits under the norm induced by the inner product  $\langle R(s, \cdot), R(t, \cdot) \rangle = R(s, t)$ . As for Theorem 5, it is easy to verify that  $R_0$  corresponds to the space of polynomials  $\mathcal{H}_0 = \{f : f^{(m)} = 0\}$  with an inner product  $\langle f, g \rangle_0 = \sum_{\nu=0}^{m-1} f^{(\nu)}(0)g^{(\nu)}(0)$  and  $R_1$  corresponds to the orthogonal complement of  $\mathcal{H}_0$ , that is  $\mathcal{H}_1 = \left\{ f : f^{(\nu)}(0) = 0, \nu = 0, \dots, m-1, \int_0^1 (f^{(m)})^2 dt < \infty \right\}$  with an inner product  $\langle f, g \rangle_1 = \int_0^1 f^{(m)}g^{(m)} dt$ .

### 3.2.3 Polynomial Smoothing Splines as Bayes Estimates

Because it is possible to interpret the smoothing spline regression estimator as a Bayes estimate when the mean function  $r(\cdot)$  is given an improper prior distribution (Wahba, 1990; Berlinet and Thomas-Agnan, 2011). Therefore, we will find that the posterior mean of  $f = f_0 + f_1$  on  $[0, 1]$  with proper priors is the polynomial smoothing spline of (3.1).

In fact, it can be found that for each  $f = f_0 + f_1$  on  $[0, 1]$ , with  $f_0$  and  $f_1$  having independent Gaussian priors with zero means and covariances, it satisfies:

$$\begin{aligned} \mathbb{E}[f_0(s)f_0(t)] &= \tau^2 R_0(s, t) = \tau^2 \sum_{\nu=0}^{m-1} \frac{s^\nu}{\nu!} \frac{t^\nu}{\nu!}, \\ \mathbb{E}[f_1(s)f_1(t)] &= bR_1(s, t) = b \int_0^1 \frac{(s-u)_+^{m-1}}{(m-1)!} \frac{(t-u)_+^{m-1}}{(m-1)!}, \end{aligned}$$

where  $R_0$  and  $R_1$  are from (3.5). Because of the observations are normally distributed as  $y_i \sim N(f(t_i), \sigma^2)$ , then the joint distribution for  $\mathbf{y} = \{y_1, \dots, y_n\}$  and  $f(t)$  is normal with zero mean and the following covariance matrix

$$\text{Cov}(f, \mathbf{y}) = \begin{bmatrix} bQ + \tau SS^\top + \sigma^2 I & b\xi + \tau^2 S\phi \\ b\xi^\top + \tau^2 \phi^\top S^\top & bR_1(t, t) + \tau^2 \phi^\top \phi \end{bmatrix},$$

where  $\{Q_{i,j}\}_{n \times n} = R_1(t_i, t_j)$ ,  $\{S_{i,\nu}\}_{n \times m} = t_i^{\nu-1}/(\nu-1)!$ ,  $\{\xi_{i,1}\}_{n \times 1} = R_1(t_i, t)$  and  $\{\phi_{\nu,1}\}_{m \times 1} = t^{\nu-1}/(\nu-1)!$ . Consequently, the posterior is

$$\begin{aligned} \mathbb{E}[f(t) | \mathbf{y}] &= (b\xi^\top + \tau\phi^\top s^\top) (bQ + \tau^2 SS^\top + \sigma^2 I)^{-1} \mathbf{y} \\ &= \xi^\top (Q + \rho SS^\top + n\lambda I)^{-1} \mathbf{y} + \phi^\top \rho S^\top (Q + \rho SS^\top + n\lambda I)^{-1} \mathbf{y}, \end{aligned} \quad (3.6)$$

where  $\rho = \tau^2/b$  and  $n\lambda = \sigma^2/b$ . Furthermore, by denoting  $M = Q + n\lambda I$ , Gu (2013) gives that, when  $\rho \rightarrow \infty$ , the posterior mean is in the form  $\mathbb{E}[f(t) | y_{1:n}] = \xi^\top \mathbf{c} + \phi^\top \mathbf{d}$  with coefficients

$$\mathbf{c} = \left( M^{-1} - M^{-1} S (S^\top M^{-1} S)^{-1} S^\top M^{-1} \right) \mathbf{y}, \quad (3.7)$$

$$\mathbf{d} = (S^\top M^{-1} S)^{-1} S^\top M^{-1} \mathbf{y}. \quad (3.8)$$

**Theorem 6.** (Gu, 2013) *The polynomial smoothing spline of (3.1) is the posterior mean of  $f = f_0 + f_1$ , where  $f_0$  diffuses in span  $\{t^{\nu-1}, \nu = 1, \dots, m\}$  and  $f_1$  has a Gaussian process prior with mean zero and a covariance function*

$$bR_1(s, t) = b \int_0^1 \frac{(s-u)_+^{m-1}}{(m-1)!} \frac{(t-u)_+^{m-1}}{(m-1)!},$$

for  $b = \sigma^2/n\lambda$ .

### 3.2.4 Gaussian Process Regression

Gaussian processes are the extension of multivariate Gaussian to infinite-sized collections of real value variables, any finite number of which have a joint Gaussian distribution (Rasmussen and Williams, 2006). Gaussian process regression is a probability distribution over functions. It is fully defined by its mean  $m(t)$  and covariance  $K(s, t)$  function as

$$m(t) = \text{E}[f(t)] \\ K(s, t) = \text{E}[(f(s) - m(s))(f(t) - m(t))],$$

where  $s$  and  $t$  are two variables. A function  $f$  distributed as such is denoted in form of

$$f \sim GP(m(t), K(s, t)).$$

Usually the mean function is assumed to be zero everywhere.

Given a set of input variables  $\mathbf{t} = \{t_1, \dots, t_n\}$  for function  $f(t)$  and the output  $\mathbf{y} = f(\mathbf{t}) + \varepsilon$  with i.i.d. Gaussian noise  $\varepsilon$  of variance  $\sigma_n^2$ , we can use the above definition to predict the value of the function  $f_* = f(t_*)$  at a particular input  $t_*$ . As the noisy observations becoming

$$\text{Cov}(y_p, y_q) = K(t_p, t_q) + \sigma_n^2 \delta_{pq}$$

where  $\delta_{pq}$  is a Kronecker delta which is one if and only if  $p = q$  and zero otherwise, the joint distribution of the observed outputs  $\mathbf{y}$  and the estimated output  $f_*$  according to prior is

$$\begin{bmatrix} \mathbf{y} \\ f_* \end{bmatrix} \sim N \left( 0, \begin{bmatrix} K(\mathbf{t}, \mathbf{t}) + \sigma_n^2 I & K(\mathbf{t}, t_*) \\ K(t_*, \mathbf{t}) & K(t_*, t_*) \end{bmatrix} \right). \quad (3.9)$$

The posterior distribution over the predicted value is obtained by conditioning on the observed data

$$f_* | \mathbf{y}, \mathbf{t}, t_* \sim N(\bar{f}_*, \text{Cov}(f_*))$$

where

$$\bar{f}_* = \text{E}(f_* | \mathbf{y}, \mathbf{t}, t_*) = K(t_*, \mathbf{t}) (K(\mathbf{t}, \mathbf{t}) + \sigma_n^2 I)^{-1} \mathbf{y}, \quad (3.10)$$

$$\text{Cov}(f_*) = K(t_*, t_*) - K(t_*, \mathbf{t}) (K(\mathbf{t}, \mathbf{t}) + \sigma_n^2 I)^{-1} K(\mathbf{t}, t_*). \quad (3.11)$$

Therefore, it can be seen that the Bayesian estimation of a smoothing spline is a special format of Gaussian process regression with diffuse prior and the covariance matrix  $R(s, t)$ .

### 3.3 V-Spline as Bayes Estimate

Recall the definition of V-spline introduced in Section 2.2. It is the solution to the objective function (2.5), where an extra term for  $f'(t) - v$  and an extra parameter  $\gamma$  are incorporated. The penalty parameter  $\lambda(t)$  is a function varying on different domains. If  $\lambda(t) = \lambda$  is constant and  $\gamma = 0$ , the V-spline degenerate to a conventional cubic smoothing spline consisting of a set of given basis functions.

However, the Bayes estimate for a polynomial smoothing spline requires fixed interval on  $[0, 1]$  and the penalty parameter is constant. For the first constraint, without loss of generality, an arbitrary interval  $[a, b]$  can be transformed to  $[0, 1]$ . For the second constraint, it is assumed that  $\lambda(t)$  stays the same constant in each subinterval of  $[0, 1]$  and name the solution "trivial V-spline". In this section, we are still using the name "V-spline" for sake of simplicity.

In the following, we are going to prove that this kind of trivial V-spline is corresponding to Bayes estimate in a particular reproducing kernel Hilbert space.

#### 3.3.1 Reproducing Kernel Hilbert Space $\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$

The space  $\mathcal{C}^{(m)}[0, 1] = \{f : f^{(m)} \in L_2[0, 1]\}$  is a set of functions  $f$  whose  $m$ th derivatives are square integrable on the domain  $[0, 1]$ . For a V-spline, it only requires  $m = 2$ . In fact, its second derivative is piecewise linear but is not necessarily continuous at joint knots. Besides, only if  $\lambda(t)$  is constant and  $\gamma = 0$ , the second derivative is piecewise linear and continuous at joint knots. Here we are introducing the space

$$\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1] = \{f : f'' \in L_2[0, 1], f, f' \text{ are continuous and } f'' \text{ is piecewise linear}\},$$

in which the second derivative of any function  $f$  is not necessarily continuous.

Given a sequence of paired data  $\{(t_1, y_1, v_1), \dots, (t_n, y_n, v_n)\}$ , the the minimizer of

$$\frac{1}{n} \sum_{i=1}^n (y_i - f(t_i))^2 + \frac{\gamma}{n} \sum_{i=1}^n (v_i - f'(t_i))^2 + \lambda \int_0^1 f''^2 dt \quad (3.12)$$

in the space  $\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$  is a V-spline. Equipped with an appropriate inner product

$$\langle f, g \rangle = f(0)g(0) + f'(0)g'(0) + \int_0^1 f''g'' dx, \quad (3.13)$$

the space  $\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$  is made a reproducing kernel Hilbert space. In fact, the representer  $R_s(\cdot)$  is

$$R_s(t) = 1 + st + \int_0^1 (s - u)_+ (t - u)_+ du. \quad (3.14)$$

It can be seen that  $R_s(0) = 1$ ,  $R'_s(0) = s$ , and  $R''_s(t) = (s - t)_+$ . The two terms of the reproducing kernel  $R(s, t) = R_s(t) \triangleq R_0(s, t) + R_1(s, t)$ , where

$$R_0(s, t) = 1 + st$$

$$R_1(s, t) = \int_0^1 (s - u)_+ (t - u)_+ du$$

are both non-negative definite themselves.

According to Theorem 5,  $R_0$  can correspond the space of polynomials  $\mathcal{H}_0 = \{f : f'' = 0\}$  with an inner product  $\langle f, g \rangle_0 = f(0)g(0) + f'(0)g'(0)$ , and  $R_1$  corresponds the orthogonal complement of  $\mathcal{H}_0$

$$\mathcal{H}_1 = \left\{ f : f(0) = 0, f'(0) = 0, \int_0^1 f''^2 dt < \infty \right\}$$

with inner product  $\langle f, g \rangle_1 = \int_0^1 f'' g'' dt$ . Thus,  $\mathcal{H}_0$  and  $\mathcal{H}_1$  are two subspaces of the  $\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$ , and the reproducing kernel is  $R_s(\cdot) = R_0(s, \cdot) + R_1(s, \cdot)$ .

Define a new notation  $\dot{R}(s, t) = \frac{\partial R}{\partial s}(s, t) = \frac{\partial R_0}{\partial s}(s, t) + \frac{\partial R_1}{\partial s}(s, t) = t + \int_0^s (t - u)_+ du$ . Obviously  $\dot{R}_s(t) \in \mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$ . Additionally, we have  $\dot{R}_s(0) = 0$ ,  $\dot{R}'_s(0) = \frac{\partial \dot{R}_s}{\partial t}(0) = 1$ , and  $\dot{R}''_s(t) = \begin{cases} 0 & s \leq t \\ 1 & s > t \end{cases}$ . Then, for any  $f \in \mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$ , we have

$$\langle \dot{R}_s, f \rangle = \dot{R}_s(0)f(0) + \dot{R}'_s(0)f'(0) + \int_0^1 \dot{R}''_s f'' du = f'(0) + \int_0^t f'' du = f'(t).$$

It can be seen that the first term  $\dot{R}_0 = t \in \mathcal{H}_0$ , and the space spanned by the second term  $\dot{R}_1 = \int_0^s (t - u)_+ du$ , denoted as  $\dot{\mathcal{H}}$ , is a subspace of  $\mathcal{H}_1$ , and  $\dot{\mathcal{H}} \ominus \mathcal{H}_1 \neq \emptyset$ . Given the sample points  $t_j$ ,  $j = 1, \dots, n$ , in equation (3.12) and noting that the space

$$\mathcal{A} = \left\{ f : f = \sum_{j=1}^n \alpha_j R_1(t_j, \cdot) + \sum_{j=1}^n \beta_j \dot{R}_1(t_j, \cdot) \right\}$$

is a closed linear subspace of  $\mathcal{H}_1$ . Then, we have a new space  $\mathcal{H}_* = \dot{\mathcal{H}} \cup \mathcal{A}$ . Thus, the two new sub spaces in  $\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$  are  $\mathcal{H}_0$  and  $\mathcal{H}_*$ .

For any  $f \in \mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$ , it can be written as

$$f(t) = d_1 + d_2 t + \sum_{j=1}^n c_j R_1(t_j, t) + \sum_{j=1}^n b_j \dot{R}_1(t_j, \cdot) + \rho(t) \quad (3.15)$$

where  $\mathbf{d}, \mathbf{c}$  and  $\mathbf{b}$  are coefficients, and  $\rho(t) \in \mathcal{H}_1 \ominus \mathcal{H}_*$ . Thus, by substituting to the

equation (3.12), it can be written as

$$\begin{aligned} & \frac{1}{n} \sum_{i=1}^n \left( y_i - d_1 - d_2 t - \sum_{j=1}^n c_j R_1(t_j, t_i) - \sum_{j=1}^n b_j \dot{R}_1(t_j, t_i) - \rho(t_i) \right)^2 \\ & \frac{\gamma}{n} \sum_{i=1}^n \left( v_i - d_2 - \sum_{j=1}^n c_j R'_1(t_j, t_i) - \sum_{j=1}^n b_j \dot{R}'_1(t_j, t_i) - \rho'(t_i) \right)^2 \\ & + \lambda \int_0^1 \left( \sum_{j=1}^n c_j R''_1(t_j, t) + \sum_{j=1}^n b_j \dot{R}''_1(t_j, t) + \rho''(t) \right)^2 dt \end{aligned} \quad (3.16)$$

Because of orthogonality,  $\rho(t_i) = (R_1(t_i, \cdot), \rho) = 0$ ,  $\rho'(t_i) = (\dot{R}_1(t_i, \cdot), \rho') = 0$ ,  $i = 1, \dots, n$ . By denoting that

$$\begin{aligned} S &= \{S_{ij}\}_{n \times 2} = \begin{bmatrix} 1 & t_i \end{bmatrix}, \quad Q = \{Q_{ij}\}_{n \times n} = R_1(t_j, t_i), \quad P = \{P_{ij}\}_{n \times n} = \dot{R}_1(t_j, t_i), \\ S' &= \{S'_{ij}\}_{n \times 2} = \begin{bmatrix} 0 & 1 \end{bmatrix}, \quad Q' = \{Q'_{ij}\}_{n \times n} = R'_1(t_j, t_i), \quad P' = \{P'_{ij}\}_{n \times n} = \dot{R}'_1(t_j, t_i). \end{aligned}$$

and noting that  $\int_0^1 R''_1(t_i, t) R''_1(t_j, t) dt = R_1(t_i, t_j)$ ,  $\int_0^1 R''_1(t_i, t) \dot{R}''_1(t_j, t) dt = \int_0^v (t_i - t) dt = \dot{R}_1(t_j, t_i)$ , and  $\int_0^1 \dot{R}''_1(t_i, t) \dot{R}''_1(t_j, t) dt = \int_0^v 1 dt = \dot{R}'_1(t_i, t_j)$ , where  $v = \min(t_i, t_j)$ , the above equation (3.16) can be written as

$$\begin{aligned} & (\mathbf{y} - S\mathbf{d} - Q\mathbf{c} - P\mathbf{b})^\top (\mathbf{y} - S\mathbf{d} - Q\mathbf{c} - P\mathbf{b}) + \\ & \gamma (\mathbf{v} - S'\mathbf{d} - Q'\mathbf{c} - P'\mathbf{b})^\top (\mathbf{v} - S'\mathbf{d} - Q'\mathbf{c} - P'\mathbf{b}) \\ & + n\lambda (\mathbf{c}^\top Q\mathbf{c} + 2\mathbf{c}^\top P\mathbf{b} + \mathbf{b}^\top P'\mathbf{b}) + n\lambda(\rho, \rho). \end{aligned} \quad (3.17)$$

Note that  $\rho$  only appears in the third term and is minimized at  $\rho = 0$ . Hence, a V-spline resides in the space  $\mathcal{H}_0 \oplus \mathcal{H}_*$  of finite dimension. Thus, the solution to (3.12) is computed via the minimization of the first three terms in (3.17) with respect to  $\mathbf{d}$ ,  $\mathbf{c}$  and  $\mathbf{b}$ .

### 3.3.2 Posterior of Bayes Estimates

Consider the independent observations  $y_i \sim N(f(t_i), \sigma^2)$  and  $v_i \sim N(f'(t_i), \frac{\sigma^2}{\gamma})$ , with a prior  $f \sim N(0, \beta I)$ , it is easy to see that the posterior mean of  $f$  is the minimizer of

$$\frac{1}{\sigma^2} \sum_{i=1}^n (y_i - f(t_i))^2 + \frac{\gamma}{\sigma^2} \sum_{i=1}^n (v_i - f'(t_i))^2 + \frac{1}{\beta} \sum_{t \in [0,1]} f^2(t),$$

and defines a shrinkage estimate being shrunk toward zero.

According to equation (3.15), let  $f(t) \in \mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$ , has the prior distribution

$$f(t) = (d_1 + d_2 t) + \sum_{i=1}^n c_i R_1(t_i, t) + \sum_{i=1}^n b_i \dot{R}_1(t_i, t), \quad (3.18)$$

where  $d \sim N(0, \tau^2 I)$ . The covariance functions for  $y, v$  and  $f, f'$  are

$$\begin{aligned} E[f(s)f(t)] &= \tau^2 R_0(s, t) + \beta R_1(s, t) & E[f(s)f'(t)] &= \tau^2 R'_0(s, t) + \beta R'_1(s, t) \\ E[f'(s)f(t)] &= \tau^2 \dot{R}_0(s, t) + \beta \dot{R}_1(s, t) & E[f'(s)f'(t)] &= \tau^2 \dot{R}'_0(s, t) + \beta \dot{R}'_1(s, t) \\ E[y_i, y_j] &= \tau^2 R_0(s_i, s_j) + \beta R_1(s_i, s_j) + \sigma^2 \delta_{ij} & E[v_i, v_j] &= \tau^2 \dot{R}'_0(s_i, s_j) + \beta \dot{R}'_1(s_i, s_j) + \frac{\sigma^2}{\gamma} \delta_{ij} \\ E[v_i, y_j] &= \tau^2 \dot{R}_0(s_i, s_j) + \beta \dot{R}_1(s_i, s_j) & E[y_i, v_j] &= \tau^2 R'_0(s_i, s_j) + \beta R'_1(s_i, s_j) \\ E[y_i, f(s)] &= \tau^2 R_0(s_i, s) + \beta R_1(s_i, s) & E[y_i, f'(s)] &= \tau^2 R'_0(s_i, s) + \beta R'_1(s_i, s) \\ E[v_i, f(s)] &= \tau^2 \dot{R}_0(s_i, s) + \beta \dot{R}_1(s_i, s) & E[v_i, f'(s)] &= \tau^2 \dot{R}'_0(s_i, s) + \beta \dot{R}'_1(s_i, s) \end{aligned}$$

where  $R(s, t)$  is taken from (3.14) and  $\beta$  is fixed.

Observing  $y_i \sim N(f(t_i), \sigma^2)$  and  $v_i \sim N(f(t_i), \frac{\sigma^2}{\gamma})$ ,  $i = 1, \dots, n$ , the joint distribution of  $\mathbf{y}, \mathbf{v}$  and  $f(t)$  is normal with mean zero and a covariance matrix can be found.

The posterior mean of  $f(t)$  is seen to be

$$\begin{aligned} E(f | \mathbf{y}, \mathbf{v}) &= \begin{bmatrix} \text{Cov}(\mathbf{y}, f) & \text{Cov}(f, \mathbf{v}) \end{bmatrix} \begin{bmatrix} \text{Var}(\mathbf{y}) & \text{Cov}(\mathbf{y}, \mathbf{v}) \\ \text{Cov}(\mathbf{v}, \mathbf{y}) & \text{Var}(\mathbf{v}) \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} \\ &= \begin{bmatrix} \tau^2 \phi^\top S^\top + \beta \xi^\top & \tau^2 \phi^\top S'^\top + \beta \psi^\top \end{bmatrix} \begin{bmatrix} \tau^2 S S^\top + \beta Q + \sigma^2 I & \tau^2 S S'^\top + \beta P \\ \tau^2 S' S^\top + \beta Q' & \tau^2 S' S'^\top + \beta P' + \frac{\sigma^2}{\gamma} I \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} \\ &= \begin{bmatrix} \rho \phi^\top S^\top + \xi^\top & \rho \phi^\top S'^\top + \psi^\top \end{bmatrix} \begin{bmatrix} \rho S S^\top + Q + n\lambda I & \rho S S'^\top + P \\ \rho S' S^\top + Q' & \rho S' S'^\top + P' + \frac{n\lambda}{\gamma} I \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} \\ &= \left( \phi^\top \rho \begin{bmatrix} S \\ S' \end{bmatrix}^\top + \begin{bmatrix} \xi^\top & \psi^\top \end{bmatrix} \right) \left( \rho \begin{bmatrix} S \\ S' \end{bmatrix}^\top \begin{bmatrix} S \\ S' \end{bmatrix} + \begin{bmatrix} Q + n\lambda I & P \\ Q' & P' + \frac{n\lambda}{\gamma} I \end{bmatrix} \right)^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} \\ &\triangleq \phi^\top \rho T^\top (\rho T^\top T + M)^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} + \begin{bmatrix} \xi^\top & \psi^\top \end{bmatrix} (\rho T^\top T + M)^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} \end{aligned} \quad (3.19)$$

where  $\phi$  is  $2 \times 1$  matrix with entry 1 and  $t$ ,  $\xi$  is  $n \times 1$  matrix with  $i$ th entry  $R(t_i, t)$ ,  $T^\top = [S^\top \quad S'^\top]$  and  $\psi$  is  $n \times 1$  matrix with  $i$ th entry  $\dot{R}(t_i, t)$ ,  $\rho = \tau^2/\beta$  and  $n\lambda = \sigma^2/\beta$ .

**Lemma 3.** Suppose  $M$  is symmetric and nonsingular and  $T$  is of full column rank.

$$\lim_{\rho \rightarrow \infty} (\rho T T^\top + M)^{-1} = M^{-1} - M^{-1} T (T^\top M^{-1} T)^{-1} T^\top M^{-1},$$

$$\lim_{\rho \rightarrow \infty} \rho T^\top (\rho T T^\top + M)^{-1} = (T^\top M^{-1} T)^{-1} T^\top M^{-1}.$$

Setting  $\rho \rightarrow \infty$  in equation (3.19) and applying Lemma 3, the posterior mean  $E(f(t) | \mathbf{y}, \mathbf{v})$  is  $\hat{f} = \phi^\top \mathbf{d} + \xi^\top \mathbf{c} + \psi^\top \mathbf{b}$ , with the coefficients given by

$$\begin{aligned}\mathbf{d} &= (T^\top M^{-1} T)^{-1} T^\top M^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix}, \\ \begin{bmatrix} \mathbf{c} \\ \mathbf{b} \end{bmatrix} &= \left( M^{-1} - M^{-1} T (T^\top M^{-1} T)^{-1} T^\top M^{-1} \right) \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix},\end{aligned}$$

$$\text{where } T = \begin{bmatrix} S \\ S' \end{bmatrix} \text{ and } M = \begin{bmatrix} Q + n\lambda I & P \\ Q' & P' + \frac{n\lambda}{\gamma} I \end{bmatrix}.$$

It is easy to verify that  $\mathbf{d}, \mathbf{c}, \mathbf{b}$  are the solutions to

$$\begin{cases} S^\top (S\mathbf{d} + Q\mathbf{c} + P\mathbf{b} - \mathbf{y}) + \gamma S'^\top (S'\mathbf{b} + P^\top \mathbf{c} + S'^\top P'\mathbf{b} - \mathbf{v}) = 0, \\ Q(S\mathbf{d} + (Q + n\lambda I)\mathbf{c} + P\mathbf{b} - \mathbf{y}) + P(\gamma S'\mathbf{b} + \gamma P^\top \mathbf{c} + (\gamma P' + n\lambda I)\mathbf{b} - \gamma \mathbf{v}) = 0, \\ P^\top (S\mathbf{d} + (Q + n\lambda I)\mathbf{c} + P\mathbf{b} - \mathbf{y}) + P'(\gamma S'\mathbf{b} + P^\top \mathbf{c} + (\gamma P' + n\lambda I)\mathbf{b} - \gamma \mathbf{v}) = 0. \end{cases}$$

Finally we obtain the following theorem:

**Theorem 7.** *The smoothing V-spline of (3.12) is the posterior mean of  $f = f_0 + f_1 + \dot{f}_1$ , where  $f_0$  diffuses in  $\text{span}\{1, t\}$  and  $f_1, \dot{f}_1$  have Gaussian process priors with mean zero and covariance functions*

$$\begin{aligned}\text{Cov}(f_1, f_1) &= R_1(s, t) = \beta \int_0^1 (s-u)_+ (t-u)_+ du, \\ \text{Cov}(\dot{f}_1, f_1) &= \dot{R}(s, t) = \beta \left( t + \int_0^s (t-u)_+ du \right)\end{aligned}$$

for  $\beta = \sigma^2/n\lambda$ .

### 3.4 V-Spline with Correlated Random Errors

In most of the studies on polynomial smoothing splines, the random errors are assumed being independent. In contrast, in applications, observations are often correlated, such as time series data and spatial data. It is known that the correlation greatly affects the selection of smoothing parameters, which are critical to the performance of smoothing spline estimates (Wang, 1998). The parameter selection methods, such as generalized maximum likelihood (GML), generalized cross-validation (GCV), underestimate smoothing parameters when data are correlated.

Diggle and Hutchinson (1989) extend GCV for choosing the degree of smoothing spline to accommodate an autocorrelated error sequence, by which the smoothing parameter and autocorrelation parameters are estimated simultaneously. Kohn *et al.* (1992) propose an algorithm to evaluate the cross-validation functions, whose autocorrelated errors are modeled by an autoregressive moving average. Wang (1998) extend GML and unbiased risk (UBR), other than GCV, to estimate the smoothing parameters and correlation parameters simultaneously. In this section, we are exploring the extended GCV for V-spline with correlated errors.

First of all, consider observations  $y = f(t) + \varepsilon_1$  and  $v = f'(t) + \varepsilon_2$ , where  $\varepsilon_1 \sim N(0, \sigma^2 W^{-1})$ ,  $\varepsilon_2 \sim N\left(0, \frac{\sigma^2}{\gamma} U^{-1}\right)$  with variance parameter  $\sigma^2$ . The V-spline  $\hat{f}$  with correlated errors in space  $C_{p,w}^{(2)}[0, 1]$  is the minimizer of

$$\frac{1}{n} (\mathbf{y} - \mathbf{f})^\top W (\mathbf{y} - \mathbf{f}) + \frac{\gamma}{n} (\mathbf{v} - \mathbf{f}')^\top U (\mathbf{v} - \mathbf{f}') + \lambda \int_0^1 (f'')^2 dt. \quad (3.20)$$

Because  $f = \sum_{i=1}^{2n} \theta_i N_i(t)$  is a linear combination of basis functions, extended to the solution with covariance matrices, the coefficients is found by

$$\hat{\theta} = (B^\top WB + \gamma C^\top UC + n\Omega_\lambda)^{-1} (B^\top Wy + \gamma C^\top Uv). \quad (3.21)$$

Furthermore, in Gaussian process regression, the covariance matrix with correlated variances becomes  $M = \begin{bmatrix} Q + n\lambda W & P \\ Q' & P' + \frac{n\lambda}{\gamma} U \end{bmatrix}$  and the rest stays the same.

Recall the leave-one-out cross-validation score of a V-spline,

$$\text{LOOCV}(\lambda, \gamma) = \frac{1}{n} \sum_{i=1}^n \left( \frac{\hat{f}(t_i) - y_i + \frac{\gamma T_{ii}}{1-\gamma V_{ii}} (\hat{f}'(t_i) - v_i)}{1 - S_{ii} - \frac{\gamma T_{ii}}{1-\gamma V_{ii}} U_{ii}} \right)^2.$$

Followed by the approximation  $S_{ii} \approx \frac{1}{n} \text{tr}(S)$ ,  $T_{ii} \approx \frac{1}{n} \text{tr}(T)$ ,  $U_{ii} \approx \frac{1}{n} \text{tr}(U)$  and  $V_{ii} \approx \frac{1}{n} \text{tr}(V)$  (Syed, 2011), the V-spline GCV will be

$$\text{GCV}(\lambda, \gamma) = \frac{1}{n} \sum_{i=1}^n \left( \frac{\hat{f}(t_i) - y_i + \frac{\gamma \text{tr}(T)/n}{1-\gamma \text{tr}(V)/n} (\hat{f}'(t_i) - v_i)}{1 - \text{tr}(S)/n - \frac{\gamma \text{tr}(T)/n}{1-\gamma \text{tr}(V)/n} \text{tr}(U)/n} \right)^2,$$

which may provide further computational savings since it requires finding the trace rather than the individual diagonal entries of the hat matrix. Hence, it can be written in the form of

$$\text{GCV}(\lambda, \gamma) = \frac{(\hat{\mathbf{f}} - \mathbf{y})^\top (\hat{\mathbf{f}} - \mathbf{y}) + \frac{2\text{tr}(\gamma T)}{\text{tr}(I - \gamma V)} (\hat{\mathbf{f}} - \mathbf{y})^\top (\hat{\mathbf{f}}' - \mathbf{v}) + \left(\frac{\text{tr}(\gamma T)}{\text{tr}(I - \gamma V)}\right)^2 (\hat{\mathbf{f}}' - \mathbf{v})^\top (\hat{\mathbf{f}}' - \mathbf{v})}{\left(\text{tr}(I - S - \frac{\text{tr}(\gamma T)}{\text{tr}(I - \gamma V)} U)\right)^2}.$$

A natural extension to the above GCV for V-spline with correlated errors is

$$\text{GCV}(\lambda, \gamma) = \frac{\left(\hat{\mathbf{f}} - \mathbf{y}\right)^T W \left(\hat{\mathbf{f}} - \mathbf{y}\right) + \frac{2\text{tr}(\gamma T)}{\text{tr}(I - \gamma V)} \left(\hat{\mathbf{f}} - \mathbf{y}\right)^T W^{1/2} U^{1/2} \left(\hat{\mathbf{f}}' - \mathbf{v}\right) + \left(\frac{\text{tr}(\gamma T)}{\text{tr}(I - \gamma V)}\right)^2 \left(\hat{\mathbf{f}}' - \mathbf{v}\right)^T U \left(\hat{\mathbf{f}}' - \mathbf{v}\right)}{\left(\text{tr}(I - S - \frac{\text{tr}(\gamma T)}{\text{tr}(I - \gamma V)} U)\right)^2}. \quad (3.22)$$

The GCV is used for finding the unknown constant parameter  $\lambda$ , instead of a piecewise  $\lambda(t)$  at different intervals, and the parameter  $\gamma$ . The structure of covariance matrices  $W$  and  $U$  is supposed to be known. If the errors are independent, in which way  $W$  and  $U$  become identity matrices, the solution  $\hat{f}$  degenerate to a conventional V-spline with constant  $\lambda$  through over the entire interval  $[0, 1]$ .

### 3.5 A Numeric Simulation

Consider a length of 100 even spaced simulation data on  $[0, 1]$  and the model  $f(t) = \sin(2\pi t)$ ,  $f'(t) = \cos(2\pi t)$ . Given parameters  $\sigma^2 = 0.01$ ,  $\gamma = 0.02$  and covariance matrices  $W$ ,  $U$ , then the simulated observation is

$$\begin{cases} y_i = f(t_i) + \varepsilon_i^{(1)}, \\ v_i = f'(t_i) + \varepsilon_i^{(2)}, \end{cases} \quad (3.23)$$

where  $\varepsilon^{(1)} \sim N(0, \sigma^2 W^{-1})$ ,  $\varepsilon^{(2)} \sim N\left(0, \frac{\sigma^2}{\gamma} U^{-1}\right)$ ,  $0 \leq t_1 < \dots < t_n \leq 1$ .

With the same parameter found by GCV, V-spline and its Bayes estimate return the same reconstruction. However, because we are using constant  $\lambda$  rather than a piecewise  $\lambda(t)$ , the trivial V-spline might not be the optimal solution compared with the one consisting an adaptive penalty term in Section 2.2.

### 3.6 Conclusion

In this chapter, we take a review of the work that has been done in the last few decades for the relationship between polynomial smoothing spline and the Bayes estimates. With improper priors, the two methods are corresponding to each other. In fact, smoothing spline is a particular case of Gaussian process regression. By following the work done by Gu (2013), we find the Bayes estimate for V-spline with a constant penalty parameter  $\lambda$ . However, it is a particular scenario of V-spline whose  $\lambda(t)$  varying on domains. So the trivial V-spline might not be an optimal solution. Additionally, we give the formula of GCV for V-spline with correlated errors on  $y$  and  $v$ .

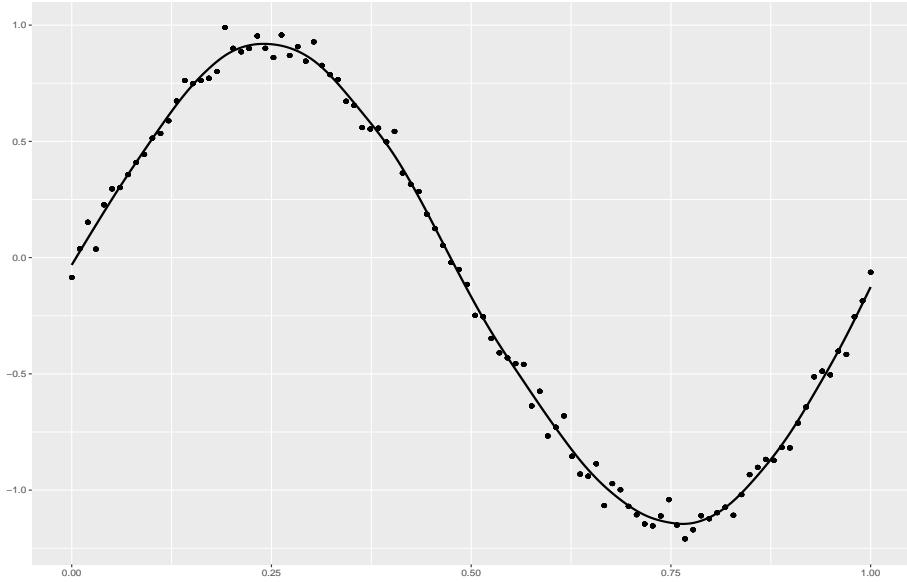


Figure 3.1: Comparing (trivial) V-spline and its Bayes estimate. Two methods are corresponding to each other. In this figure, black dots indicate observations and solid line stands for the reconstruction. The V-spline and its posterior  $E(f(t) \mid \mathbf{y}, \mathbf{v})$  of Bayes estimate give the same results.

A further work is to find the Bayes estimate for the real V-spline with a piecewise penalty term  $\lambda(t)$ . Besides GCV, other methods, such as EM and UBR are worth being invested in further research.

# Chapter 4

## An Overview of On-line State and Parameter Estimation

### 4.1 Introduction

As the development of the technology of science and real life, the "big data" challenge becomes ubiquitous. Classical methods, such as MCMC, are normally suitable and good at handling a batch of data forecasting and analyzing. However, for big data and instant updating data stream, more robust and efficient methods are required.

Alternative approaches, such as Sequential Monte Carlo, for on-line updating and estimating are well studied in scientific literature and prevalent in academic research in the last decades. When it embraced with state-space model, which is a popular class of time series models that have found numerous of applications in fields as diverse as statistics, ecology, econometrics, engineering and environmental sciences (Cappé *et al.*, 2009; Arnaud Doucet, 2011; Robert J Elliott, 1995; Cargnoni *et al.*, 1997), it allows us to establish complex linear and nonlinear Bayesian estimations in time series patterns (Vieira and Wilkinson, 2016).

### State-Space Model

State-space models are models that rely on the concept of state variables. If we describe a system as an operator mapping from the space of inputs to the space of outputs, then we may need the entire input-output history of the system together with the planned input in order to compute the future output values (Hangos *et al.*, 2006). In an alternative way, by using new information at time  $t$  containing all the past

information up to the current state and initial conditions to get the current output is possible, which is known as a sequential method. A genetic state-space model consists of two sets of equations: state equation and output equation. The state equation describes the evolution of the true input and state variables sequentially as a function and passes the variable one after one, generally, with some noises. The output equation catches the input values and interprets it out by an algebraic equation. A general state-space model has the form of

$$\text{State equation } x_t = G_t(x_{t-1}) + w_t, \quad (4.1)$$

$$\text{Output equation } y_t = F_t(x_t) + \varepsilon_t \quad (4.2)$$

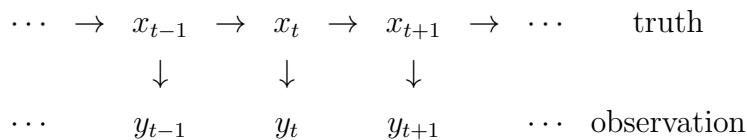
with an initial state  $x_0$ , where  $w_t$  and  $\varepsilon_t$  are noise terms.  $x_t$  are true status variables and  $y_t$  are output values. Many researchers have been interested in this model and its application because of its good property. It can be used to model univariate or multivariate time series and can be applied to a system that exhibits non-stationarity, structural changes, and irregular patterns (Petris *et al.*, 2009).

The most simple and important system is given by Gaussian linear state-space models, also known by dynamic linear models (DLM), which defines a very general class of non-stationary time series models. First of all, the model is linear, that means  $G_t$  and  $F_t$  are linear processes and satisfy linearity property. Secondly, it is specified by a normal prior distribution for the  $p$ -dimensional state vector at initial state  $t = 0$ ,

$$x_0 \sim N_p(m_0, C_0)$$

and two independent zero-mean normal distributed noises  $\varepsilon_t \sim N_p(0, V_t)$  and  $w_t \sim N_p(0, W_t)$  (Petris *et al.*, 2009). The celebrated Kalman filter is a particular algorithm that is used to solve state-space models in the linear case. This was first derived by Kalman (Kalman *et al.*, 1960).

The assumption Markovian keeps the current state  $x_t$  only depending on the previous one step  $x_{t-1}$  and the observed  $y_t$  depending on  $x_t$ . A state-space is shown in the diagram below:



In applications, the process functions  $G_t$  and  $F_t$  contain one or more unknown parameters that need to be estimated (De Jong, 1988) and the goal is to estimate

the true states on sequential observations  $y_1, \dots, y_t$ . Then it becomes to estimate the joint density of  $p(x_{1:t}, \theta | y_{1:t})$ , where  $x_{1:t} = \{x_1, x_2, \dots, x_t\}$  are the hidden states and  $y_{1:t} = \{y_1, y_2, \dots, y_t\}$  are the observed outcomes and  $\theta$  is a set of unknown parameters.

## Contents

In this chapter, an overview of existing methods for sequential state and parameter inference is given with discussions and a numerical study. In Section 4.2, the concepts and popular algorithms of sequential state estimation are introduced. These algorithms are the fundamental of advanced methods. In Section 4.3, we will have a look at on-line algorithms that can estimate both unknown state and parameter in different ways. In Section 4.4, a numerical study is to analyze and compare the performances of these methods, including the proposed Algorithm 5.2 in Section 5.5.

## 4.2 State Estimation Filters

State estimation is the fundamental problem in a target-tracking system. A general approach is using the system functional form to perform the state estimation with the assumption that all parameters are known. Indeed, two aspects of the functional form that mainly affect the analysis of such systems: (i) is the system model linear or non-linear in the state, and (ii) is the noise modeled as a random variable or a non-random bounded variable.

The following sections, we explore state filters that are not restricted by assumptions of linearity and may be applied to non-Gaussian noise models.

### 4.2.1 Sequential Monte Carlo Method

The use of *Monte Carlo* methods for filtering can be traced back to the pioneering contributions of (Handschin and Mayne, 1969; Handschin, 1970). These researchers tried to use an importance sampling paradigm to approximate the target distributions and. Later on, an importance sampling algorithms were implemented sequentially in the filtering context. This algorithm is named *sequential importance sampling*, often abbreviated SIS, and has been known since the early 1970s. Limited by the power of computers and suffering from sample impoverishment or weight degeneracy, the SIS did not develop well until 1993. Gordon used this a technique based on sampling and importance sampling methods to find the best state estimation (Gordon *et al.*, 1993).

A particle filter algorithm was proposed to allow rejuvenation of the set of samples by duplicating the samples with high importance weights and, on the contrary, removing samples with low weights (Cappé *et al.*, 2009). Since then, sequential Monte Carlo (SMC) methods have been applied in many different fields including but not limited to computer vision, signal processing, control, econometrics, finance, robotics, and statistics (Arnaud Doucet, 2011; Ristic *et al.*, 2004).

In the state-space model, a generic particle filter estimates the posterior distribution of the hidden states using the observation measurement process. The filtering problem is to estimate sequentially the values of the hidden states  $x_t$  given the values of the observation process  $y_{1:t}$  at any time  $t$ . In another word, it is to find the value of  $p(x_t | y_{1:t})$ . The process is divided into two steps: prediction and updating. In the prediction step, the assumption of Markov chain is the current status  $x_t$  only depends on the previous one  $x_{t-1}$ . Then we can calculate the probability of  $x_t$  by

$$\begin{aligned} p(x_t | y_{1:t-1}) &= \int p(x_t, x_{t-1} | y_{1:t-1}) dx_{t-1} \\ &= \int p(x_t | x_{t-1}, y_{1:t-1}) p(x_{t-1} | y_{1:t-1}) dx_{t-1} \\ &= \int p(x_t | x_{t-1}) p(x_{t-1} | y_{1:t-1}) dx_{t-1}. \end{aligned}$$

In the updating step, once  $p(x_t | y_{1:t-1})$  is known,  $p(x_t | y_{1:t})$  can be found by

$$\begin{aligned} p(x_t | y_{1:t}) &= \frac{p(y_t | x_t, y_{1:t-1}) p(x_t | y_{1:t-1})}{p(y_t | y_{1:t-1})} \\ &= \frac{p(y_t | x_t) p(x_t | y_{1:t-1})}{p(y_t | y_{1:t-1})}, \end{aligned}$$

where the normalization  $p(y_t | y_{1:t-1}) = \int p(y_t | x_t) p(x_t | y_{1:t-1}) dx_t$  (Arulampalam *et al.*, 2002).

Imagine that the state-space is partitioned as many parts, in which the particles are filled according to some probability measure. The higher probability, the denser the particles are concentrated. Suppose the particles  $x_k^{(1)}, \dots, x_k^{(N)}$  at time  $k$  are drawn from the target probability density function  $p(x)$ , then these particles are used to estimate the expectation and variance of  $f(x)$  by

$$\begin{aligned} \text{E}[f(x)] &= \int_a^b f(x) p(x) dx \\ \text{Var}[f(x)] &= \text{E}[f(x) - \text{E}(f(x))]^2 p(x) dx. \end{aligned}$$

Back to our target, the posterior distribution or density is empirically represented by a weighted sum of samples  $x_k^{(1)}, \dots, x_k^{(N)}$

$$\hat{p}(x_k | y_{1:t}) = \frac{1}{N} \sum_{i=1}^N \delta(x_k - x_k^{(i)}) \approx p(x_k | y_{1:t}), \quad (4.3)$$

where  $f(x) = \delta(x_k - x_k^{(i)})$  is Dirac delta function. Hence, a continuous variable is approximated by a discrete one with a random support. When  $N$  is sufficiently large,  $\hat{p}(x_k | y_{1:t})$  was treated by particle filter as the true posterior  $p(x_k | y_{1:t})$ . By this approximation, the filtering problem becomes to get the expectation of current status

$$\begin{aligned} \mathbb{E}[f(x_k)] &\approx \int f(x_k) \hat{p}(x_k | y_{1:t}) dx_k \\ &= \frac{1}{N} \sum_{i=1}^N \int f(x_k) \delta(x_k - x_k^{(i)}) dx_k \\ &= \frac{1}{N} \sum_{i=1}^N f(x_k^{(i)}). \end{aligned}$$

The expectation is the mean of the status of all particles  $x_k^{(1)}, \dots, x_k^{(N)}$ .

However, the posterior distribution is unknown and impossible to sample from the true posterior. To solve this issue, some sampling methods are introduced in the following sections.

### 4.2.2 Importance sampling

It is common to sample from an easy-to-implement distribution, the so-called proposal distribution  $q(x | y)$ , hence

$$\begin{aligned} \mathbb{E}[f(x)] &= \int f(x_t) \frac{p(x_t | y_{1:t})}{q(x_t | y_{1:t})} q(x_t | y_{1:t}) dx_x \\ &= \int f(x_t) \frac{p(x_t)p(y_{1:t} | x_t)}{p(y_{1:t})q(x_t | y_{1:t})} q(x_t | y_{1:t}) dx_x \\ &= \int f(x_t) \frac{W_t(x_t)}{p(y_{1:t})} q(x_t | y_{1:t}) dx_x, \end{aligned}$$

where  $W_t(x_t) = \frac{p(x_t)p(y_{1:t}|x_t)}{q(x_t|y_{1:t})} \propto \frac{p(x_t|y_{1:t})}{q(x_t|y_{1:t})}$ . Because  $p(y_{1:t}) = \int p(y_{1:t} | x_t)p(x_t)dx_t$ , so the above equation can be rewritten as

$$\begin{aligned}\mathbb{E}[f(x)] &= \frac{1}{p(y_{1:t})} \int f(x_t) W_t(x_t) q(x_t | y_{1:t}) dx_t \\ &= \frac{\int f(x_t) W_t(x_t) q(x_t | y_{1:t}) dx_t}{\int p(y_{1:t} | x_t) p(x_t) dx_t} \\ &= \frac{\int f(x_t) W_t(x_t) q(x_t | y_{1:t}) dx_t}{\int W_t(x_t) q(x_t | y_{1:t}) dx_t} \\ &= \frac{\mathbb{E}_{q(x_t|y_{1:t})}[W_t(x_t)f(x_t)]}{\mathbb{E}_{q(x_t|y_{1:t})}[W_t(x_t)]}.\end{aligned}$$

To solve the above equation, we can use Monte Carlo method by drawing samples  $\{x_t^{(i)}\}$  from  $q(x_t | y_{1:t})$  and get its expectation, which is approximated by

$$\begin{aligned}\mathbb{E}[f(x_t)] &\approx \frac{\frac{1}{N} \sum_{i=1}^N W_t(x_t^{(i)}) f(x_t^{(i)})}{\frac{1}{N} \sum_{i=1}^N W_t(x_t^{(i)})} \\ &= \sum_{i=1}^N \tilde{W}_t(x_t^{(i)}) f(x_t^{(i)}),\end{aligned}\tag{4.4}$$

where  $\tilde{W}_t(x_t^{(i)}) = \frac{W_t(x_t^{(i)})}{\sum_{i=1}^N W_t(x_t^{(i)})}$  is factorized weight. Each particle has its own weighted value, so the overall expectation is a weighted mean. However, the drawback of this method is that the computation is expensive. A smarter way is to update  $W_t^{(i)}$  recursively. Suppose the proposal distribution

$$q(x_{0:t} | y_{1:t}) = q(x_{0:t-1} | y_{1:t-1})q(x_t | x_{0:t-1}, y_{1:t}),$$

then the recursive form of the posterior distribution is

$$\begin{aligned}p(x_{0:t} | y_{1:t}) &= \frac{p(y_t | x_{0:t}, y_{1:t-1})p(x_{0:t} | y_{1:t-1})}{p(y_t | y_{1:t-1})} \\ &= \frac{p(y_t | x_{0:t}, y_{1:t-1})p(x_t | x_{0:t-1}, y_{1:t-1})p(x_{0:t-1} | y_{1:t-1})}{p(y_t | y_{1:t-1})} \\ &= \frac{p(y_t | x_t)p(x_t | x_{t-1})p(x_{0:t-1} | y_{1:t-1})}{p(y_t | y_{1:t-1})} \\ &\propto p(y_t | x_t)p(x_t | x_{t-1})p(x_{0:t-1} | y_{1:t-1}),\end{aligned}$$

the recursive form of the weights are

$$\begin{aligned}
W_t^{(i)} &\propto \frac{p(x_{0:t}^{(i)} | y_{1:t})}{q(x_{0:t}^{(i)} | y_{1:t})} \\
&= \frac{p(y_{1:t} | x_{0:t}^{(i)}) p(x_t^{(i)} | x_{t-1}^{(i)}) p(x_{0:t-1}^{(i)} | y_{1:t-1})}{q(x_t^{(i)} | x_{0:t-1}^{(i)}, y_t) q(x_{0:t-1}^{(i)} | y_{1:t-1})} \\
&= W_{t-1}^{(i)} \frac{p(y_{1:t} | x_{0:t}^{(i)}) p(x_t^{(i)} | x_{t-1}^{(i)})}{q(x_t^{(i)} | x_{0:t-1}^{(i)}, y_t)}.
\end{aligned}$$

### 4.2.3 Sequential Importance Sampling and Resampling

In practice, we are interested in the current filtered estimate  $p(x_t | y_{1:t})$  instead of  $p(x_{0:t} | y_{1:t})$ . Provided

$$q(x_t | x_{0:t-1}, y_{1:t}) = q(x_t | x_{t-1}, y_t),$$

the importance weights  $W_t^{(i)}$  can be updated recursively via

$$W_t^{(i)} \propto W_{t-1}^{(i)} \frac{p(y_t | x_t^{(i)}) p(x_t^{(i)} | x_{t-1}^{(i)})}{q(x_t^{(i)} | x_{t-1}^{(i)}, y_t)}.$$

The problem of SIS filter is that the distribution of importance weights becomes more and more skewed as time increases. Hence, after several iterations, only few particles have non-zero importance weights. This phenomenon is called *weight degeneracy* or *sample impoverishment* (Arnaud Doucet, 2011).

The effective sample size  $N_{\text{eff}}$  is suggested to monitor how bad the degeneration is, which is

$$N_{\text{eff}} = \frac{N}{1 + \text{Var}(w_t^{*(i)})},$$

where  $w_t^{*(i)} = \frac{p(x_t^{(i)} | y_{1:t})}{q(x_t^{(i)} | x_{t-1}^{(i)}, y_{1:t})}$ . The more different between the biggest weight and smallest weight, the worse the degeneration is. In practice, the effective sample size is approximated by

$$\hat{N}_{\text{eff}} \approx \frac{1}{\sum_{i=1}^N (w_t^{(i)})^2}.$$

If the value of  $N_{\text{eff}}$  is less than some threshold, some procedure should be used to avoid a worse degeneration. There are two ways one can do: choose an appropriate probability density function for importance sampling, or use resampling after SIS.

The idea of resampling is keeping the same size of particles, replacing the low weights particles with new ones. As discussed before,

$$p(x_t | y_{1:t}) = \sum_{i=1}^N w_t^{(i)} \delta(x_t - x_t^{(i)}) .$$

After resampling, it becomes

$$\tilde{p}(x_t | y_{1:t}) = \sum_{j=1}^N \frac{1}{N} \delta(x_t - x_t^{(j)}) = \sum_{i=1}^N \frac{n_i}{N} \delta(x_t - x_t^{(i)}) ,$$

where  $n_i$  represents how many times the new particles  $x_t^{(j)}$  were duplicated from  $x_t^{(i)}$ .

Then the process of SIS particle filter with resampling is summarized in following Algorithm 4.1.

---

**Algorithm 4.1:** Sampling and Importance Sampling

---

- 1 Initialization: Initial particles when  $t = 0$ . For  $i = 1, \dots, N$ , draw samples  $\{x_0^{(i)}\}$  from  $p(x_0)$ .
  - 2 **for**  $t = 1, 2, \dots, n$  **do**
  - 3     Importance sampling: draw sample  $\{\tilde{x}_t^{(i)}\}_{i=1}^N$  from  $q(x_t | y_{1:t})$ , calculate their weights  $\tilde{w}_t^{(i)}$  and normalize them.
  - 4     Resampling: Resample  $\{\tilde{x}_t^{(i)}, \tilde{w}_t^{(i)}\}$  and get a new set  $\{x_t^{(i)}, \frac{1}{N}\}$ .
  - 5     Output the status at time  $t$ :  $\hat{x}_t = \sum_{i=1}^N \tilde{x}_t^{(i)} \tilde{w}_t^{(i)}$ .
  - 6 **end**
- 

In SIR, if we choose

$$q(x_t^{(i)} | x_{t-1}^{(i)}, y_t) = p(x_t^{(i)} | x_{t-1}^{(i)}) ,$$

the weights become

$$\begin{aligned} w_t^{(i)} &\propto w_{t-1}^{(i)} \frac{p(y_t | x_t^{(i)}) p(x_t^{(i)} | x_{t-1}^{(i)})}{q(x_t^{(i)} | x_{t-1}^{(i)}, y_t)} \\ &\propto w_{t-1}^{(i)} p(y_t | x_t^{(i)}) . \end{aligned}$$

Because  $w_{t-1}^{(i)} = \frac{1}{N}$ , thus we have  $w_t^{(i)} \propto p(y_t | x_t^{(i)})$  and

$$w = \frac{1}{\sqrt{2\pi\Sigma}} \exp\left(-\frac{1}{2}(y_{\text{true}} - y)\Sigma^{-1}(y_{\text{true}} - y)\right).$$

However, SMC methods are suffering some drawbacks. At any time point  $k (k < t)$ , if  $t - k$  is too large, the approximation to marginal  $p(x_k | y_{1:t})$  is likely to be rather poor as the successive resampling steps deplete the number of distinct particle co-ordinates  $x_k$  (Andrieu *et al.*, 2010), which is also the difficulty of approximating  $p(\theta, x_{1:t} | y_{1:t})$  with SMC algorithms (Andrieu *et al.*, 1999; Fearnhead, 2002; Storvik, 2002).

#### 4.2.4 Auxiliary Particle Filter

The *auxiliary particle filter* (APF) was first introduced by Pitt and Shephard (1999) as an extension of SIR to perform inference in state-space model. The author uses the idea of stratification into particle filter to solve particle degeneracy by pre-selecting particles before propagation.

At each step, the algorithm draws a sample of the particle index  $i$ , which will be propagated from  $t - 1$  into the  $t$ , on the mixture in (4.4). These indexes are auxiliary variables only used as an intermediary step, hence the name of the algorithm (Pitt and Shephard, 1999). Thus, the task becomes to sample from the joint density  $p(x_t, i | y_{1:t})$ . Define

$$p(x_t, i | y_{1:t}) \propto p(y_t | x_t)p(x_t | x_{t-1}^{(i)})w_{t-1}^{(i)}, \quad (4.5)$$

and define  $\mu_t^{(i)}$  as some characterization of  $x_t | x_{t-1}$ , which suggested by the author could be mean, mode, a sample and so on, then the joint density can be approximated by

$$\pi(x_t, i | y_{1:t}) \propto p(y_t | \mu_t^{(i)})p(x_t | x_{t-1}^{(i)})w_{t-1}^{(i)}, \quad (4.6)$$

with weights

$$w_t^{(i)} \propto \frac{p(y_t | x_t^{(i)})}{p(y_t | \mu_t^{(i)})}.$$

This auxiliary variable based SIR requires only the ability to propagate and evaluate the likelihood, just as the original SIR suggestion of Gordon *et al.* (1993).

The main idea behind the APF is modifying the original sequence of target distributions to guide particles in promising regions, can be extended outside the filtering framework (Johansen and Doucet, 2008). It is also recommended in the literature (Liu, 2008) that the particles can be resampled not according to the normalized weights

$w_t^{\text{SISR}}(x_{1:t}) = \frac{p(x_{1:t})}{p(x_{1:t-1}q(x_t|x_{1:t-1}))}$  but according to a generic score function  $w_t(x_{1:t}) > 0$  at time  $t$

$$w_t(x_{1:t}) = g(w_t^{\text{SISR}}(x_{1:t})),$$

where  $g : \mathbb{R}^+ \mapsto \mathbb{R}^+$  is a monotonously increasing function, such as  $g(x) = x^\alpha$ , where  $0 < \alpha \leq 1$ .

#### 4.2.5 Sequential Particle Filter

SMC method is effective for exploring the sequence of posteriors distribution  $\pi(x_t | \theta) = p(x_t | y_{1:t}, \theta)$ , where the static parameters are treated as known. An inference about  $\pi_{t-1}$  is used to draw an inference on  $\pi_t$  by SIS and resampling. Its interest is focusing on  $x_t$  instead of the whole path  $x_{0:t}$ , that is the filtering problem. However, this algorithm evolves weighting and resampling a population of  $N$  particles,  $x_t^{(1)}, \dots, x_t^{(N)}$ , so that at each time  $t$  they are properly weighted samples from  $\pi(x_t | \theta)$ . Additionally, it is not practicable on huge size datasets, due to numerous iterations in the sampling process.

As a complementary solution, *sequential particle filter* method was proposed by Chopin (2002) in the first part of his doctorate thesis. Instead, sequential particle filter is using preliminary explorations of partial distribution  $\pi(\theta | y_{1:k})$  ( $k < t$ ). The concept is: an inference of  $\pi(\theta)$  is drawn from the first  $k$  observations, named as learning phase, and it is updated through importance sampling to incorporate the following  $l$  observations, named as updating phase, (Chopin, 2002). This method is the *iterated batch importance sampling* (IBIS) algorithm, which is used for the recursive exploration of the sequence of the parameter posterior distributions  $\pi(\theta)$ . It updates a population of  $N$  particles for  $\theta, \theta^{(1)}, \dots, \theta^{(N)}$ , so that at each time  $t$  they are a properly weighted sample from  $\pi(\theta)$ . The algorithm includes occasional MCMC steps for rejuvenating the current population of particles of  $\theta$  to prevent the number of distinct from decreasing over time.

In a batch mode, we are assuming that the parameter  $\theta$  is static. When the first  $k$  observations become available, we can find the posterior distribution  $\pi(\theta | y_{1:k})$ . After that, with length of  $l (< \infty)$  observations coming into data stream, the posterior becomes  $\pi(\theta | y_{1:k+l})$  and it is likely to be similar with  $\pi(\theta | y_{1:k})$ . Hence, a set of

proper re-weighted particles by the incremental weight is

$$\begin{aligned} w_{k,l}(\theta) &\propto \frac{\pi(\theta | y_{1:k+l})}{\pi(\theta | y_{1:k})} \\ &\propto \frac{p(y_{1:k+l} | \theta)}{p(y_{1:k} | \theta)} \\ &= p(y_{k+1:k+l} | y_{1:k}, \theta). \end{aligned}$$

Sequentially, the iterated batch importance sampling algorithm is in the following Algorithm 4.2.

---

**Algorithm 4.2:** Sequential Particle Filter

---

- 1 Initialization: General particles of  $\theta_i$  and  $w_i$ ,  $i = 1, \dots, N$ .
  - 2 **while**  $k < t$  **do**
  - 3     Re-weighting. Update the weights by  $w_i^* = w_i \times w_{k,l}$ , where  $w_{k,l}(\theta_i) \propto p(y_{k+1:k+l} | y_{1:k}, \theta_i)$ ,  $i = 1, \dots, N$ .
  - 4     Resampling. Normalize  $\theta_i$  and  $w_i^*$  to  $\theta_i^*$  and  $\frac{1}{N}$  according to  $p(\theta_i^* = \theta_i) = \frac{w_i^*}{\sum w_i^*}$ ,  $i = 1, \dots, N$ .
  - 5     Propagating. Draw  $\theta_i^m$  from  $K_{k+l}(\theta_i^*)$ , where  $K_{k+l}$  is a predefined transition kernel function with stationary distribution  $\pi_{k+l}$ .
  - 6     Set  $(\theta_i^m, \frac{1}{N})$  to  $(\theta_i, w_i)$ ,  $k + l$  to  $k$ .
  - 7 **end**
- 

The algorithm stops at  $k = t$ , where the particle system targets the distribution of interest  $\pi(\theta | y_{1:t})$ .

#### 4.2.6 MCMC-Based Particle Algorithm

It is discussed that the sequential Monte Carlo approaches are powerful methodologies to cope with large data set recursively, but unfortunately, they are inefficient when apply to high dimensional problems (Septier *et al.*, 2009). An alternative set of powerful stochastic algorithms that allow us to solve most of Bayesian computational problems is MCMC method. However, as dataset becomes larger and larger, it requires numerous computing in the process.

A natural extension is whether there exists a sequential MCMC method to diversify the degenerate particle population thus improving the empirical approximation for multi-target tracking or high dimensional space. Luckily, sequential approaches using

MCMC is proposed by Berzuini *et al.* (1997), in which the author combines MCMC with importance resampling to sequentially update the posterior distribution. Other discussions, such as (Khan *et al.*, 2005; Golightly and Wilkinson, 2006; Pang *et al.*, 2008), are using either resampling nor importance sampling.

As we discussed before, the a filtering problem is to find the posterior distribution recursively, like

$$p(x_t | y_{1:t}) \propto \int p(y_t | x_t) p(x_t | x_{t-1}) p(x_{t-1} | y_{1:t-1}) dx_{t-1}. \quad (4.7)$$

In particle filter, the posterior is approximated by particles  $x_t^{(1)}, \dots, x_t^{(N)}$  in equation (4.3). A MCMC procedure is designed using (4.3) as the target distribution with a proposal distribution of  $q(x_t | x_t^{(i)})$ . Therefore, like MCMC, the desired approximation  $\hat{p}(x_t | y_{1:t})$  is obtained by storing every accepted samples after the initial burn-in iterations (Septier *et al.*, 2009). The drawback is excessive computation occurs as the number of particles increases at each iteration.

To avoid this issue, an MCMC-based particle algorithm in (Pang *et al.*, 2008) considers the joint posterior distribution of  $x_t$  and  $x_{t-1}$ :

$$p(x_t, x_{t-1} | y_{1:t}) \propto p(y_t | x_t) p(x_t | x_{t-1}) p(x_{t-1} | y_{1:t-1}), \quad (4.8)$$

which becomes the new target distribution. At the  $i$ th sampling iteration, the joint  $x_k$  and  $x_{k-1}$  was proposed in a Metropolis-Hastings sampling step. After that, a refinement Metropolis-within-Gibbs step update  $x_k$  and  $x_{k-1}$  individually. Hence, the algorithm is summarized in Algorithm 4.3:

Septier *et al.* (2009) discuss some attractive features of genetic algorithms and simulated annealing into the framework of MCMC based particle scheme. One may refer to the paper for details.

### 4.3 On-line State and Parameter Estimation

The state transition density and the conditional likelihood function depend not only upon the dynamic state  $x_t$ , but also on a static parameter vector  $\theta$ , which will be stressed by use of the notations  $f(x_t | x_{t-1}, \theta)$  and  $g(y_t | x_t, \theta)$ . Putting the algorithms on-line means to update the parameters and states instantly as new observations coming into the data stream. For Bayesian dynamic models, however, the most natural option consists in treating the unknown parameter  $\theta$ , using the state-space representation, as a component of the state which lacks dynamic evolution, also referred to

---

**Algorithm 4.3:** MCMC-Based Particle Algorithm

---

```

1 Initialization: Initialize particles  $x_0^{(j)}, j = 1, \dots, N$ .
2 for  $k = 1, \dots, t$  do
3   for  $i = 1, \dots, M$  do
4     Propose  $\{x_k^*, x_{k-1}^*\} \sim q_1(x_k, x_{k-1} | x_k^{(i-1)}, x_{k-1}^{(i-1)})$ .
5     Accept  $\{x_k^*, x_{k-1}^*\}$  with probability
6       
$$\alpha_1 = \min \left\{ 1, \frac{p(x_k^*, x_{k-1}^* | y_{1:t})}{p(x_k^{(i-1)}, x_{k-1}^{(i-1)} | y_{1:t})} \frac{q_1(x_k^{(i-1)}, x_{k-1}^{(i-1)} | x_k^*, x_{k-1}^*)}{q_1(x_k^{(i-1)}, x_{k-1}^{(i-1)} | x_k^{(i-1)}, x_{k-1}^{(i-1)})} \right\}$$

7       Propose  $x_{k-1}^* \sim q_2(x_{k-1} | x_k^{(i)}, x_{k-1}^{(i)})$ 
8       Accept  $x_{k-1}^{(i)} = x_{k-1}^*$  with probability
9         
$$\alpha_2 = \min \left\{ 1, \frac{p(x_{k-1}^{(i)} | x_k^{(i)}, y_{1:t})}{p(x_{k-1}^{(i)} | x_k^{(i)}, y_{1:t})} \frac{q_2(x_{k-1}^{(i)} | x_{k-1}^*, x_k^{(i)})}{q_2(x_{k-1}^* | x_k^{(i)}, x_{k-1}^{(i)})} \right\}$$
.
10      Propose  $x_k^* \sim q_3(x_k | x_k^{(i)}, x_{k-1}^{(i)})$ .
11      Accept  $x_k^{(i)} = x_k^*$  with probability
12        
$$\alpha_3 = \min \left\{ 1, \frac{p(x_k^* | x_{k-1}^{(i)}, y_{1:t})}{p(x_k^{(i)} | x_{k-1}^{(i)}, y_{1:t})} \frac{q_3(x_k^{(i)} | x_k^*, x_{k-1}^{(i)})}{q_3(x_k^* | x_k^{(i)}, x_{k-1}^{(i)})} \right\}$$
.
13      After burn-in points, keep  $x_k^{(j)} = x_k^{(i)}$  as new particles for approximating
14       $p(x_k | y_{1:k})$ .
15    end
16  end
17
```

---

as a static parameter (Cappé *et al.*, 2007). The standard SMC is deficient for on-line parameter estimation. As a result of the successive resampling steps, after a certain time  $t$ , the approximation  $\hat{p}(\theta | y_{1:t})$  will only contain a single unique value for  $\theta$ . In other words, SMC approximation of the marginalized parameter posterior distribution is represented by a single Dirac delta function. It also causes error accumulation in successive Monte Carlo (MC) steps grows exponentially or polynomially in time (Kantas *et al.*, 2009).

Therefore, in this section, we are introducing some methods that will estimate combined state and parameter by either jointly estimating of state and parameter or by marginalizing the parameter using sufficient statistics.

### 4.3.1 Artificial Dynamic Noise

Some methods are trying to solve the posterior distribution  $p(\theta | y_{1:t})$  by

$$p(\theta | y_{1:t}) \propto p(y_{1:t} | \theta)p(\theta) \quad (4.9)$$

through maximize the likelihood function without introducing any bias or controlling the bias in states propagation. A pragmatic approach to reduce parameter sample degeneracy and error accumulation in successive MC approximations is to adding an artificial dynamic equation on  $\theta$ , (Higuchi, 2001; Kitagawa, 1998), which gives

$$\theta_{n+1} = \theta_n + \varepsilon_{n+1}.$$

The artificial noise  $\varepsilon_{t+1} \sim N(0, W_{t+1})$  is specified by a covariance matrix  $W_{t+1}$ . With this noise, SMC can now be applied to approximate  $p(x_{1:t}, \theta | y_{1:t})$ . A related kernel density estimation method proposes a kernel density estimate of the target (Liu and West, 2001)

$$\hat{p}(\theta | y_{1:t}) = \frac{1}{N} \sum M(\theta - \theta_n^{(i)}).$$

At time  $t + 1$ , the samples obtain a new set of particles.

### 4.3.2 Practical Filtering

A *fixed-lag* approach to filtering and sequential parameter learning was proposed in (Polson *et al.*, 2008). Its key idea is to express the filtering distribution as a mixture of lag-smoothing distributions and to implement it sequentially.

With a fixed-lag  $l$ , the state filtering and parameter learning require the sequence of the joint distribution  $p(x_t, \theta | y_{1:t})$ , which implies the desired filtering distribution  $p(x_t | y_{1:t})$  being marginalized as

$$p(x_t | y_{1:t}) = \int p(x_{t-l+1:t} | y_{1:t}) dx_{t-l+1:t-1},$$

and the parameter posterior distribution  $p(\theta | y_{1:t})$ . Arguing that the approximation that draws from  $p(x_{0:t-l} | y_{1:t-1})$  are approximate draws from  $p(x_{0:t-l} | y_{1:t})$ , the state filtering with static parameter  $\theta$  is

$$\begin{aligned} p(x_{t-l+1:t}, \theta | y_{1:t}) &= \int p(x_{t-l+1,t}, \theta | x_{0:t-l}, y_{1:t}) dp(x_{0:t-l} | y_{1:t}) \\ &\approx \int p(x_{t-l+1,t}, \theta | x_{0:t-l}, y_{1:t}) dp(x_{0:t-l} | y_{1:t-1}). \end{aligned}$$

Therefore, we can firstly draw some samples  $x_{0:t-l}^{(i)}$  from  $p(x_{0:t-l} \mid y_{1:t-1})$ , which is approximately the same as  $p(x_{0:t-l} \mid y_{1:t})$  and  $i = 1, \dots, M$ . Then, use these samples to estimate states and parameter by

$$x_{t-l+1} \sim p\left(x_{t-l+1} \mid x_{0:t-l}^{(i)}, \theta, y_{t-l+1:t}\right),$$

$$\theta \sim p\left(\theta \mid x_{0:t-l}^{(i)}, x_{t-l+1}, y_{t-l+1:t}\right),$$

with two-step Gibbs sampler. The algorithm is summarized in the following.

---

**Algorithm 4.4:** Practical Filtering Algorithm

---

```

1 Initialization: Set  $\theta^{(i)} = \theta_0$  as initial values,  $i = 1, \dots, N$ .
2 Burn-In: for  $k = 1, \dots, l$  do
3   for  $i = 1, \dots, N$  do
4     Initialize  $\theta = \theta^{(i)}$ .
5     Generate  $x_{0:k} \sim p(x_{0:k} \mid \theta, y_{1:k})$  and  $\theta \sim p(\theta \mid x_{0:k}, y_{1:k})$ .
6     After a few iterations, achieve a set of  $\{\tilde{x}_{0:k}^{(i)}, \theta^{(i)}\}$ .
7   end
8 end
9 Sequential Updating: for  $k = l + 1, \dots, t$  do
10  for  $i = 1, \dots, N$  do
11    initialize  $\theta = \theta^{(i)}$ .
12    Generate  $x_{k-l+1:k} \sim p\left(x_{k-l+1:k} \mid \tilde{x}_{k-l}^{(i)}, \theta, y_{k-l+1:k}\right)$  and
13     $\theta \sim p\left(\theta \mid \tilde{x}_{0:k-l}^{(i)}, x_{k-l+1:k}, y_{1:k}\right)$ .
14    Achieve a set of  $\{\tilde{x}_{k-l+1}^{(i)}, \theta^{(i)}\}$  and leave  $\tilde{x}_{0:k-l}^{(i)}$  unchanged.
15 end
16 end
```

---

The speed and accuracy of this algorithm depend on the choice of sample size  $M$  and the lag  $l$ , which is difficult, and there is a non-vanishing bias that is difficult to quantify (Polson *et al.*, 2008; Kantas *et al.*, 2009).

### 4.3.3 Liu and West's Filter

Particles degeneracy is inevitable in SMC. A method in Section 4.3.1 reduces the degeneracy by adding artificial noise to the parameters, however, that will also lead to

the variance of estimates. Liu and West (2001) use a kernel smoothing approximation combined with a neat shrinkage idea to kill over-dispersion.

At time  $t$ , suppose we have particles  $\{x_t^{(i)}\}$  and associated weights  $\{w_t^{(i)}\}$ ,  $i = 1, \dots, N$ , Bayes' theorem tells us that approximation to the posterior distribution  $p(x_{t+1} | y_{1:t+1})$  at time  $t + 1$  of the state is

$$p(x_{t+1} | y_{1:t+1}) \propto \sum_{i=1}^N w_t^{(i)} p\left(x_{t+1} | x_t^{(i)}\right) p(y_{t+1} | x_{t+1}).$$

However, variance increases through over  $t$  by the Gaussian mixture. In (West, 1993), the author is utilizing a smooth kernel density

$$p(\theta | y_{1:t}) \approx \sum_{i=1}^N w_t^{(i)} N\left(\theta | m_t^{(i)}, h^2 V_t\right) \quad (4.10)$$

to against the sample dispersion. Here,  $V_t$  is the Monte Carlo variance matrix of  $p(\theta | y_{1:t})$ . Because  $N(\cdot | m, C)$  is a multivariate normal density with mean  $m$  and covariance matrix  $C$ , so the above density (4.10) is a mixture of  $N\left(\theta | m_t^{(i)}, h^2 V_t\right)$  distributions weighted by the sample weights  $w_t^{(i)}$ . Without this shrinkage approach, the standard kernel locations would be  $m_t^{(i)} = \theta_t^{(i)}$ , by which there is an over dispersed kernel density, because of  $(1 = h^2)V_t$  is always large than  $V_t$ .  $\theta_t$  indicates that the samples are from the posterior at a specific time  $t$  instead of time-varying.

To correct it, the idea of shrinkage kernel is taking

$$m_t^{(i)} = \alpha \theta_t^{(i)} + (1 - \alpha) \bar{\theta}_t, \quad (4.11)$$

where  $\alpha = \sqrt{1 - h^2}$  and  $h > 0$  is the smoothing parameter. Consequently, the resulting normal mixture retains the mean  $\bar{\theta}_t$  and now has the correct covariance  $V_t$ , hence the over dispersion is trivially corrected (Liu and West, 2001).

A general algorithm is summarized bellow:

#### 4.3.4 Storvik Filter

*Storvik filter*, presented in (Storvik, 2002), is assuming that the posterior  $p(\theta | x_{0:t}, y_{1:t})$  depends on a low dimensional set of sufficient statistics  $s_t$  with an associated recursive update via  $s_t = S(s_{t-1}, x_t, y_t)$ . This approach is based on marginalizing the static parameters out of the posterior distribution, in which only the state vector needs to be considered, and aiming at reducing the particle impoverishment. It can be thought of as an extension of particle filters with additional steps of updating sufficient

---

**Algorithm 4.5:** Liu and West's Filter

---

```

1 for  $k = 1, \dots, t$  do
2   for  $i = 1, \dots, N$  do
3     Identify the prior estimation of  $(x_k, \theta)$  by  $(\mu_{k+1}^{(i)}, m_k^{(i)})$ , where
4      $\mu_{k+1}^{(i)} = E(x_{k+1} | x_k^{(i)}, \theta_k^{(i)})$ , and  $m_k^{(i)} = \alpha\theta_k^{(i)} + (1 - \alpha)\bar{\theta}_k$ .
5     Sample an auxiliary integer index  $I$  from  $\{1, \dots, N\}$  with probability
6     proportional to  $g_{k+1}^{(i)} \propto w_k^{(i)} p(y_{k+1} | \mu_{k+1}^{(i)}, m_k^{(i)})$ .
7     Sample a new parameter vector  $\theta_{k+1}^{(I)}$  from  $N(\theta_{k+1} | m_k^{(I)}, h^2 V_k)$ .
8     Sample current state vector  $x_{k+1}^{(I)}$  from  $p(x_{k+1} | x_k^{(I)}, \theta_{k+1}^{(I)})$ .
9     Evaluate weights  $\tilde{w}_{k+1}^{(i)} \propto \frac{p(y_{k+1} | x_{k+1}^{(I)}, \theta_{k+1}^{(I)})}{p(y_{k+1} | \mu_{k+1}^{(I)}, m_k^{(I)})}$ 
10    end
11  Normalize weights:  $w_{k+1}^{(i)} = \frac{\tilde{w}_{k+1}^{(i)}}{\sum \tilde{w}_{k+1}^{(i)}}$ .
12 end

```

---

statistics and sampling parameters sequentially (Lopes and Tsay, 2011). In particular, models for which the underlying process is Gaussian and linear in the parameters can be handled by this approach (Storvik, 2002). Furthermore, some other observational distributions with unknown parameters can be handled by this approach but subject to unavailable sufficient statistics.

The Storvik filter is summarized bellow:

---

**Algorithm 4.6:** Storvik Filter

---

```

1 for  $k = 1, \dots, t$  do
2   for  $i = 1, \dots, N$  do
3     Sample  $x_k^{(i)}$  from  $p(x_k | x_{k-1}^{(i)}, y_{1:k}, \theta^{(i)})$ .
4     Calculate weights  $\tilde{w}_k \propto p(y_k | x_k^{(i)}, \theta^{(i)})$  and normalize it by  $w_k^{(i)} = \frac{\tilde{w}_k^{(i)}}{\sum \tilde{w}_k^{(i)}}$ .
5     Re-sample  $\{\theta_k^{(i)}, x_k^{(i)}, s_k^{(i)}\}$  according to  $w_k^{(i)}$ .
6     Update sufficient statistics  $s_k^{(i)} = S(s_{k-1}^{(i)}, x_k, y_k)$ .
7     Sample  $\theta^{(i)}$  from  $p(\theta | s_k^{(i)})$ .
8   end
9 end

```

---

### 4.3.5 Particle Learning

*Particle Learning*, proposed by Carvalho *et al.* (2010), uses the similar sufficient statistics as Storvik filter does, in which the set of sufficient statistics is used for parameters estimation only. As an extension to the mixture Kalman filter (Chen and Liu, 2000), Particle Learning allows parameters learning throughout the process and utilize a resampling propagate framework together with a set of particles that includes a set of sufficient statistics (if it is available) for the states.

By denoting  $s_t$  and  $s_t^x$  the sufficient statistics for the parameter and state respectively, the updating rules are satisfied:  $s_t = S(s_{t-1}, x_t, y_t)$  and  $s_t^x = K(s_{t-1}^x, \theta, y_t)$ , where  $K(\cdot)$  is the Kalman filter recursions. In Particle Learning, the prior to sampling from the proposal distribution uses a predictive likelihood and takes  $y_{t+1}$  into account (Vieira and Wilkinson, 2016). This algorithm is summarized as following:

---

**Algorithm 4.7: Particle Learning Algorithm**


---

```

1 for  $k = 1, \dots, t$  do
2   for  $i = 1, \dots, N$  do
3     Re-sample  $\tilde{z}_k^{(i)} = (\tilde{s}_k^{x(i)}, \tilde{s}_k^{(i)}, \tilde{\theta}^{(i)})$  from  $p(z_k | s_k^x, s_k, \theta)$  with weight
4        $w \propto p(y_{k+1} | s_k^x, \theta)$ .
5     Draw  $x_{k+1}^{(i)}$  from  $p(x_{k+1} | \tilde{s}_k^x, \tilde{\theta}, y_{1:k+1})$ .
6     Update sufficient statistics  $s_{k+1} = S(\tilde{s}_k, x_{k+1}, y_{k+1})$ .
7     Sample  $\theta^{(i)}$  from  $p(\theta | s_{k+1})$ .
8   end
9 end

```

---

### 4.3.6 Adaptive Ensemble Kalman Filter

Storvik filter and Particle learning algorithms are efficient in some ways, however, the drawbacks are obvious. One of them is that the sufficient statistics are not always available, or hard to find, for complex models. They are trying to reduce the problem of particle impoverishment, although in practice they did not solve the problem completely (Chopin *et al.*, 2010). An ensemble Kalman filter method was proposed for sequential state and parameter estimation (Stroud *et al.*, 2016). It is fully Bayesian and propagates the joint posterior density of states and parameters through over the

process.

The ensemble Kalman filter, which is an extension to the standard Kalman filter, is an approximate filtering method introduced in the geophysics literature by Evensen (1994). Instead of working with the entire distribution, the ensemble Kalman filter stores propagates and updates an ensemble of vectors that approximates the state distribution (Katzfuss *et al.*, 2016).

Recall that an on-line combined parameters and state estimation relies on the decomposition of the joint posterior distribution

$$p(x_{t+1}, \theta | y_{1:t+1}) \propto p(x_{t+1} | y_{1:t+1}, \theta) p(\theta | y_{1:t+1}).$$

To implement on-line sequential estimation, the first term on the right side of the above formula should be written in the following recursive form as

$$p(x_{t+1} | \theta, y_{1:t+1}) \propto p(y_{t+1} | x_{t+1}, \theta) \int p(x_{t+1} | x_t, \theta) p(x_t | \theta, y_{1:t}) dx_t, \quad (4.12)$$

and the second term in the recursive form is

$$\begin{aligned} p(\theta | y_{1:t+1}) &\propto p(y_{1:t+1} | \theta) p(\theta) \\ &= p(y_{t+1} | \theta, y_{1:t}) p(\theta | y_{1:t}). \end{aligned} \quad (4.13)$$

The ensemble Kalman filter is used to find (4.12), which is the state inference. The estimated Kalman gain is

$$\hat{K}_{t+1}(\theta) = F_{t+1}(\theta) \hat{P}_{t+1}^f(\theta) F_{t+1}^\top(\theta) \hat{\Sigma}_{t+1}^{-1}(\theta),$$

where  $F_{t+1}$  is the observation map. The posterior ensemble at time  $t + 1$  based on parameter  $\theta$  is

$$x_{t+1}^{(i)} = x_{t+1}^{f(i)} + \hat{K}_{t+1}(\theta) \left( y_{t+1} + v_{t+1}^{(i)} + F_{t+1}(\theta) x_{t+1}^{f(i)} \right), \quad (4.14)$$

where  $\left\{ x_t^{(i)} \right\}_1^N$  is an ensemble of states representing the filtering distribution at time  $t$ .  $x_{t+1}^{f(i)}$  is the forecast ensemble from the forward map by  $x_{t+1}^{f(i)} = x_{t+1}^{p(i)} + w_{t+1}^{(i)} = G(x_t^{(i)}) + w_{t+1}^{(i)}$ . For the second term (4.13), Stroud *et al.* (2016) propose a feasible likelihood approximation by a multivariate Gaussian distribution (Mitchell and Houtekamer, 2000) for high-dimensional states:

$$p(y_{t+1} | \theta, y_{1:t}) \propto \left| \hat{\Sigma}_t(\theta) \right|^{-\frac{1}{2}} \exp \left( -\frac{1}{2} \hat{e}_{t+1}(\theta)^\top \hat{\Sigma}_t(\theta)^{-1} \hat{e}_{t+1}(\theta) \right), \quad (4.15)$$

where  $\hat{e}_{t+1}(\theta) = y_{t+1} - F_{t+1}(\theta) \hat{a}_{t+1}$ , and  $\hat{a}_{t+1} = \frac{1}{N} x_{t+1}^{p(i)}$

To find  $p(\theta | y_{1:t})$ , a generic way is using normal approximation, where the posterior density is given by

$$p(\theta | y_{1:t}) \propto \exp\left(-\frac{1}{2}(\theta - m_t)^\top C_t^{-1}(\theta - m_t)\right).$$

A grid-based representation is writing the posterior in the way that  $p(\theta | y_{1:t}) \propto p(y_t | \theta, y_{1:t-1})p(\theta | y_{1:t-1})$  and update the recursion weights by  $\pi_{t,k} \propto p(y_t | \theta, y_{1:t-1})\pi_{t,k-1}$ .

To summarize it up, the complete algorithm is in the following

---

**Algorithm 4.8:** Adaptive Ensemble Kalman Filter

---

```

1 Initialize samples  $\theta^{(i)} \sim p(\theta)$  and  $x_1^{(i)} \sim N(x_0, P_0)$ ,  $i = 1, \dots, N$ .
2 for  $k = 1, \dots, t$  do
3   for  $i = 1, \dots, N$  do
4     Propagate.  $x_k^{p(i)} = G(x_{k-1}^{(i)})$ .
5     Approximate likelihood function by (4.15).
6     Update. Draw  $\theta$  either use normal approximation or grid-based
      approximation to find (4.13).
7     Draw  $\theta^{(i)} \sim p(\theta | y_{1:k})$ .
8     Generate forecast ensemble by  $x_k^{f(i)} = x_k^{p(i)} + w_k$ .
9     Draw posterior ensemble using (4.14).
10    end
11 end

```

---

This algorithm works well when  $\theta$  is small and the parameter in the forward map  $G(\cdot)$  is known. If the forward map parameter is not known and has a high correlation with the state, the author suggests that it can be combined with the state augmentation (Anderson, 2001) and this algorithm is still working.

### 4.3.7 On-line Pseudo-Likelihood Estimation

Bayesian estimation requires the posterior distribution of  $p(\theta | y_{1:t})$ , where the  $\theta$  is treated as a random variable. By contrast, maximum likelihood estimation is looking for a value  $\hat{\theta}$ , which maximum the likelihood  $p(y_{1:t} | \theta)$ .

The classical *expectation maximization* (EM) algorithm (Dempster *et al.*, 1977) for maximizing  $l(\theta)$  is a two step procedure:

- E-step: Compute  $Q(\theta_k, \theta) = \int \ln p_\theta(x_{0:t}, y_{1:t}) p_{\theta_k}(x_{0:t} | y_{1:t}) dx_{0:t}$ .

- M-step: Update the parameter  $\theta_k$  by  $\theta_{k+1} = \arg \max Q(\theta_k, \theta)$ .

Then  $\{l(\theta_k)_k\}$  generated by the EM is a non-decreasing sequence.

A straightforward *on-line EM* algorithm uses SMC method to maximize  $l(\theta)$ . However, it requires estimating sufficient statistics base on joint probability distributions whose dimension is increasing over time and has a computational load of  $O(N^2)$  per time step (Kantas *et al.*, 2009). To circumvent this problem, Andrieu *et al.* (2005) propose a pseudo-likelihood function for finite state-space models.

Assuming that the process is stationary, give a time lag  $L \geq 1$  and any  $k \geq 1$ ,  $x_{1:t}$  and  $y_{1:t}$  are sliced to  $X_k = x_{kL+1:(k+1)L}$  and  $Y_k = y_{kL+1:(k+1)L}$ . For example:  $X_1 = x_{L+1:2L}$  consisting of  $L$  data. Further, the joint distribution of  $p(X_k, Y_k)$  is

$$p(X_k, Y_k) = \pi(x_{kL+1})F(y_{kL+1} | x_{xL+1})\prod_{n=kL+2}^{(k+1)L}G(x_n | x_{n-1})F(y_n | x_n). \quad (4.16)$$

The likelihood of a block  $Y_k$  of observations is given by

$$p(Y_k) = \int p(X_k, Y_k) dX_k, \quad (4.17)$$

and the log pseudo-likelihood for  $m$  slices is  $\sum_{k=0}^{m-1} \ln p(Y_k)$  (Andrieu *et al.*, 2005).

The advantage of this algorithm is that it only requires an approximation of the fixed dimensional distribution  $p(X_k | Y_k)$  and don't suffer degeneracy for small  $L$  (Kantas *et al.*, 2009). The disadvantage is that it only applies to stationary distribution, and can be observed empirically that the algorithm might converge to incorrect values and even sometimes drift away from the correct values as  $t$  increases (Andrieu *et al.*, 2010).

## 4.4 Simulation Study

In this section, we are comparing the performance of Liu and West's filter (LW), Storvik filter (St), Particle Learning (PL) and the proposed sequential MCMC Algorithm 5.2 in Section 5.5 by a simple dynamic linear model, see example (Liu and West, 2001). Explicitly, the model is

$$\begin{aligned} y_t &= Fx_t + \varepsilon_t, \\ x_t &= \phi x_{t-1} + w_t, \\ x_0 &\sim N(m_0, C_0), \end{aligned}$$

where  $\varepsilon_t \sim N(0, \sigma^2)$  and  $w_t \sim N(0, \tau^2)$ ,  $x_t$  are hidden status and  $y_t$  are observations. Assuming that  $F = 1$ ,  $\sigma^2 = 1$  and  $\tau^2 = 1$ . The initial value  $x_0 = 0$ .  $\theta = \phi$  a single static parameter without unobserved state variable.

A length of 897 simulated data set was generated from this  $AR(1)$  model at  $\phi = 0.8$ . First of all, we should find the sufficient statistics for Storvik filter and Particle Learning. For Particle Learning, the sufficient statistics  $s_t^x$  for state  $x$  and  $s_t$  for parameter  $\phi$  are satisfying the updating rules  $s_t^x = K(s_{t-1}^x, \phi, y_t)$  and  $s_t = S(s_{t-1}, x_t, y_t)$  respectively. Because of the assumption, the Kalman observation map is  $H_k = 1$  and the variances are normal distributed. Thus, the Kalman gain is  $K = 1$ . For details, the Particle Learning algorithm runs as :

- Step 1. Resample  $\left\{\tilde{z}_t^{(i)}\right\}_{i=1}^N = (\tilde{s}_t^{x(i)}, \tilde{s}_t^{(i)}, \tilde{\phi}^{(i)})$  from  $p(z_t | s_t^x, s_t, \phi)$  with weight  $w \propto p(y_{t+1} | s_t^x, \phi)$ . It is found that

$$p(y_{t+1} | s_t^x, \phi) \propto \exp\left(-\frac{1}{2}(y_{t+1} - \phi x_t)^2\right).$$

- Step 2. Draw  $x_{t+1}^{(i)}$  from  $p(x_{t+1} | \tilde{s}_t^x, \tilde{\phi}, y_{1:t+1})$ .

$$\begin{aligned} p(x_{t+1} | \tilde{s}_t^{(i)}, y_{1:t+1}) &= p(x_{t+1} | s_t^x, \phi, y_{1:t+1}) \propto p(x_{t+1}, y_{1:t+1} | s_t^x, \phi) \\ &\propto p(x_{t+1} | s_t^x, \phi) p(y_{t+1} | x_{t+1}, s_t^x, \phi) \\ &= N(x_{t+1} | \phi x_t, 1) N(y_{t+1} | x_{t+1}, 1) \\ &= N\left(x_{t+1} | \frac{1}{2}(y_{t+1} + \phi x_t), \frac{1}{\sqrt{2}}\right) \end{aligned}$$

- Step 3. Update sufficient statistics  $s_{t+1} = S(\tilde{s}_t, x_{t+1}, y_{t+1})$ .

$$\begin{aligned} s_{t+1,1} &= x_{t+1} \\ s_{t+1,2} &= x_t x_{t+1} + s_{t,2} = x_t s_{t,1} + s_{t,2} \\ s_{t+1,3} &= x_t^2 + s_{t,3} = s_{t,1}^2 + s_{t,3}. \end{aligned}$$

- Step 4. Sampling  $\phi$  from  $p(\phi | s_{t+1})$ .

$$\begin{aligned} p(\phi | x_{1:t+1}, y_{1:t+1}) &\propto p(x_{1:t+1}, y_{1:t+1} | \phi) p(\phi) \propto p(x_{1:t+1} | \phi) p(\phi) \\ &= N\left(\phi | \frac{s_{t+1,2}}{s_{t+1,3}}, \frac{1}{s_{t+1,3}}\right). \end{aligned}$$

- Step 5. Update from  $s_t^x$  to  $s_{t+1}^x$  via  $s_{t+1}^x = K(s_t^x, \phi, y_{t+1})$ .

Notice that the proposed sliding window MCMC algorithm requires using a few data to learn the parameter's mean and variance in the learning phase. Besides, LW, St and PL do not converge at the first few data. Then, to be fair, we take the first

300 data out and use them in the learning phase of the proposed algorithm. In the estimation phase, we are using three different strategies: a fixed length of 100, a fixed length of 300 and an expanding length including all the historical data along time  $t$ . In the former three algorithms, we are using 5 000 particles to infer state and parameter. In the latter MCMC algorithm, we are taking 5 000 samples at each time  $t$  for  $x_t^{(i)}$  and  $\phi^{(i)}$ , where  $i = 1, \dots, 5000$  and  $t = 300, \dots, 897$ . Furthermore, we run the comparison for 50 times to check their stabilities.

From figure 4.1 it can be seen that the former three algorithms converge to the true parameter  $\phi$  with similar speeds along time  $t$ . LW filter has a larger distance to the true parameter comparing with St and PL filters. The proposed MCMC with 100 length data in estimation phase has the biggest variance. By setting a longer length, the MCMC becomes more stable.

The estimations for  $x_t$  from  $t = 300$  to 897 are very close and hard to tell visually. From table 4.2, we can see that, by repeatedly running 50 times, the proposed MCMC algorithm is more stable in estimating parameter  $\phi$  as it has the lowest standard error (SE) among all the algorithms. The MSE of all the algorithms on estimating  $x$  is on the similar levels.

## 4.5 Conclusion

In this chapter, we take a brief overview of existing sequential state estimation and combined state and parameter estimation. The particle filter is an efficient method for state estimation, although the particles impoverishment is inevitable. Extended to this method, researchers are working on killing particles degeneracy and several accomplishments have been achieved. A new challenge is estimating the unknown parameters. In no doubt, for complex stochastic processes and dynamics, both Bayesian and Frequentist methods are working well. One may refer to (Wakefield, 2013) for further discussion between Bayesian and Frequentist methods and implementation.

As a summary, most of the research issues for filtering and parameter estimation focused on

- Choices of resampling scheme to kill particles degeneracy, such as Liu and West's filter.
- Exploration of an efficient sampling algorithm, such as Metropolis-Hastings sampler and related sampling algorithms.

- Exploration of accurate estimation with low variances in higher dimensional space.

Subject to pages and time, some algorithms are not included in this chapter. For more information and interests, readers can refer to unscented Kalman filter (Wan and Van Der Merwe, 2000) and its related algorithms for non-linear estimation, particle MCMC (Andrieu *et al.*, 2010) for off-line Bayesian estimation and on-line gradient approach (Poyiadjis *et al.*, 2005) for parameter estimation.

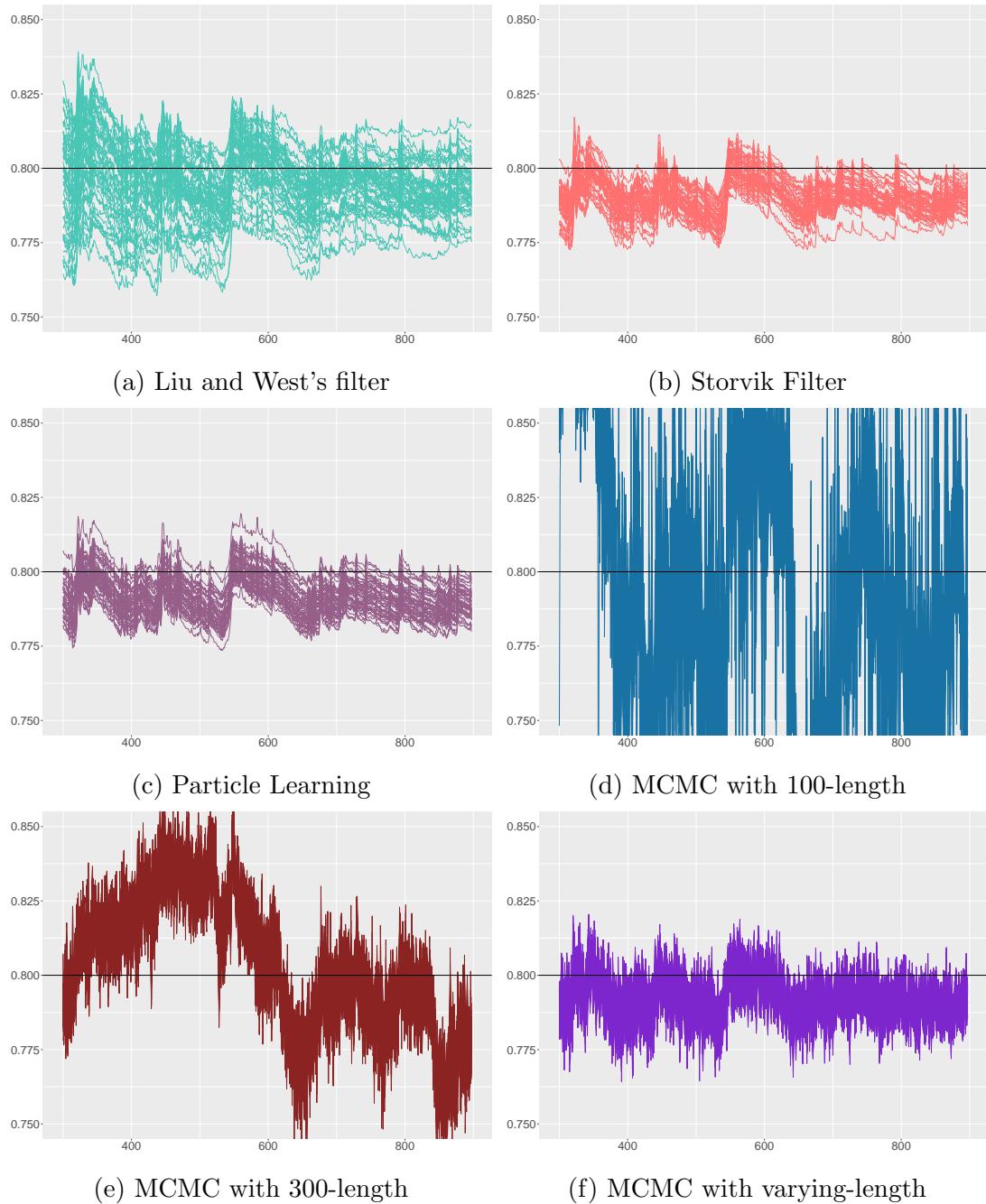
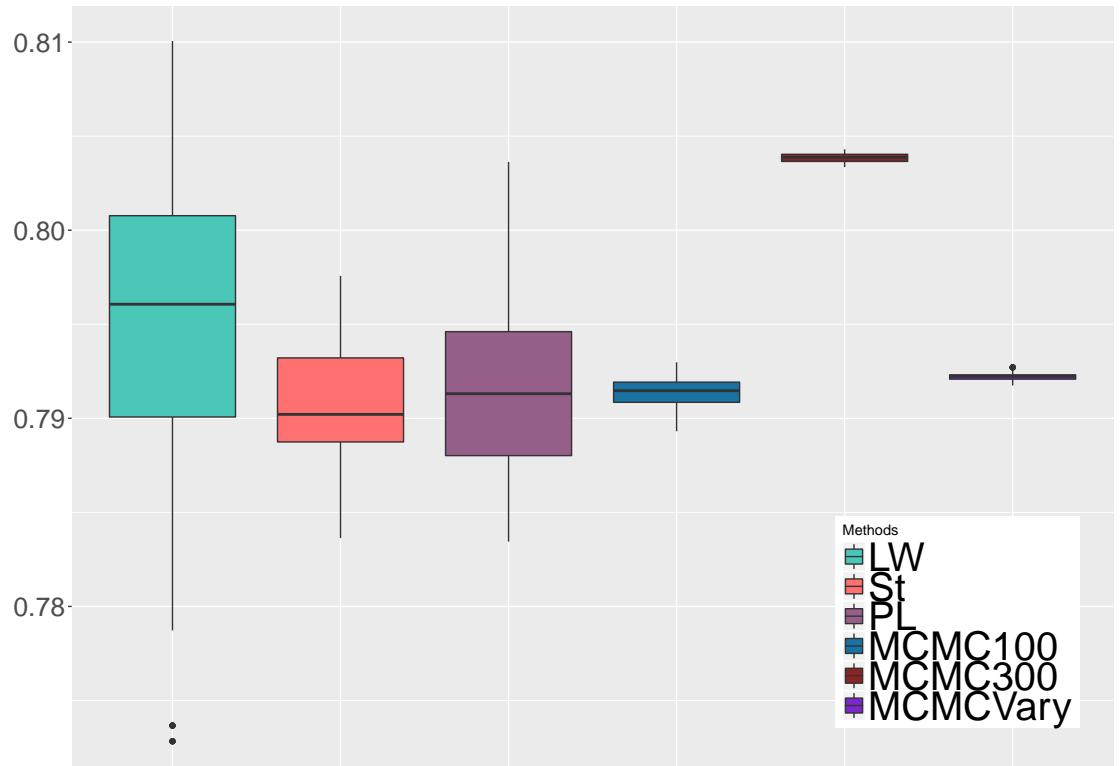


Figure 4.1: Trace plots. Repeatedly running 50 times with cutting off the first **300** data. It is apparent that all these algorithms converge to the true parameter (black horizontal line) along time. St, PL and MCMC-vary have a narrower range. MCMC-100 has a higher variability and MCMC-vary has the least. The more data incorporated in the estimation phase the better approximation to be obtained.



	LW	St	PL	MCMC-100	MCMC-300	MCMC-vary
Mean of $\hat{\phi}$	0.7947	0.7908	0.7918	0.7914	0.8038	0.7922
Se of $\hat{\phi} (\times 10^{-4})$	13.1000	4.8793	6.2877	1.1388	0.3275	0.27506
$\frac{1}{n} \sum_i (\hat{x}_i - x_i)^2$	0.5745	0.5739	0.5737	0.5875	0.5741	0.5740

Figure 4.2: Box-plots comparison of all the algorithms. The proposed MCMC algorithm is more stable than other filters.

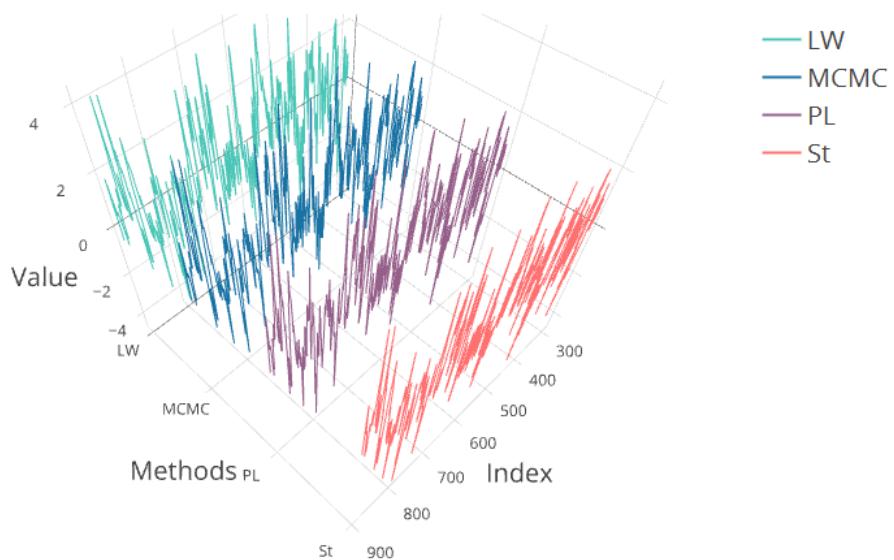


Figure 4.3: The filtering for  $x_{300:897}$  is competitive. These algorithms return close estimations.



# Chapter 5

## Adaptive Sequential MCMC for On-line State and Parameter Estimation

### 5.1 Introduction

Data assimilation is a sequential process, by which the observations are incorporated into a numerical model describing the evolution of this system throughout the whole process. It is applied in many fields, particularly in weather forecasting and hydrology. The quality of the numerical model determines the accuracy of this system, which requires sequential combined state and parameter inferences. An enormous literature has been done on discussing pure state estimation, however, less research is talking about estimating combined state and parameter, particularly in a sequential updating way.

Sequential Monte Carlo method is well studied in the scientific literature and quite prevalent in academic research in the last decades. It allows us to specify complex, non-linear time series patterns and enables performing real-time Bayesian estimations when it is coupled with Dynamic Generalized Linear Models (Vieira and Wilkinson, 2016). However, model's parameters are unknown in real-world application and it is a limit for standard SMC. Extensions to this algorithm have been done by researchers. Kitagawa (1998) propose a self-organizing filter and augmenting the state vector with unknown parameters. The state and parameter are estimated simultaneously by either a non-Gaussian filter or a particle filter. Liu and West (2001) propose an improved particle filter to kill degeneracy, which is a normal issue in static parameters estimation.

They are using a kernel smoothing approximation, with a correction factor to account for over-dispersion. Alternatively, Storvik (2002) propose a new filter algorithm by assuming the posterior depends on a set of sufficient statistics, which can be updated recursively. However, this approach only applies to parameters with conjugate priors (Stroud *et al.*, 2016). Particle learning was first introduced in (Carvalho *et al.*, 2010). Unlike Storvik filter, it is using sufficient statistics solely to estimate parameters and promises to reduce particle impoverishment. These particle-like methods are all using more or less sampling and resampling algorithms to update particles recursively.

Stroud *et al.* (2016) propose an SMC algorithm by using ensemble Kalman filter framework for high dimensional space models with observations. Their approach combines information about the parameters from data at different time points in a formal way using Bayesian updating. Polson *et al.* (2008) rely on a fixed-lag length of data approximation to filtering and sequential parameter learning in a general dynamic state-space model. This approach allows for sequential parameter learning where importance sampling has difficulties and avoids degeneracies in particle filtering. A new adaptive MCMC method yields a quick and flexible way for estimating posterior distribution in parameter estimation (Haario *et al.*, 1999). This new Adaptive Proposal method depends on historical data, is introduced to avoid the difficulties of tuning the proposal distribution in Metropolis-Hastings methods.

In this chapter, an adaptive Delayed-Acceptance Metropolis-Hastings algorithm is proposed to estimate the posterior distribution for combined state and parameter with two phases. In the learning phase, a self-tuning random walk Metropolis-Hastings sampler is used to learn the parameter mean and covariance structure. In the estimation phase, the parameter mean and covariance structure informs the proposed mechanism and is also used in a delayed-acceptance algorithm, which greatly improves sampling efficiency. Information on the resulting state of the system is given by a Gaussian mixture. To keep the algorithm a higher computing efficiency for on-line estimation, it is suggested to cut off historical data and to use a fixed length of data up to the current state, like a window sliding along time. At the end of this chapter, an application of this algorithm on irregularly sampled GPS time series data is presented.

## 5.2 Bayesian Inference on Combined State and Parameter

In a general state-space model of the following form, either the forward map  $F$  in hidden states or the observation transition matrix  $G$  is linear or non-linear. We are considering the model

$$\text{Observation: } y_t = G(x_t, \theta), \quad (5.1)$$

$$\text{Hidden State: } x_t = F(x_{t-1}, \theta), \quad (5.2)$$

where  $G$  and  $F$  are linear processes with Gaussian white noises  $\varepsilon \sim N(0, R(\theta))$  and  $\varepsilon' \sim N(0, Q(\theta))$ . This model has an initial state  $p(x_0 | \theta)$  and a prior distribution of the parameter  $p(\theta)$  is known or can be estimated. Therefore, for a general Bayesian filtering problem with known static parameter  $\theta$ , it requires computing the posterior distribution of current state  $p(x_t | y_{1:t})$  at each time  $t = 1, \dots, T$  by marginalizing the previous state

$$p(x_t | y_{1:t}) = \int p(x_t | x_{t-1}, y_{1:t})p(x_{t-1} | y_{1:t})dx_{t-1},$$

where  $y_{1:t} = \{y_1, \dots, y_t\}$  is the observation information up to time  $t$ . However, if  $\theta$  is unknown, one has to marginalize the posterior distribution for parameter by

$$p(x_t | y_{1:t}) = \int p(x_t | y_{1:t}, \theta)p(\theta | y_{1:t})d\theta. \quad (5.3)$$

The approach in equation (5.3) relies on the two terms : (i) a conditional posterior distribution for the states given parameters and observations; (ii) a marginal posterior distribution for parameter  $\theta$ . Several methods can be used in finding the second term, such as cross validation, Expectation Maximization algorithm, Gibbs sampling, Metropolis-Hastings algorithm and so on. A Monte Carlo method is popular in research area solving this problem. Monte Carlo method is an algorithm that relies on repeated random sampling to obtain numerical results. To compute an integration of  $\int f(x)dx$ , one has to sampling as many independent  $x_i$  ( $i = 1, \dots, N$ ) as possible and numerically to find  $\frac{1}{N} \sum_i f(x_i)$  to approximate the target function. In the target function, we draw samples of  $\theta$  and use a numerical way to calculate its posterior  $p(\theta | y_{1:t})$ .

Additionally, the marginal posterior distribution for the parameter can be written in two different ways:

$$p(\theta | y_{1:t}) \propto p(y_{1:t} | \theta)p(\theta), \quad (5.4)$$

$$p(\theta | y_{1:t}) \propto p(y_t | y_{1:t-1}, \theta)p(\theta | y_{1:t-1}). \quad (5.5)$$

The above formula (5.4) is a standard Bayesian inference requiring a prior distribution  $p(\theta)$ . It can be used in off-line methods, in which  $\hat{\theta}$  is inferred by iterating over a fixed observation record  $y_{1:t}$ . In contrast, formula (5.5) is defined in a recursive way over time depending on the previous posterior at time  $t - 1$ , which is known as on-line method.  $\hat{\theta}$  is estimated sequentially as a new observation  $y_{t+1}$  becomes available.

Therefore, the question becomes finding an efficient way to sampling  $\theta$ , such as Importance sampling (Hammersley and Handscomb, 1964; Geweke, 1989), Rejection sampling (Casella *et al.*, 2004; Martino and Míguez, 2010), Gibbs sampling (Geman and Geman, 1984), Metropolis-Hastings method (Metropolis *et al.*, 1953; Hastings, 1970) and so on.

### 5.2.1 Log-likelihood Function of Parameter Posterior

To sample  $\theta$ , firstly we should find its distribution function by starting from the joint covariance matrix of  $x_{0:t}$  and  $y_{1:t}$ . With a given  $\theta$ , suppose the joint covariance matrix is in the form of

$$\begin{bmatrix} x_{1:t} \\ y_{1:t} \end{bmatrix} \sim N(0, \Sigma_t), \quad (5.6)$$

where  $x_{1:t}$  represents the hidden states  $\{x_0, x_1, \dots, x_t\}$ ,  $y_{1:t}$  represents observed  $\{y_1, \dots, y_t\}$  and  $\theta$  is the set of all known and unknown parameters. The inverse of the covariance matrix  $\Sigma_t^{-1}$  is the precision matrix. In fact, it is a block matrix in the form of

$$\Sigma_t^{-1} = \begin{bmatrix} A_t & -B_t \\ -B_t^\top & B_t \end{bmatrix},$$

where  $A_t$  is a  $t \times t$  matrix of forward map hidden states,  $B_t$  is a  $t \times t$  matrix of observation errors up to time  $t$ . The structure of the matrices, such as bandwidth, sparse density, depending on the structure of the model. Temporally, we are using  $A$  and  $B$  to represent the matrices  $A_t$  and  $B_t$  here. Then, we may find the covariance matrix easily by calculating the inverse of the precision matrix

$$\begin{aligned} \Sigma &= \begin{bmatrix} (A - B^\top B^{-1} B)^{-1} & -(A - B^\top B^{-1} B)^{-1} B^\top B^{-1} \\ -B^{-1} B (A - B^\top B^{-1} B)^{-1} & (B - B^\top A^{-1} B)^{-1} \end{bmatrix} \\ &= \begin{bmatrix} (A - B)^{-1} & (A - B)^{-1} \\ (A - B)^{-1} & (I - A^{-1} B)^{-1} B^{-1} \end{bmatrix} \\ &\triangleq \begin{bmatrix} \Sigma_{XX} & \Sigma_{XY} \\ \Sigma_{YX} & \Sigma_{YY} \end{bmatrix}. \end{aligned}$$

Because of the covariance  $\Sigma_{YY} = (I - A^{-1}B)^{-1} B^{-1}$ , therefore the inverse is

$$\Sigma_{YY}^{-1} = B(I - A^{-1}B) = BA^{-1}\Sigma_{XX}^{-1}.$$

Given the Choleski decomposition  $LL^\top = A$ , we have

$$\begin{aligned}\Sigma_{YY}^{-1} &= BL^{-\top}L^{-1}\Sigma_{XX}^{-1} \\ &= (L^{-1}B)^\top(L^{-1}\Sigma_{XX}^{-1})\end{aligned}$$

More usefully, by given another Choleski decomposition  $RR^\top = A - B = \Sigma_{XX}^{-1}$ ,

$$\begin{aligned}y_{1:t}^\top \Sigma_{YY}^{-1} y_{1:t} &= (L^{-1}By_{1:t})^\top (L^{-1}\Sigma_{XX}^{-1} y_{1:t}) \\ &\triangleq W^\top (L^{-1}\Sigma_{XX}^{-1} y_{1:t})\end{aligned}\tag{5.7}$$

$$\begin{aligned}\det \Sigma_{YY}^{-1} &= \det B \det L^{-\top} \det L^{-1} \det R \det R^\top \\ &= \det B (\det L^{-1})^2 (\det R)^2.\end{aligned}\tag{5.8}$$

From the objective function (5.4), the posterior distribution of  $\theta$  is

$$p(\theta | y_{1:t}) \propto p(y_{1:t} | \theta) p(\theta) \propto \exp\left(-\frac{1}{2} y_{1:t}^\top \Sigma_{YY}^{-1} y_{1:t}\right) \sqrt{\det \Sigma_{YY}^{-1}} p(\theta).$$

Then, by taking natural logarithm on the posterior of  $\theta$  and using the useful solutions in equations (5.7) and (5.8), we will have

$$\ln L(\theta) = -\frac{1}{2} y_{1:t}^\top \Sigma_{YY}^{-1} y_{1:t} + \frac{1}{2} \sum \ln \text{tr}(B) - \sum \ln \text{tr}(L) + \sum \ln \text{tr}(R) + \ln p(\theta).\tag{5.9}$$

### 5.2.2 The Forecast Distribution

From equation (5.5), a sequential way for estimating the forecast distribution is needed. Suppose it is

$$p(y_t | y_{1:t-1}, \theta) \sim N(\bar{\mu}_t, \bar{\sigma}_t).\tag{5.10}$$

Look back to the covariance matrices of observations that we found in the previous section

$$\begin{aligned}p(y_{1:t-1}, \theta) &\sim N(0, \Sigma_{YY}^{(t-1)}), \\ p(y_t, y_{1:t-1}, \theta) &\sim N(0, \Sigma_{YY}^{(t)}),\end{aligned}$$

where the covariance matrix of the joint distribution is  $\Sigma_{YY}^{(t)} = (I_t - A_t^{-1}B_t)^{-1}B_t^{-1}$ ,  $I_t$  is a  $t \times t$  identity matrix. Then, by taking its inverse, we will get

$$\begin{aligned}\Sigma_{YY}^{(t)(-1)} &= B_t(I_t - A_t^{-1}B_t) \\ &= B_t(B_t^{-1} - A_t^{-1})B_t \\ &\triangleq \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} \begin{bmatrix} Z_t & b_t \\ b_t^\top & K_t \end{bmatrix} \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix}\end{aligned}$$

where  $Z_t$  is a  $t \times t$  matrix,  $b_t$  is a  $t \times 1$  matrix and  $K_t$  is a  $1 \times 1$  matrix. Thus, by taking its inverse again, we will get

$$\Sigma_{YY}^{(t)} = \begin{bmatrix} B_t^{-1}(Z_t - b_t K_t^{-1} b_t^\top)^{-1} B_t^{-1} & -B_t^{-1} Z_t^{-1} b_t (K_t - b_t^\top Z_t^{-1} b_t)^{-1} B_1^{-1} \\ -B_1^{-1} K_t^{-1} b_t^\top (Z_t - b_t K_t^{-1} b_t^\top)^{-1} B_t^{-1} & B_1^{-1} (K_t - b_t^\top Z_t^{-1} b_t)^{-1} B_1^{-1} \end{bmatrix}.$$

So, from the above covariance matrix, we can find the mean and variance of  $p(y_t | y_{1:t-1}, \theta)$  are

$$\bar{\mu}_t = B_1^{-1} K_t^{-1} b_t^\top B_{t-1}^{-1} y_{1:t-1}, \quad (5.11)$$

$$\bar{\sigma}_t = B_1^{-1} K_t B_1^{-1}. \quad (5.12)$$

### 5.2.3 The Estimation Distribution

From the joint distribution (5.6), one can find the best estimation with a given  $\theta$  by

$$\begin{aligned}\hat{x}_{1:t} | y_{1:t}, \theta &\sim N(A_t^{-1}B_t y_{1:t}, A_t^{-1}) \\ &\sim N(L^{-\top} L^{-1} B_t y_{1:t-1}, L^{-\top} L^{-1}) \\ &\sim N(L^{-\top} W, L^{-\top} L^{-1}).\end{aligned}$$

Consequently

$$\hat{x}_{1:t} = L^{-\top} (W + Z),$$

where  $Z \sim N(0, I(\varepsilon))$  is independent and identically distributed and drawn from a zero-mean normal distribution with variance  $I(\varepsilon)$ .

For sole  $x_t$ , its joint distribution with  $y_{1:t}$  is

$$x_t, y_{1:t} | \theta \sim N \left( 0, \begin{bmatrix} C_t^\top (A_t - B_t)^{-1} C_t & C_t^\top (A_t - B_t)^{-1} \\ (A_t - B_t)^{-1} C_t & (I - A_t^{-1} B_t)^{-1} B_t^{-1} \end{bmatrix} \right),$$

where  $C_t^\top = \begin{bmatrix} 0 & \cdots & 0 & 1 \end{bmatrix}$  helps to achieve the last element in the matrix. Thus, the filtering distribution of the state is

$$p(x_t | y_{1:t}, \theta) \sim N\left(\mu_t^{(x)}, \text{Var}(x_t)\right),$$

where, after simplifying, the mean and variance are

$$\mu_t^{(x)} = C_t^\top A_t^{-1} B_t y_{1:t}, \quad (5.13)$$

$$\text{Var}(x_t) = C_t^\top A_t^{-1} C_t. \quad (5.14)$$

Generally, researchers would like to find the combined estimation for  $x_t$  and  $\theta$  at time  $t$  by

$$p(x_t, \theta | y_{1:t}) = p(x_t | y_{1:t}, \theta)p(\theta | y_{1:t}).$$

Differently, from the target equation (5.3), the state inference containing  $N$  samples is a mixture Gaussian distribution in the following form

$$p(x_t | y_{1:t}) = \int p(x_t | y_{1:t}, \theta)p(\theta | y_{1:t})d\theta \doteq \frac{1}{N} \sum_{i=1}^N p(x_t | \theta^{(i)}, y_{1:t}). \quad (5.15)$$

Suppose  $x_t | y_{1:t}, \theta_i \sim N\left(\mu_{ti}^{(x)}, \text{Var}(x_{ti})\right)$  is found from equation (5.13) and (5.14) for each  $\theta_i$ , then its mean is

$$\mu_t^{(x)} = \frac{1}{N} \sum_i \mu_{ti}^{(x)} \quad (5.16)$$

and the unconditional variance of  $x_t$ , by law of total variance, is

$$\begin{aligned} \text{Var}(x_t) &= \text{E}[\text{Var}(x_t | y_{1:t}, \theta)] + \text{Var}[\text{E}(x_t | y_{1:t}, \theta)] \\ &= \frac{1}{N} \sum_i \left( \mu_{ti}^{(x)} \mu_{ti}^{(x)\top} + \text{Var}(x_{ti}) \right) - \frac{1}{N^2} \left( \sum_i \mu_{ti}^{(x)} \right) \left( \sum_i \mu_{ti}^{(x)} \right)^\top. \end{aligned} \quad (5.17)$$

### 5.3 Random Walk Metropolis-Hastings Algorithm

Metropolis-Hastings algorithm is an important class of MCMC algorithms (Smith and Roberts, 1993; Tierney, 1994; Gilks *et al.*, 1995). This algorithm has been used extensively in physics but was little known to others until Müller (1991); Tierney (1994) expounded the value of this algorithm to statisticians. The algorithm is extremely powerful and versatile and has been included in a list of "The Top 10 Algorithms" with the greatest influence on the development and practice of science and engineering in the 20th century (Dongarra and Sullivan, 2000; Medova, 2008).

Given essentially a probability distribution  $\pi(\cdot)$  (the "target distribution"), MH algorithm provides a way to generate a Markov chain  $x_1, x_2, \dots, x_t$ , who has the target distribution as a stationary distribution, for the uncertain parameters  $x$  requiring only that this density can be calculated at  $x$ . Suppose that we can evaluate  $\pi(x)$  for any  $x$ . The transition probabilities should satisfy the detailed balance condition

$$\pi(x^{(t)}) q(x', x^{(t)}) = \pi(x') q(x^{(t)}, x'),$$

which means that the transition from the current state  $\pi(x^{(t)})$  to the new state  $\pi(x')$  has the same probability as that from  $\pi(x')$  to  $\pi(x^{(t)})$ . In sampling method, drawing  $x_i$  first and then drawing  $x_j$  should have the same probability as drawing  $x_j$  and then drawing  $x_i$ . However, in most situations, the details balance condition is not satisfied. Therefore, we introduce a function  $\alpha(x, y)$  satisfying

$$\pi(x') q(x', x^{(t)}) \alpha(x', x^{(t)}) = \pi(x^{(t)}) q(x^{(t)}, x') \alpha(x^{(t)}, x').$$

In this way, a tentative new state  $x'$  is generated from the proposal density  $q(x'; x^{(t)})$  and it is accepted or rejected according to acceptance probability

$$\alpha = \frac{\pi(x')}{\pi(x^{(t)})} \frac{q(x^{(t)}, x')}{q(x', x^{(t)})}. \quad (5.18)$$

If  $\alpha \geq 1$ , the new state is accepted. Otherwise, the new state is accepted with probability  $\alpha$ .

Here comes an issues of how to choose  $q(\cdot | x^{(t)})$ . The most widely used subclass of MCMC algorithms is based around the Random Walk Metropolis (RWM). The RWM updating scheme was first applied by Metropolis *et al.* (1953) and proceeds as follows. Given a current value of the  $d$ -dimensional Markov chain  $x^{(t)}$ , a new value  $x'$  is obtained by proposing a jump  $\epsilon = |x' - x^{(t)}|$  from the pre-specified Lebesgue density

$$\tilde{\gamma}(\epsilon^*; \lambda) = \frac{1}{\lambda^d} \gamma\left(\frac{\epsilon^*}{\lambda}\right), \quad (5.19)$$

with  $\gamma(\epsilon) = \gamma(-\epsilon)$  for all  $\epsilon$ . Here, the positive  $\lambda$  governs the overall distance of the proposed jump and plays a crucial role in determining the efficiency of any algorithm. In a random walk, the proposal density function  $q(\cdot)$  can be chosen for some suitable normal distribution, and hence  $q(x' | x^{(t)}) = N(x' | x^{(t)}, \epsilon^2)$  and  $q(x^{(t)} | x') = N(x^{(t)} | x', \epsilon^2)$  cancel in the above equation (5.18) (Sherlock *et al.*, 2016). Therefore, to decide whether to accept the new state, we compute the quantity

$$\alpha = \min \left\{ 1, \frac{\pi(x') q(x^{(t)} | x')}{\pi(x^{(t)}) q(x' | x^{(t)})} \right\} = \min \left\{ 1, \frac{\pi(x')}{\pi(x^{(t)})} \right\}. \quad (5.20)$$

If the proposed value is accepted it becomes the next current value  $x^{(t+1)} = x'$ ; otherwise the current value is left unchanged  $x^{(t+1)} = x^{(t)}$  (Sherlock *et al.*, 2010).

### 5.3.1 Self-tuning Metropolis-Hastings Algorithm

In this section, a self-tuning MH algorithm, which automatically tunes the step sizes by one-variable-at-a-time Random Walk to gain the target acceptance rates, is proposed to estimate the structure of parameters in a  $d$ -dimensional space. Suppose the parameters are independent, the idea of this algorithm is that in each iteration, only one parameter is proposed and the others remain to be changed. After sampling, take  $n$  samples out of the total amount of  $N$  as new sequences. In figure 5.1, examples of different proposing methods are compared. To gain the target acceptance rates  $\alpha_i$ ,

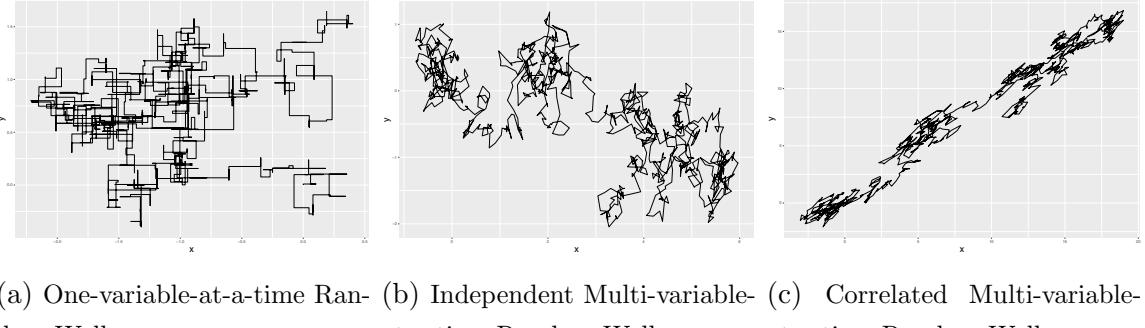


Figure 5.1: Examples of 2-Dimension Random Walk Metropolis-Hastings algorithm. Figure 5.1a is using one-variable-at-a-time proposal Random Walk. At each time, only one variable is changed and the other one stay constant. Figure 5.1b and 5.1c are using multi-variable-at-a-time Random Walk. The difference is in figure 5.1b, every forward step are proposed independently, but in 5.1c are proposed according to the covariance matrix.

( $i = 1, \dots, d$ ), the step sizes  $s_i$  for each parameter can be tuned automatically. The concept of the algorithm is if the proposal is accepted, we have more confidence on the direction and step size that were made. In this scenario, the next movement should be further, that means the step size  $s_{t+1}$  in the next step is bigger than  $s_t$ ; otherwise, a conservative proposal is made with a shorter distance, which is  $s_{t+1} \leq s_t$ .

Supposing  $a$  and  $b$  are non-negative numbers indicating the distances of a forward

movement, the new step size  $s_{t+1}$  from current  $s_t$  is

$$\ln s_{t+1} = \begin{cases} \ln s_t + a & \text{with probability } \alpha \\ \ln s_t - b & \text{with probability } 1 - \alpha \end{cases}, \quad (5.21)$$

where the logarithm guarantees the step size is positive. By taking its expectation

$$E(\ln s_{t+1} | \ln s_t) = \alpha(\ln s_t + a) + (1 - \alpha)(\ln s_t - b),$$

and simplifying to

$$\mu = \alpha(\mu + a) + (1 - \alpha)(\mu - b),$$

we can find that

$$a = \frac{1 - \alpha}{\alpha}b. \quad (5.22)$$

Thus, if the proposal is accepted, the step size  $s_t$  is tuned to  $s_{t+1} = s_t e^a$ , otherwise  $s_{t+1} = s_t / e^b$ .

The complete one-variable-at-a-time MH is illustrated in the following table:

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**Algorithm 5.1:** Self-tuning Random Walk Metropolis-Hastings Algorithm

---

- 1 Initialization: Given an arbitrary positive step size  $s_i^{(1)}$  for each parameter. Set up a value for  $b$  and find  $a$  by using formula (5.22). Set up a target acceptance rate  $\alpha_i$  for each parameter, where  $i = 1, \dots, d$ .
  - 2 Run sampling algorithm: **for**  $k$  from 1 to  $N$  **do**
  - 3     Randomly select a parameter  $\theta_i^{(k)}$ , propose a new one by  $\theta'_i \sim N(\theta_i^{(k)}, \epsilon s_i^{(k)})$  and leave the rest unchanged.
  - 4     Accept  $\theta'_i$  with probability  $\alpha = \min \left\{ 1, \frac{\pi(\theta') q(\theta^{(k)}, \theta')}{\pi(\theta^{(k)}) q(\theta', \theta^{(k)})} \right\}$ .
  - 5     If it is accepted, tune step size to  $s_i^{(k+1)} = s_i^{(k)} e^a$ , otherwise  $s_i^{(k+1)} = s_i^{(k)} / e^b$ .
  - 6     Set  $k = k + 1$  and move to step 3 until  $N$ .
  - 7 Take  $n$  samples out from  $N$  with equal spaced index for each parameter being a new sequence.
- 

The advantage of the Algorithm 5.1 is that it returns a more accurate estimation for  $\theta$  and it is more reliable to learn the structure of parameter space. However, if  $\pi(\cdot)$  is in an irregular structure, the algorithm is really time-consuming and that cause a lower efficiency. To accelerate the computation, we are introducing the Delayed-Acceptance Metropolis-Hastings (DA MH) algorithm.

### 5.3.2 Adaptive Delayed-Acceptance Metropolis-Hastings Algorithm

The DA MH algorithm proposed in (Christen and Fox, 2005) is a two-stage Metropolis-Hastings algorithm in which, typically, proposed parameter values are accepted or rejected at the first stage based on a computationally cheap surrogate  $\hat{\pi}(x)$  for the likelihood  $\pi(x)$ . In stage one, the quantity  $\alpha_1$  is found by a standard MH acceptance formula

$$\alpha_1 = \min \left\{ 1, \frac{\hat{\pi}(x') q(x^{(t)}, x')}{\hat{\pi}(x^{(t)}) q(x', x^{(t)})} \right\},$$

where  $\hat{\pi}(\cdot)$  is a cheap estimation for  $x$  and a simple form is  $\hat{\pi}(\cdot) = N(\cdot | \hat{x}, \epsilon)$ . Once  $\alpha_1$  is accepted, the process goes into stage two and the acceptance probability  $\alpha_2$  is

$$\alpha_2 = \min \left\{ 1, \frac{\pi(x') \hat{\pi}(x^{(t)})}{\pi(x^{(t)}) \hat{\pi}(x')} \right\}, \quad (5.23)$$

where the overall acceptance probability  $\alpha_1 \alpha_2$  ensures that detailed balance is satisfied with respect to  $\pi(\cdot)$ ; however if a rejection occurs at stage one, the expensive evaluation of  $\pi(x)$  at stage two is unnecessary.

For a symmetric proposal density kernel  $q(x', x^{(t)})$  such as is used in the random walk MH algorithm, the acceptance probability in stage one is simplified to

$$\alpha_1 = \min \left\{ 1, \frac{\pi(x')}{\pi(x^{(t)})} \right\}. \quad (5.24)$$

If the true posterior is available, the delayed-acceptance Metropolis-Hastings algorithm is obtained by substituting this for the unbiased stochastic approximation in (5.23) (Sherlock *et al.*, 2015).

To accelerate the MH algorithm, DA MH requires a cheap approximate estimation  $\hat{\pi}(\cdot)$  in formula (5.24). Intuitively, the approximation should be efficient with respect to time and accuracy to the true posterior  $\pi(\cdot)$ . A sensible option is assuming the parameter distribution at each time  $t$  is following a normal distribution with mean  $m_t$  and covariance  $C_t$ . So the posterior density is given by

$$\hat{\pi}(\theta | y_{1:t}) \propto \exp \left( -\frac{1}{2} (\theta - m_t)^\top C_t^{-1} (\theta - m_t) \right).$$

A lazy  $C_t$  is using identity matrix, in which way all the parameters are independent. In terms of  $m_t$ , in most of circumstances, 0 is not an idea choice. To find an optimal or suboptimal  $m_t$  and  $C_t$ , several algorithms have been discussed. Stroud *et al.* (2016)

are using a second-order expansion of  $l(\theta)$  at the mode and the mean and covariance become  $m_t = \arg \max l(\theta)$  and  $C_t = -\left[\frac{\partial l(\theta)}{\partial \theta_i \partial \theta_j}\right]_{\theta=m_t}^{-1}$  respectively. The drawback of this estimation is a global optimum is not guaranteed. Mathew *et al.* (2012) propose a fast adaptive MCMC sampling algorithm, which is consist of two phases. In the learning phase, they use hybrid Gibbs sampler to learn the covariance structure of the variance components. In phase two, the covariance structure is used to formulate an effective proposal distribution for a MH algorithm.

Likewise, we are suggesting that use a batch of data with length  $L < t$  to learn the parameter space by using self-tuning random walk MH algorithm in the learning phase first. This algorithm tunes each parameter at its own optimal step size and explores the surface in different directions. When the process is done, we have a sense of Hyper-surface of  $\theta \approx \hat{\theta}$  and its mean  $\hat{\mu} \approx m_L$  and covariance  $\hat{\Sigma} \approx C_L$  can be estimated. Then, we can move to the second phase: DA MH algorithm. The new  $\theta'$  is proposed from  $N(\theta^{(t)} | m_L, C_L)$ , which is in the following form

$$\theta' = \theta^{(t)} + R\epsilon z, \quad (5.25)$$

where  $R^\top R = C_L$  is the Cholesky decomposition,  $\epsilon$  is the tuned step size and  $z \sim N(0, 1)$  is Gaussian white noise. This proposing method reduces the impact of drawing  $\theta'$  from a correlation space.

### 5.3.3 Efficiency of Metropolis-Hastings Algorithm

In equation (5.19), the jump size  $\epsilon$  determines the efficiency of RWM algorithm. For a general RWM, it is intuitively clear that we can make the algorithm arbitrarily poor by making  $\epsilon$  either very large or very small (Sherlock *et al.*, 2010). Assuming  $\epsilon$  is extremely large, the proposal  $x' \sim N(x^{(t)}, \epsilon)$ , for example, is taken a further distance from current value  $x^{(t)}$ . Therefore, the algorithm will reject most of its proposed moves and stay where it was for a few iterations. On the other hand, if  $\epsilon$  is extremely small, the algorithm will keep accepting the proposed  $x'$  since  $\alpha$  is always approximately be 1 because of the continuity of  $\pi(x)$  and  $q(\cdot)$  (Roberts *et al.*, 2001). Thus, RWM takes a long time to explore the posterior space and converge to its stationary distribution. So, the balance between these two extreme situations must exist. This appropriate step size  $\hat{\epsilon}$  is optimal, sometimes is suboptimal, the solution to gain a Markov chain. Figure 5.2 illustrates the performances of RWM with different step size  $\epsilon$ . From these plots we may see that either too large or too small  $\epsilon$  causes high correlation chains,

indicating bad samples in sampling algorithm. An appropriate  $\epsilon$  decorrelate samples and returns a stationary chain, which is said to be high efficiency.

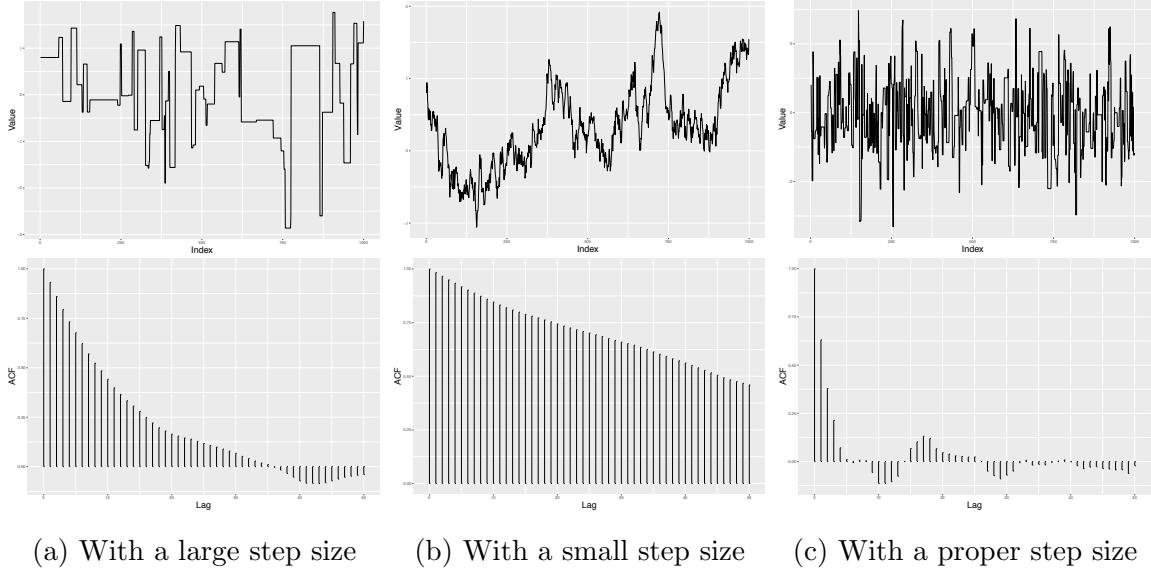


Figure 5.2: Metropolis-Hastings sampler for a single parameter with: 5.2a a large step size, 5.2b a small step size, 5.2c an appropriate step size. The upper plots show the sample chain and lower plots indicate the autocorrelation for each case.

Plenty of work has been done in determining the efficiency of Metropolis-Hastings algorithm in recent years. Gelman *et al.* (1996) work with algorithms consisting of a single Metropolis move (not multi-variable-at-a-time), and obtain many interesting results for the  $d$ -dimensional spherical multivariate normal problem with symmetric proposal distributions, including that the optimal scale is approximately  $2.4/\sqrt{d}$  times the scale of target distribution, which implies optimal acceptance rates of 0.44 for  $d = 1$  and 0.23 for  $d \rightarrow \infty$  (Gilks *et al.*, 1995). Roberts *et al.* (2001) evaluate scalings that are optimal (in the sense of integrated autocorrelation times) asymptotically in the number of components. They find that an acceptance rate of 0.234 is optimal in many random walk Metropolis situations, but their studies are also restricted to algorithms that consist of only a single step in each iteration, and in any case, they conclude that acceptance rates between 0.15 and 0.5 do not cost much efficiency. Other researchers (Roberts *et al.*, 1997; Bédard, 2007; Beskos *et al.*, 2009; Sherlock *et al.*, 2009; Sherlock, 2013) have been tackled for various shapes of target on choosing the optimal scale of the RWM proposal and led to the similar rule: choose the scale so that the acceptance rate is approximately 0.234. Although nearly all of the theoretical results are based upon limiting arguments in high dimension, the rule of thumb appears to be applicable

even in relatively low dimensions (Sherlock *et al.*, 2010).

In terms of the step size  $\epsilon$ , it is pointed out that for a stochastic approximation procedure, its step size sequence  $\{\epsilon_i\}$  should satisfy  $\sum_{i=1}^{\infty} \epsilon_i = \infty$  and  $\sum_{i=1}^{\infty} \epsilon_i^{1+\lambda} < \infty$  for some  $\lambda > 0$ . The former condition somehow ensures that any point of  $X$  can eventually be reached, while the second condition ensures that the noise is contained and does not prevent convergence (Andrieu and Thoms, 2008). Sherlock *et al.* (2010) tune various algorithms to attain target acceptance rates, and one of the algorithms tunes step sizes of univariate updates to attain the optimal efficiency of Markov chain at the acceptance rates between 0.4 and 0.45. Additionally, Graves (2011) mentioned that it is certain that one could use the actual arctangent relationship to try to choose a good  $\epsilon$ : in the univariate example, if  $\alpha$  is the desired acceptance rate, then  $\epsilon = 2\sigma / \tan(\pi/2\alpha)$ , where  $\sigma$  is the posterior standard deviation, will be obtained. In fact, some explorations infer a linear relationship between acceptance rate and step size, which is  $\text{logit}(\alpha) \approx 0.76 - 1.12 \ln \epsilon / \sigma$ , and the slope of the relationship is nearly equal to the constant -1.12 independently.

However, in multi-variable-at-a-time RWM, one expects that the proper interpretation of  $\sigma$  is not the posterior standard deviation but the average conditional standard deviation, which is presumably more difficult to estimate from a Metropolis algorithm. In a higher  $d$ -dimensional space, or propose multi-variable-at-a-time, suppose  $\Sigma$  is known or could be estimated, then  $X'$  can be proposed from  $q \sim N(X, \epsilon^2 \Sigma)$ . Thus, the optimal step size  $\epsilon$  is required. A concessive way of RWM in high dimension is proposing one-variable-at-a-time and treating them as one dimension space individually. In any case, however, the behavior of RWM on a multivariate normal distribution is governed by its covariance matrix  $\Sigma$ , and it is better than using a fixed  $N(X, \epsilon^2 I_d)$  distribution (Roberts *et al.*, 2001).

To explore the efficiency of a MCMC process, we introduce some notions first. For an arbitrary square integrable function  $g$ , Roberts *et al.* (2001) define its *integrated autocorrelation time* by

$$\tau_g = 1 + 2 \sum_{i=1}^{\infty} \text{Corr}(g(X_0), g(X_i)),$$

where  $X_0$  is assumed to be distributed according to  $\pi$ . Because central limit theorem, the variance of the estimator  $\bar{g} = \sum_{i=1}^n g(X_i)/n$  for estimating  $E[g(X)]$  is approximately  $\text{Var}_{\pi}[g(X)] \times \tau_g/n$ . The variance tells us the accuracy of the estimator  $\bar{g}$ . The smaller it is, the faster the chain converge. Therefore, they suggest that the efficiency of Markov chains can be found by comparing the reciprocal of their integrated autocorrelation

time, which is

$$e_g(\sigma) \propto (\tau_g \text{Var}_\pi[g(X)])^{-1}.$$

However, the disadvantage of their method is that the measurement of efficiency is highly dependent on the function  $g$ . Instead, an alternative approach is using *effective sample size* (ESS) (Kass *et al.*, 1998; Robert, 2004), which is defined in (Gong and Flegal, 2016) in the following form of

$$\text{ESS} = \frac{n}{1 + 2 \sum_{k=1}^{\infty} \rho_k(X)} \approx \frac{n}{1 + 2 \sum_{k=1}^{k_{\text{cut}}} \rho_k(X)} = \frac{n}{\tau},$$

where  $n$  is the number of samples,  $k_{\text{cut}}$  is lag of the first  $\rho_k < 0.01$  or  $0.05$ , and  $\tau$  is the integrated autocorrelation time. Given a Markov chain having  $n$  iterations, the ESS measures the size of i.i.d.samples with the same standard error. Moreover, a wide support among both statisticians (Geyer, 1992) and physicists (Sokal, 1997) are using the following cost of an independent sample to evaluate the performance of MCMC, that is

$$\frac{n}{\text{ESS}} \times \text{cost per step} = \tau \times \text{cost per step}.$$

Being inspired by their research, we now define the Efficiency in Unit Time (EffUT) and ESS in Unit Time (ESSUT) as follows:

$$\text{EffUT} = \frac{e_g}{T}, \quad (5.26)$$

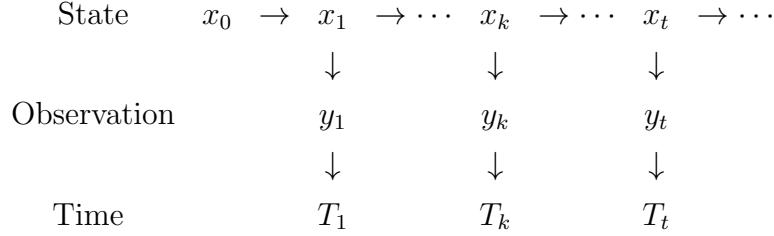
$$\text{ESSUT} = \frac{\text{ESS}}{T}, \quad (5.27)$$

where  $T$  represents the computation time, which is also known as running time. The computation time is the length of time, in minutes or hours, etc, required to perform a computational process. The best Markov chain with an appropriate step size  $\epsilon$  should not only have a lower correlation, as illustrated in figure 5.2, but also have less time-consuming. The standard efficiency  $e_g$  and ESS do not depend on the computation time, but EffUT and ESSUT do. The best-tuned step size gains the balance between the size of effective proposed samples and cost of time.

## 5.4 Simulation Studies

In this section, we consider the model in regular and irregular spaced time difference separately. For an one dimensional state-space model, we consider the hidden state process  $\{x_t, t \geq 1\}$  is a stationary and ergodic Markov process and transited by  $F(x' | x)$ . In this paper, we assume that the state of a system has an interpretation as the

summary of the past one-step behavior of the system. The states are not observed directly but by another process  $\{y_t, t \geq 1\}$ , which is assumed depending on  $\{x_t\}$  by the process  $G(y | x)$  only and independent with each other. When observed on discrete time  $T_1, \dots, T_k$ , the model is summarized on the directed acyclic following graph



We define  $\Delta_k = T_k - T_{k-1}$ . If  $\Delta_t$  is constant, we retrieve a standard  $AR(1)$  model process with regular spaced time steps; if  $\Delta_t$  is not constant, then the model becomes more complicated with irregular spaced time steps.

### 5.4.1 Simulation on Regularly Sampled Time Series Data

If the time steps are even spaced, the model can be written as a simple linear model in the following

$$\begin{aligned} y_t | x_t &\sim N(x_t, \sigma^2) \\ x_t | x_{t-1} &\sim N(\phi x_{t-1}, \tau^2), \end{aligned}$$

where  $\sigma$  and  $\tau$  are i.i.d.errors occurring in processes and  $\phi$  is a static process parameter in forward map. An initial value  $x_0 \sim N(0, L)$  is known.

To get the joint distribution for  $x_{0:t}$  and  $y_{1:t}$

$$\begin{bmatrix} x \\ y \end{bmatrix} | \theta \sim N(0, \Sigma),$$

where  $\theta = \{\phi, \sigma, \tau\}$ , we should start from the precision matrix  $\Sigma^{-1}$ , which looks like

$$\begin{bmatrix} \frac{1}{L^2} + \frac{\phi^2}{\tau^2} & \frac{-\phi}{\tau^2} & \cdots & 0 & 0 & 0 & \cdots & 0 \\ \frac{-\phi}{\tau^2} & \frac{1+\phi^2}{\tau^2} + \frac{1}{\sigma^2} & \cdots & 0 & -\frac{1}{\sigma^2} & 0 & \cdots & 0 \\ 0 & \frac{-\phi}{\tau^2} & \cdots & 0 & 0 & -\frac{1}{\sigma^2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{1}{\tau^2} + \frac{1}{\sigma^2} & 0 & 0 & \cdots & -\frac{1}{\sigma^2} \\ 0 & -\frac{1}{\sigma^2} & \cdots & 0 & \frac{1}{\sigma^2} & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 0 & \frac{1}{\sigma^2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -\frac{1}{\sigma^2} & 0 & 0 & \cdots & \frac{1}{\sigma^2} \end{bmatrix},$$

and denoted as  $\Sigma^{-1} = \begin{bmatrix} A & -B \\ -B & B \end{bmatrix}$ . Its inverse is the covariance matrix

$$\Sigma = \begin{bmatrix} (A - B)^{-1} & (A - B)^{-1} \\ (A - B)^{-1} & (I - A^{-1}B)^{-1}B^{-1} \end{bmatrix} \triangleq \begin{bmatrix} \Sigma_{XX} & \Sigma_{XY} \\ \Sigma_{YX} & \Sigma_{YY} \end{bmatrix}, \quad (5.28)$$

where  $B$  is a  $t \times t$  diagonal matrix with elements  $\frac{1}{\sigma^2}$ . The covariance matrices  $\Sigma_{XX} = (A - B)^{-1}$  and  $\Sigma_{YY} = (I - A^{-1}B)^{-1}B^{-1}$  are easily found.

## Parameter Estimation

In formula (5.4), the parameter posterior is estimated with observation data  $y_{1:t}$ . By using the Algorithm 5.1, although it may take a longer time, we will achieve a precise estimation. Similarly with Section 5.2.1, from the objective function, the posterior distribution of  $\theta$  is

$$p(\theta | Y) \propto p(Y | \theta)p(\theta) \propto \exp\left(-\frac{1}{2}Y\Sigma_{YY}^{-1}Y\right)\sqrt{\det\Sigma_{YY}^{-1}}p(\theta).$$

Then, by taking natural logarithm on the posterior of  $\theta$  and using the useful solutions in equations (5.7) and (5.8), we will have

$$\ln L(\theta) = -\frac{1}{2}Y^\top\Sigma_{YY}^{-1}Y + \frac{1}{2}\sum \ln \text{tr}(B) - \sum \ln \text{tr}(L) + \sum \ln \text{tr}(R) + \ln p(\theta). \quad (5.29)$$

In a simple linear case, we are choosing the parameter  $\theta = \{\phi = 0.9, \tau^2 = 0.5, \sigma^2 = 1\}$  as the author did in (Lopes and Tsay, 2011) and using  $n = 500$  dataset, setting initial  $L = 0$ . Instead of inferring  $\tau$  and  $\sigma$ , we are estimating  $\nu_1 = \ln \tau^2$  and  $\nu_2 = \ln \sigma^2$  in the RW-MH to avoid singular proposals. After the process, the parameters can be transformed back to original scale. Therefore, the new parameter  $\theta^* = \{\phi, \nu_1, \nu_2\} = \{\phi, \ln \tau^2, \ln \sigma^2\}$ .

By using Algorithm 5.1 and aiming the optimal acceptance rate at 0.44, after 10 000 iterations we get the acceptance rates for each parameters are  $\alpha_\phi = 0.4409$ ,  $\alpha_{\nu_1} = 0.4289$  and  $\alpha_{\nu_2} = 0.4505$ , and the estimations are  $\phi = 0.8794$ ,  $\nu_1 = -0.6471$  and  $\nu_2 = -0.0639$  respectively. Thus, we have the cheap surrogate  $\hat{\pi}(\cdot)$ . Keep going to the DA MH with another 10 000 iterations, the algorithm returns the best estimation with  $\alpha_1 = 0.1896$  and  $\alpha_2 = 0.8782$ . In figure 5.3, the trace plots illustrates that the Markov chain of  $\hat{\theta}$  is stably fluctuating around the true  $\theta$ .

## Recursive Forecast Distribution

Calculating the log-posterior of parameters requires finding out the forecast distribution of  $p(y_{1:t} | y_{1:t-1}, \theta)$ . A general way is using the joint distribution of  $y_t$  and  $y_{1:t-1}$ ,

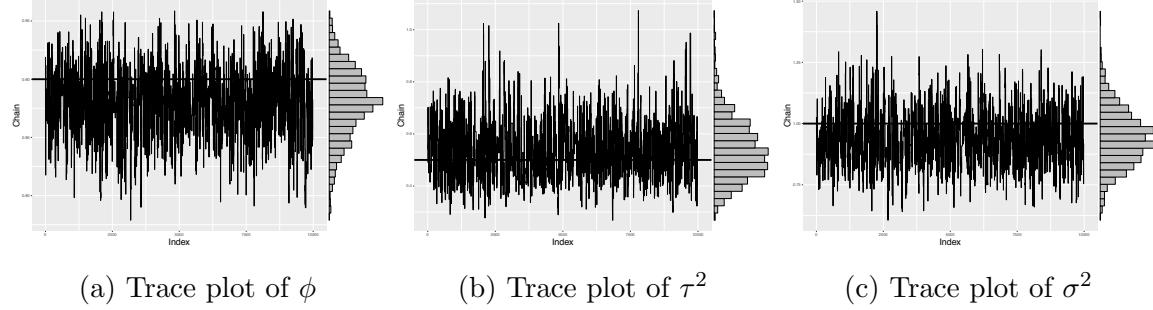


Figure 5.3: Linear simulation with true parameter  $\theta = \{\phi = 0.9, \tau^2 = 0.5, \sigma^2 = 1\}$ . By transforming back to the original scale, the estimation of  $\hat{\theta}$  is  $\{\phi = 0.8810, \tau^2 = 0.5247, \sigma^2 = 0.9416\}$ .

which is  $p(y_{1:t} | \theta) \sim N(0, \Sigma_{YY})$ , and following the procedure in Section 5.2.2 to work out the inverse matrix of a multivariate normal distribution. For example, one may find the inverse of the covariance matrix

$$\Sigma_{YY}^{-1} = B_t(I - A_t^{-1}B_t) = \frac{1}{\sigma^4}(\sigma^2 I_t - A_t^{-1}) \triangleq \frac{1}{\sigma^4} \begin{bmatrix} Z_t & b_t \\ b_t^\top & K_t \end{bmatrix}.$$

Therefore, the original form of this covariance is

$$\Sigma_{YY} = \sigma^4 \begin{bmatrix} (Z_t - b_t K_t^{-1} b_t^\top)^{-1} & -Z_t^{-1} b_t (K_t - b_t^\top Z_t^{-1} b_t)^{-1} \\ -K_t^{-1} b_t^\top (Z_t - b_t K_t^{-1} b_t^\top)^{-1} & (K_t - b_t^\top Z_t^{-1} b_t)^{-1} \end{bmatrix}.$$

By denoting  $C_t^\top = [0 \ \dots \ 0 \ 1]$  and post-multiplying  $\Sigma_{YY}^{-1}$ , we will have

$$\Sigma_{YY}^{-1} C_t = \frac{1}{\sigma^4} (\sigma^2 I - A^{-1}) C_t = \frac{1}{\sigma^4} \begin{bmatrix} b_t \\ K_t \end{bmatrix}. \quad (5.30)$$

A recursive way of calculating  $b_t$  and  $K_t$  is to use the Sherman-Morrison-Woodbury formula. In the late 1940s and the 1950s, Sherman and Morrison (1950); Woodbury (1950); Bartlett (1951); Bodewig (1956) discovered the following Theorem 8. The original Sherman-Morrison-Woodbury (for short SMW) formula has been used to consider the inverse of matrices (Deng, 2011). In this paper, we will consider the more generalized case.

**Theorem 8.** (*Sherman-Morrison-Woodbury formula*). *Let  $A \in B(H)$  and  $G \in B(K)$  both be invertible, and  $Y, Z \in B(K, H)$ . Then,  $A + YGZ^*$  is invertible if and only if  $G^{-1} + ZA^{-1}Y$  is invertible. In which case,*

$$(A + YGZ^*)^{-1} = A^{-1} - A^{-1}Y (G^{-1} + ZA^{-1}Y)^{-1} ZA^{-1}. \quad (5.31)$$

A simple form of SMW formula is Sherman-Morrison formula represented in the following statement (Bartlett, 1951): Suppose  $A \in R^{n \times n}$  is an invertible square matrix and  $u, v \in R^n$  are column vectors. Then,  $A + uv^\top$  is invertible  $\iff 1 + u^\top A^{-1}v \neq 0$ . If  $A + uv^\top$  is invertible, then its inverse is given by

$$(A + uv^\top)^{-1} = A^{-1} - \frac{A^{-1}uv^\top A^{-1}}{1 + v^\top A^{-1}u}. \quad (5.32)$$

By using the formula (5.32), one can find a recursive way to update  $K_t$  and  $b_{t-1}$ , which is

$$K_t = \frac{\sigma^4}{\tau^2 + \sigma^2 + \phi^2(\sigma^2 - K_{t-1})}, \quad (5.33)$$

$$b_t = \begin{bmatrix} \frac{b_{t-1}\phi K_t}{\sigma^2} \\ \frac{K_t(\sigma^2 + \tau^2) - \sigma^4}{\phi\sigma^2} \end{bmatrix}. \quad (5.34)$$

With the above formula, the recursive way of updating the mean and covariance is in the following formula:

$$\bar{\mu}_t = \frac{\phi}{\sigma^2} K_{t-1} \bar{\mu}_{t-1} + \phi \left( 1 - \frac{K_{t-1}}{\sigma^2} \right) y_{t-1}, \quad (5.35)$$

$$\bar{\Sigma}_t = \sigma^4 K_t^{-1}, \quad (5.36)$$

where  $K_1 = \frac{\sigma^4}{\sigma^2 + \tau^2 + L^2\phi^2}$ . For calculation details, we refer readers to Appendix B.1.

## The Estimation Distribution

As introduced in Section 5.2.3, from the joint distribution of  $x_{1:t}$  and  $y_{1:t}$ , one can find the best estimation with a given  $\theta$  by

$$\hat{x}_{1:t} | y_{1:t}, \theta \sim N(L^{-\top} W, L^{-\top} L^{-1}),$$

where  $W = L^{-1} B_t y_{1:t-1}$ . Consequently

$$\hat{x}_{1:t} = L^{-\top} (W + Z),$$

where  $Z \sim N(0, I(\varepsilon))$  is independent and identically distributed and drawn from a zero-mean normal distribution with variance  $I(\varepsilon)$ . Moreover, the mixture Gaussian distribution  $p(x_t | y_{1:t})$  can be found by

$$\mu_t^{(x)} = \frac{1}{N} \sum_i \mu_{ti}^{(x)} \quad (5.37)$$

$$\text{Var}(x_t) = \frac{1}{N} \sum_i \left( \mu_{ti}^{(x)} \mu_{ti}^{(x)\top} + \text{Var}(x_{ti}) \right) - \frac{1}{N^2} \left( \sum_i \mu_{ti}^{(x)} \right) \left( \sum_i \mu_{ti}^{(x)} \right)^\top. \quad (5.38)$$

To find  $\mu_{ti}^{(x)}$  and  $\text{Var}(x_{ti})$ , we will use the joint distribution of  $x_t$  and  $y_{1:t}$ , which is  $p(x_t, y_{1:t} | \theta) \sim N(0, \Gamma)$  and

$$\Gamma = \begin{bmatrix} C_t^\top (A_t - B_t)^{-1} C_t & C_t^\top (A_t - B_t)^{-1} \\ (A_t - B_t)^{-1} C_t & (I_t - A_t^{-1} B_t)^{-1} B_t^{-1} \end{bmatrix}.$$

Because of

$$C_t^\top A_t^{-1} = \begin{bmatrix} -b_t^\top & \sigma^2 - K_t \end{bmatrix},$$

thus, for any given  $\theta$ , we have  $\hat{x}_t | y_{1:t}, \theta \sim N\left(\mu_t^{(x)}, \text{Var}(x_t)\right)$ , where

$$\mu_t^{(x)} = \frac{K_t \bar{\mu}_t}{\sigma^2} + \left(1 - \frac{K_t}{\sigma^2}\right) y_t \quad (5.39)$$

$$\text{Var}(x_t) = \sigma^2 - K_t. \quad (5.40)$$

By substituting them into the equation (5.37) and (5.38), the estimated  $\hat{x}_t$  is easily got. For calculation details, we refer readers to Appendix B.1.

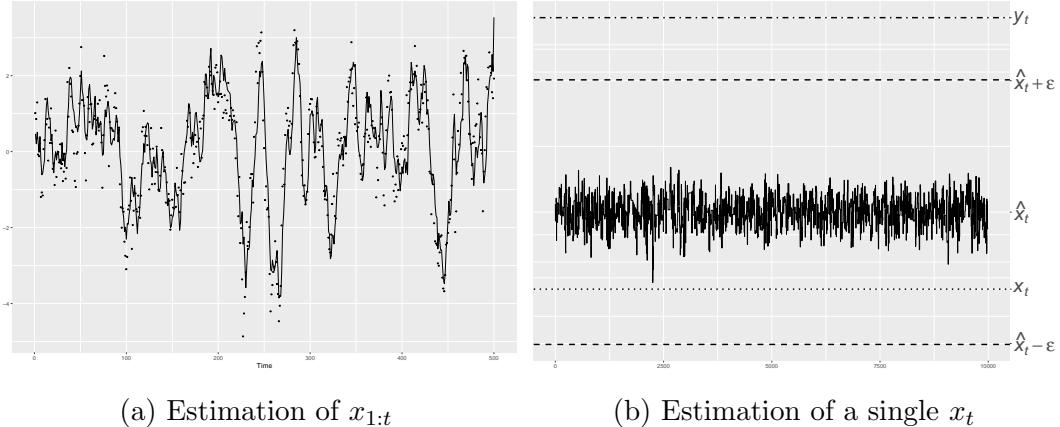


Figure 5.4: Linear simulation of  $x_{1:t}$  and single  $x_t$ . In figure 5.4a, the dots is the true  $x_{1:t}$  and the solid line is the estimation  $\hat{x}_{1:t}$ . In figure 5.4b, the estimation  $\hat{x}_t$  is very close to the true  $x$ . In fact, the true  $x$  falls in the interval  $[\hat{x} - \varepsilon, \hat{x} + \varepsilon]$ .

### 5.4.2 Simulation on Irregularly Sampled Time Series Data

Irregularly sampled time series data is painful for scientists and researchers. In spatial data analysis, several satellites and buoy networks provide continuous observations of wind speed, sea surface temperature, ocean currents, etc. However, data was

recorded with irregular time-step, with generally several data each day but also sometimes gaps of several days without any data. Tandeo *et al.* (2011) adopt a continuous-time state-space model to analyze this kind of irregular time-step data, in which the state is supposed to be an Ornstein-Uhlenbeck process.

The OU process is an adaptation of Brownian Motion, which models the movement of a free particle through a liquid and was first developed by Einstein (1956). By considering the velocity  $u_t$  of a Brownian motion at time  $t$ , over a small time interval, two factors affect the change in velocity: the frictional resistance of the surrounding medium whose effect is proportional to  $u_t$  and the random impact of neighboring particles whose effect can be represented by a standard Wiener process. Thus, because mass times velocity equals force, the process in a differential equation form is

$$mdu_t = -\omega u_t dt + dW_t,$$

where  $\omega > 0$  is called the friction coefficient and  $m > 0$  is the mass. If we define  $\gamma = \omega/m$  and  $\lambda = 1/m$ , we obtain the OU process (Vaughan, 2015), which was first introduced with the following differential equation:

$$du_t = -\gamma u_t dt + \lambda dW_t.$$

The OU process is used to describe the velocity of a particle in a fluid and is encountered in statistical mechanics. It is the model of choice for random movement toward a concentration point. It is sometimes called a continuous-time Gauss Markov process, where a Gauss Markov process is a stochastic process that satisfies the requirements for both a Gaussian process and a Markov process. Because a Wiener process is both a Gaussian process and a Markov process, in addition to being a stationary independent increment process, it can be considered a Gauss-Markov process with independent increments (Kijima, 1997).

To apply OU process on irregular sampling data, we assume that the latent process  $\{x_{1:t}\}$  is a simple OU process, that is a stationary solution of the following stochastic differential equation :

$$dx_t = -\gamma x_t dt + \lambda dW_t, \quad (5.41)$$

where  $W_t$  is a standard Brownian motion,  $\gamma > 0$  represents the slowly evolving transfer between two neighbor data and  $\lambda$  is the forward transition variability. It is not hard to find the solution of equation (5.41) is

$$x_t = x_{t-1} e^{-\gamma t} + \int_0^t \lambda e^{-\gamma(t-s)} dW_s.$$

For any arbitrary time step  $t$ , the general form of the process satisfies

$$x_t = x_{t-1} e^{-\gamma \Delta t} + \tau, \quad (5.42)$$

where  $\Delta_t = T_t - T_{t-1}$  is the time difference between two consecutive data points,  $\tau$  is a Gaussian white noise with mean zero and variances  $\frac{\lambda^2}{2\gamma} (1 - e^{-2\gamma\Delta_t})$ .

The observed  $y_{1:t}$  is measured by

$$y_t = Hx_t + \varepsilon, \quad (5.43)$$

where  $\varepsilon \sim N(0, \sigma)$  is a Gaussian white noise.

To run simulations, we firstly generate irregular time lag sequence  $\{\Delta_t\}$  from an *Inverse Gamma* distribution with parameters  $\alpha = 2, \beta = 0.1$ . Then, the following parameters were chosen for the numerical simulation:  $\gamma = 0.5, \lambda^2 = 0.1, \sigma^2 = 1$ .

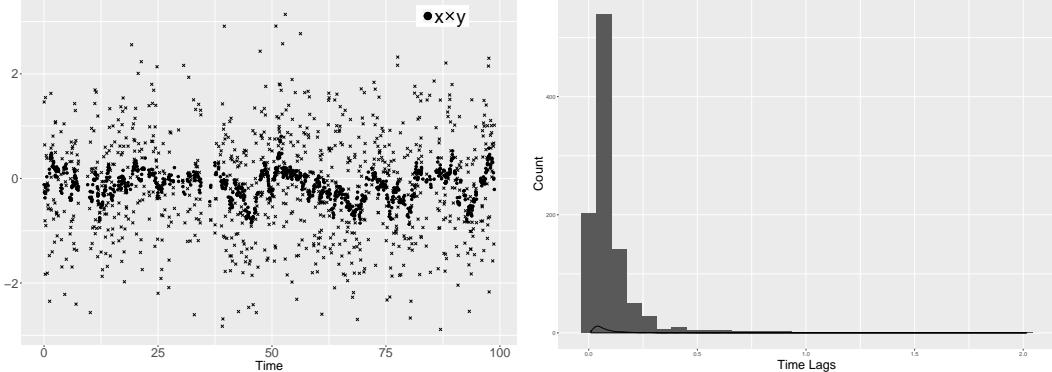


Figure 5.5: Simulated data. The solid dots indicate the true state  $x$  and cross dots indicate observation  $y$ . Irregular time lag  $\Delta_t$  are generated from  $\text{Inverse Gamma}(2,0.1)$  distribution.

Similarly, we can get the joint distribution for  $x_{0:t}$  and  $y_{1:t}$

$$\begin{bmatrix} x \\ y \end{bmatrix} \Big| \theta \sim N(0, \Sigma),$$

from the precision matrix

$$\begin{bmatrix} \frac{1}{L^2} + \frac{\phi_1^2}{\tau_1^2} & \frac{-\phi_1}{\tau_1^2} & \cdots & 0 & 0 & 0 & \cdots & 0 \\ \frac{-\phi_1}{\tau_1^2} & \frac{1}{\tau_1^2} + \frac{\phi_2^2}{\tau_2^2} + \frac{1}{\sigma^2} & \cdots & 0 & -\frac{1}{\sigma^2} & 0 & \cdots & 0 \\ 0 & \frac{-\phi_2}{\tau_2^2} & \cdots & 0 & 0 & -\frac{1}{\sigma^2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{1}{\tau_t^2} + \frac{1}{\sigma^2} & 0 & 0 & \cdots & -\frac{1}{\sigma^2} \\ 0 & -\frac{1}{\sigma^2} & \cdots & 0 & \frac{1}{\sigma^2} & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 0 & \frac{1}{\sigma^2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -\frac{1}{\sigma^2} & 0 & 0 & \cdots & \frac{1}{\sigma^2} \end{bmatrix}$$

where  $\phi_t = e^{-\gamma\Delta_t}$ ,  $\tau_t^2 = \frac{\lambda^2}{2\gamma} (1 - e^{-2\gamma\Delta_t})$ ,  $\theta$  represents unknown parameters. Denoted by  $\Sigma^{-1} = \begin{bmatrix} A_t & -B_t \\ -B_t & B_t \end{bmatrix}$ , covariance matrix is

$$\Sigma = \begin{bmatrix} (A_t - B_t)^{-1} & (A_t - B_t)^{-1} \\ (A_t - B_t)^{-1} & (I - A_t^{-1}B_t)^{-1} B_t^{-1} \end{bmatrix} \triangleq \begin{bmatrix} \Sigma_{XX} & \Sigma_{XY} \\ \Sigma_{YX} & \Sigma_{YY} \end{bmatrix}, \quad (5.44)$$

where  $B_t$  is a  $t \times t$  diagonal matrix with elements  $\frac{1}{\sigma^2}$ . The covariance matrices  $\Sigma_{XX} = (A_t - B_t)^{-1}$  and  $\Sigma_{YY} = (I - A_t^{-1}B_t)^{-1} B_t^{-1}$ .

## Parameter Estimation

To use the Algorithm 5.1, similarly with Section 5.2.1, we firstly need to find the posterior distribution of  $\theta$  with observations  $y_{1:t}$ , which in fact is

$$p(\theta | Y) \propto p(Y | \theta)p(\theta) \propto \exp\left(-\frac{1}{2}Y\Sigma_{YY}^{-1}Y\right)\sqrt{\det\Sigma_{YY}^{-1}}p(\theta).$$

By taking natural logarithm on the posterior of  $\theta$  and using the useful solutions in equations (5.7) and (5.8), we have

$$\ln L(\theta) = -\frac{1}{2}Y^\top\Sigma_{YY}^{-1}Y + \frac{1}{2}\sum \ln \text{tr}(B) - \sum \ln \text{tr}(L) + \sum \ln \text{tr}(R) + \ln p(\theta). \quad (5.45)$$

Because of all parameters are positive, we are estimating  $\nu_1 = \ln \lambda$ ,  $\nu_2 = \ln \gamma^2$  and  $\nu_3 = \ln \sigma^2$  instead. When the estimation process is done, we can transform them back to the original scale by taking exponential.

After running the whole process, it gives us the best estimation of  $\hat{\theta}$  is  $\{\gamma = 0.4841, \lambda^2 = 0.1032, \sigma^2 = 0.9276\}$ . In figure 5.6, we can see that the  $\theta$  chains are skew to the true value with tails.

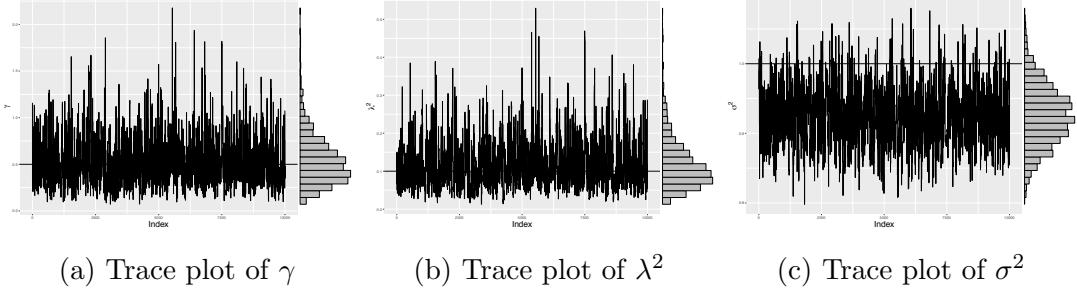


Figure 5.6: Irregular time step OU process simulation. The estimation of  $\hat{\theta}$  is  $\{\gamma = 0.4841, \lambda^2 = 0.1032, \sigma^2 = 0.9276\}$ . In the plots, the horizontal dark lines are the true  $\theta$ .

### Recursive Calculation and State Estimation

Follow the procedure in Section 5.2.2 and do similar calculation with Section 5.4.1, one can find a recursive way to update  $K_t$  and  $b_{t-1}$ , which are

$$K_t = \frac{\sigma^4}{\tau_t^2 + \sigma^2 + \phi_t^2(\sigma^2 - K_{t-1})}, \quad (5.46)$$

$$b_t = \begin{bmatrix} \frac{b_{t-1}\phi_t K_t}{\sigma^2} \\ \frac{K_t(\sigma^2 + \tau_t^2) - \sigma^4}{\phi_t \sigma^2} \end{bmatrix}. \quad (5.47)$$

With the above formula, the recursive way of updating the mean and covariance are

$$\bar{\mu}_t = \frac{\phi_t}{\sigma^2} K_{t-1} \bar{\mu}_{t-1} + \phi_t \left( 1 - \frac{K_{t-1}}{\sigma^2} \right) y_{t-1}, \quad (5.48)$$

$$\bar{\Sigma}_t = \sigma^4 K_t^{-1}, \quad (5.49)$$

where  $K_1 = \frac{\sigma^4}{\sigma^2 + \tau_1^2 + L^2 \phi_1^2}$ .

Additionally, as introduced in Section 5.2.3, the best estimation of  $x_{1:t}$  with a given  $\theta$  is

$$\hat{x}_{1:t} \mid y_{1:t}, \theta \sim N(L^{-\top} W, L^{-\top} L^{-1}),$$

where  $W = L^{-1} B_t y_{1:t-1}$ , and the mixture Gaussian distribution for  $p(x_t \mid y_{1:t})$  is

$$\mu_t^{(x)} = \frac{1}{N} \sum_i \mu_{ti}^{(x)} \quad (5.50)$$

$$\text{Var}(x_t) = \frac{1}{N} \sum_i \left( \mu_{ti}^{(x)} \mu_{ti}^{(x)\top} + \text{Var}(x_{ti}) \right) - \frac{1}{N^2} \left( \sum_i \mu_{ti}^{(x)} \right) \left( \sum_i \mu_{ti}^{(x)} \right)^{\top}, \quad (5.51)$$

The same as we did in Section 5.4.1, for any given  $\theta$ , we have  $\hat{x}_t \mid y_{1:t}, \theta \sim N\left(\mu_t^{(x)}, \text{Var}(x_t)\right)$ , where

$$\mu_t^{(x)} = \frac{K_t \bar{\mu}_t}{\sigma^2} + \left(1 - \frac{K_t}{\sigma^2}\right) y_t$$

$$\text{Var}(x_t) = \sigma^2 - K_t.$$

By substituting them into the equation (5.37) and (5.38), the estimated  $\hat{x}_t$  is easily got. The difference at this time is the  $\mu_t^{(x)}$  and  $\text{Var}(x_t)$  are dependent on time lag  $\Delta_t$ , that can be seen from formula (5.46) and (5.48).

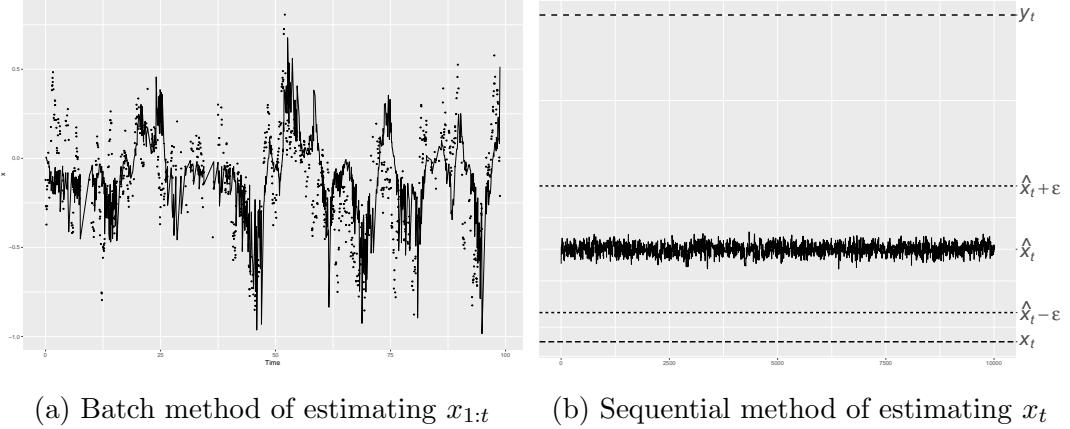


Figure 5.7: Irregular time step OU process simulation of  $x_{1:t}$  and sole  $x_t$ . In figure 5.7a, the dots is the true  $x_{1:t}$  and the solid line is the estimation  $\hat{x}_{1:t}$ . In figure 5.7b, the chain in solid line is the estimation  $\hat{x}_t$ ; dotted line is the true value of  $x$ ; dot-dash line on top is the observed value of  $y$ ; dashed lines are the estimated error.

## 5.5 High Dimensional Ornstein-Uhlenbeck Process Application

Tractors moving on an orchard are mounted with GPS units, which are recording data and transfer to the remote server. This data infers longitude, latitude, bearing, etc, with unevenly spaced time mark. However, one dimensional OU process containing either only position or velocity is not enough to infer a complex movement.

Therefore, in this section, we are introducing an Ornstein-Uhlenbeck process (OU-process) model combining both position and velocity with the following equations

$$\begin{cases} du_t = -\gamma u_t dt + \lambda dW_t, \\ dx_t = u_t dt + \xi dW'_t. \end{cases} \quad (5.52)$$

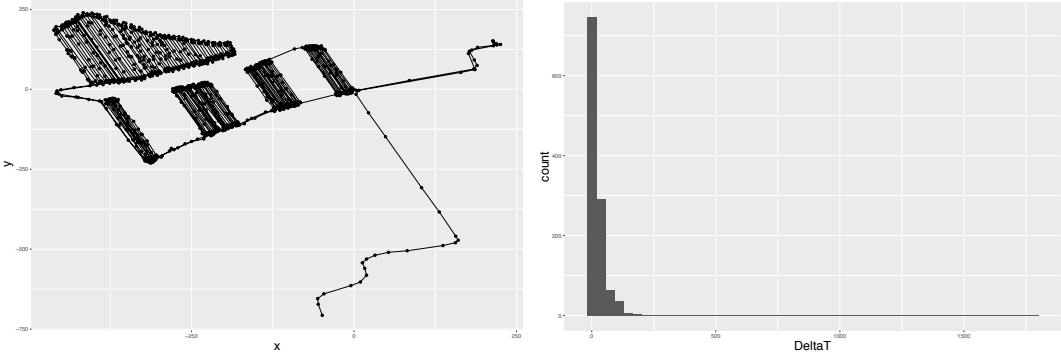


Figure 5.8: The trajectory of a moving tractor. The time lags (right side figure) obtained from GPS units are irregular.

The solution can be found by integrating  $dt$  out, that gives us

$$\begin{cases} u_t = u_{t-1} e^{-\gamma t} + \int_0^t \lambda e^{-\gamma(t-s)} dW_s, \\ x_t = x_{t-1} + \frac{u_{t-1}}{\gamma} (1 - e^{-\gamma t}) + \int_0^t \frac{\lambda}{\gamma} e^{\gamma s} (1 - e^{-\gamma t}) dW_s + \int_0^t \xi dW'_s. \end{cases} \quad (5.53)$$

As a result, the joint distribution is

$$\begin{bmatrix} x_t \\ u_t \end{bmatrix} \sim N \left( \begin{bmatrix} \mu_t^{(x)} \\ \mu_t^{(u)} \end{bmatrix}, \begin{bmatrix} \sigma_t^{(x)2} & \rho_t \sigma_t^{(x)} \sigma_t^{(u)} \\ \rho_t \sigma_t^{(x)} \sigma_t^{(u)} & \sigma_t^{(u)2} \end{bmatrix} \right), \quad (5.54)$$

where  $\mu_t^{(x)}$  and  $\mu_t^{(u)}$  are from the forward map process

$$\begin{bmatrix} \mu_t^{(x)} \\ \mu_t^{(u)} \end{bmatrix} = \begin{bmatrix} 1 & \frac{1-e^{-\gamma\Delta_t}}{\gamma} \\ 0 & e^{-\gamma\Delta_t} \end{bmatrix} \begin{bmatrix} x_{t-1}^{(x)} \\ u_{t-1} \end{bmatrix} \triangleq \Phi \begin{bmatrix} x_{t-1}^{(x)} \\ u_{t-1} \end{bmatrix}, \quad (5.55)$$

and

$$\begin{cases} \sigma_t^{(x)2} &= \frac{\lambda^2 (e^{2\gamma\Delta_t} - 1) (1 - e^{-\gamma\Delta_t})^2}{2\gamma^3} + \xi^2 \Delta_t \\ \sigma_t^{(u)2} &= \frac{\lambda^2 (1 - e^{-2\gamma\Delta_t})}{2\gamma} \\ \rho_t \sigma_t^{(x)} \sigma_t^{(u)} &= \frac{\lambda^2 (e^{\gamma\Delta_t} - 1) (1 - e^{-2\gamma\Delta_t})}{2\gamma^2} \end{cases}$$

In the above equations  $\Delta_t = T_t - T_{t-1}$  and initial values are  $\Delta_1 = 0$ ,  $x_0 \sim N(0, L_x^2)$ ,  $u_0 \sim N(0, L_u^2)$ ,  $\rho_t^2 = 1 - \frac{\xi^2 \Delta_t}{\sigma_t^{(x)2}}$ . To be useful, we are using  $\frac{1}{1 - \rho_t^2} = \frac{\sigma_t^{(x)2}}{\xi^2 \Delta_t}$  instead in the calculation.

Furthermore, the independent observation process is

$$\begin{cases} y_t = x_t + \varepsilon_t, \\ v_t = u_t + \varepsilon'_t, \end{cases} \quad (5.56)$$

where  $\varepsilon_t \sim N(0, \sigma)$ ,  $\varepsilon'_t \sim N(0, \tau)$  are normally distributed independent errors. Thus, the joint distribution of observations is

$$\begin{bmatrix} y_t \\ v_t \end{bmatrix} \sim N \left( \begin{bmatrix} x_t \\ u_t \end{bmatrix}, \begin{bmatrix} \sigma^2 & 0 \\ 0 & \tau^2 \end{bmatrix} \right). \quad (5.57)$$

Consequently, the parameter  $\theta$  of an entire Ornstein-Uhlenbeck process is a set of five parameters from both hidden status and observation process, which is represented as  $\theta = \{\gamma, \xi^2, \lambda^2, \sigma^2, \tau^2\}$ .

Starting from the joint distribution of  $x_{0:t}, u_{0:t}$  and  $y_{1:t}, v_{1:t}$  by given  $\theta$ , it can be found that

$$\begin{bmatrix} \tilde{X} \\ \tilde{Y} \end{bmatrix} \mid \theta \sim N \left( 0, \tilde{\Sigma} \right), \quad (5.58)$$

where  $\tilde{X}$  represents for the hidden statuses  $\{x, u\}$ ,  $\tilde{Y}$  represents for observed  $\{y, v\}$ ,  $\theta$  is the set of five parameters. The inverse of the covariance matrix  $\tilde{\Sigma}^{-1}$  is the precision matrix in the form of

$$\tilde{\Sigma}^{-1} = \begin{bmatrix} Q_{xx} & Q_{xu} & -\frac{1}{\sigma^2} I & 0 \\ Q_{ux} & Q_{uu} & 0 & -\frac{1}{\tau^2} I \\ -\frac{1}{\sigma^2} I & 0 & \frac{1}{\sigma^2} I & 0 \\ 0 & -\frac{1}{\tau^2} I & 0 & \frac{1}{\tau^2} I \end{bmatrix}.$$

To make the covariance matrix a more beautiful form and convenient computing,  $\tilde{X}, \tilde{Y}$  and  $\tilde{\Sigma}$  can be rearranged in a time series order, that makes  $X_{1:t} = \{x_1, u_1, x_2, u_2, \dots, x_t, u_t\}$ ,  $Y_{1:t} = \{y_1, v_1, y_2, v_2, \dots, y_t, v_t\}$  and the new precision matrix  $\Sigma^{-1}$  looks like

$$\begin{aligned} \Sigma^{-1} &= \begin{bmatrix} \sigma_{11}^{(x)2} + \frac{1}{\sigma^2} & \sigma_{11}^{(xu)2} & \dots & \sigma_{1t}^{(x)2} & \sigma_{1t}^{(xu)2} & -\frac{1}{\sigma^2} & 0 & \dots & 0 & 0 \\ \sigma_{11}^{(ux)2} & \sigma_{11}^{(u)2} + \frac{1}{\tau^2} & \dots & \sigma_{1t}^{(ux)2} & \sigma_{1t}^{(x)2} & 0 & -\frac{1}{\tau^2} & \dots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ \sigma_{t1}^{(x)2} & \sigma_{t1}^{(xu)2} & \dots & \sigma_{tt}^{(x)2} + \frac{1}{\sigma^2} & \sigma_{tt}^{(xu)2} & 0 & 0 & \dots & -\frac{1}{\sigma^2} & 0 \\ \sigma_{t1}^{(ux)2} & \sigma_{t1}^{(u)2} & \dots & \sigma_{tt}^{(ux)2} & \sigma_{tt}^{(u)2} + \frac{1}{\tau^2} & 0 & 0 & \dots & 0 & -\frac{1}{\tau^2} \\ -\frac{1}{\sigma^2} & 0 & \dots & 0 & 0 & \frac{1}{\sigma^2} & 0 & \dots & 0 & 0 \\ 0 & -\frac{1}{\tau^2} & \dots & 0 & 0 & 0 & \frac{1}{\tau^2} & \dots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \dots & -\frac{1}{\sigma^2} & 0 & 0 & 0 & \dots & \frac{1}{\sigma^2} & 0 \\ 0 & 0 & \dots & 0 & -\frac{1}{\tau^2} & 0 & 0 & \dots & 0 & \frac{1}{\tau^2} \end{bmatrix} \\ &\triangleq \begin{bmatrix} A_t & -B_t \\ -B_t^\top & B_t \end{bmatrix}, \end{aligned}$$

where  $B_t$  is a  $2t \times 2t$  diagonal matrix of observation errors at time  $t$  in the form of

$$\begin{bmatrix} \frac{1}{\sigma^2} & \cdot & \cdot & \cdot & \cdot \\ \cdot & \frac{1}{\tau^2} & \cdot & \cdot & \cdot \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ \cdot & \cdot & \cdot & \frac{1}{\sigma^2} & \cdot \\ \cdot & \cdot & \cdot & \cdot & \frac{1}{\tau^2} \end{bmatrix}.$$

In fact, the matrix  $A_t$  is a  $2t \times 2t$  bandwidth six sparse matrix at time  $t$  in the process. For sake of simplicity, we are using  $A$  and  $B$  to represent the matrices  $A_t$  and  $B_t$  here. Then, we may find the covariance matrix by calculating the inverse of the precision matrix as

$$\begin{aligned} \Sigma &= \begin{bmatrix} (A - B^\top B^{-1}B)^{-1} & -(A - B^\top B^{-1}B)^{-1} B^\top B^{-1} \\ -B^{-1}B (A - B^\top B^{-1}B)^{-1} & (B - B^\top A^{-1}B)^{-1} \end{bmatrix} \\ &= \begin{bmatrix} (A - B)^{-1} & (A - B)^{-1} \\ (A - B)^{-1} & (I - A^{-1}B)^{-1} B^{-1} \end{bmatrix} \\ &\triangleq \begin{bmatrix} \Sigma_{XX} & \Sigma_{XY} \\ \Sigma_{YX} & \Sigma_{YY} \end{bmatrix}. \end{aligned}$$

A detailed structure of the covariance matrix  $\Sigma_{XX}$  is presented in Appendix B.3.

### 5.5.1 Approximation of The Parameter Posterior

To find the log-posterior distribution of  $X_{1:t}$  and  $Y_{1:t}$ , we start from the joint distribution. Similarly, the inverse of the covariance matrix is

$$\Sigma_{YY}^{-1} = B(I - A^{-1}B) = BA^{-1}\Sigma_{XX}^{-1}.$$

By using Choleski decomposition and similar technical solution, second term in the integrated objective function is

$$p(\theta | Y) \propto p(Y | \theta)p(\theta) \propto \exp\left(-\frac{1}{2}Y\Sigma_{YY}^{-1}Y\right) \sqrt{\det \Sigma_{YY}^{-1}} P(\theta).$$

Then, by taking natural logarithm on the posterior of  $\theta$  and using the useful solutions in equations (5.7) and (5.8), we will have

$$\ln L(\theta) = -\frac{1}{2}Y^\top \Sigma_{YY}^{-1}Y + \frac{1}{2} \sum \ln \text{tr}(B) - \sum \ln \text{tr}(L) + \sum \ln \text{tr}(R). \quad (5.59)$$

### 5.5.2 The Forecast Distribution

It is known that

$$\begin{aligned} p(Y_{1:t-1}, \theta) &\sim N\left(0, \Sigma_{YY}^{(t-1)}\right) \\ p(Y_t, Y_{1:t-1}, \theta) &\sim N\left(0, \Sigma_{YY}^{(t)}\right) \\ p(Y_t | Y_{1:t}, \theta) &\sim N(\bar{\mu}_t, \bar{\Sigma}_t) \end{aligned}$$

where the covariance matrix of the joint distribution is  $\Sigma_{YY}^{(t)} = (I_t - A_t^{-1}B_t)^{-1}B_t^{-1}$ .

Then, by taking its inverse, we will get

$$\Sigma_{YY}^{(t)(-1)} = B_t(I_t - A_t^{-1}B_t).$$

To be clear, the matrix  $B_t$  is short for the matrix  $B_t(\sigma^2, \tau^2)$ , which is  $2t \times 2t$  diagonal matrix with elements  $\frac{1}{\sigma^2}, \frac{1}{\tau^2}$  repeating for  $t$  times on its diagonal. For instance, the very simple  $B_1(\sigma^2, \tau^2) = \begin{bmatrix} \frac{1}{\sigma^2} & 0 \\ 0 & \frac{1}{\tau^2} \end{bmatrix}_{2 \times 2}$  is a  $2 \times 2$  matrix.

Because of  $A_t$  is symmetric and invertible,  $B_t$  is the diagonal matrix defined as above, therefore they have the following property

$$\begin{aligned} A_t B &= A_t^\top B_t^\top = (B_t A_t)^\top, \\ A_t^{-1} B_t &= A_t^{-\top} B_t^\top = (B_t A_t^{-1})^\top. \end{aligned}$$

Followed up the form of  $\Sigma_{YY}^{(t)(-1)}$ , we can define that

$$\Sigma_{YY}^{(t)(-1)} \triangleq \begin{bmatrix} B_{t-1} & 0 \\ 0 & B_1 \end{bmatrix} \begin{bmatrix} Z_t & b_t \\ b_t^\top & K_t \end{bmatrix} \begin{bmatrix} B_{t-1} & 0 \\ 0 & B_1 \end{bmatrix}$$

where  $Z_t$  is a  $2t \times 2t$  matrix,  $b_t$  is a  $2t \times 2$  matrix and  $K_t$  is a  $2 \times 2$  matrix. Thus, by taking its inverse again, we will get

$$\Sigma_{YY}^{(t)} = \begin{bmatrix} B_{t-1}^{-1} (Z_t - b_t K_t^{-1} b_t^\top)^{-1} B_{t-1}^{-1} & -B_{t-1}^{-1} Z_t^{-1} b_t (K_t - b_t^\top Z_t^{-1} b_t)^{-1} B_1^{-1} \\ -B_1^{-1} K_t^{-1} b_t^\top (Z_t - b_t K_t^{-1} b_t^\top)^{-1} B_{t-1}^{-1} & B_1^{-1} (K_t - b_t^\top Z_t^{-1} b_t)^{-1} B_1^{-1} \end{bmatrix}.$$

It is easy to find the relationship between  $A_t$  and  $A_t$  in the Sherman-Morrison-Woodbury form, which is

$$A_t = \begin{bmatrix} A_{t-1} & \cdot & \cdot \\ \cdot & \frac{1}{\sigma^2} & \cdot \\ \cdot & \cdot & \frac{1}{\tau^2} \end{bmatrix} + U_t U_t^\top \triangleq M_t + U_t U_t^\top,$$

where, in fact,  $M_t = \begin{bmatrix} A_{t-1} & \cdot & \cdot \\ \cdot & \frac{1}{\sigma^2} & \cdot \\ \cdot & \cdot & \frac{1}{\tau^2} \end{bmatrix} = \begin{bmatrix} A_{t-1} & 0 \\ 0 & B_1 \end{bmatrix}$  and its inverse is  $M_t^{-1} = \begin{bmatrix} A_{t-1}^{-1} & 0 \\ 0 & B_1^{-1} \end{bmatrix}$ .

We may use Sherman-Morrison-Woodbury formula to find the inverse of  $A_t$  in a recursive way, which is

$$A_t^{-1} = (M_t + U_t U_t^\top)^{-1} = M_t^{-1} - M_t^{-1} U_t (I + U_t^\top M_t^{-1} U_t)^{-1} U_t^\top M_t^{-1}. \quad (5.60)$$

Consequently, with some calculations, we will get

$$K_t = B_1^{-1} D_t (I + S_t^\top (B_1^{-1} - K_{t-1}) S_t + D_t^\top B_1^{-1} D_t)^{-1} D_t^\top B_1^{-1}, \quad (5.61)$$

and

$$b_t = \begin{bmatrix} -b_{t-1} \\ B_1^{-1} - K_{t-1} \end{bmatrix} S_t (I + S_t^\top (B_1^{-1} - K_{t-1}) S_t + D_t^\top B_1^{-1} D_t)^{-1} D_t^\top B_1^{-1},$$

that are updating in a recursive way. As a result, one can achieve the following recursive updating formula for the mean and covariance matrix

$$\begin{aligned} \bar{\mu}_t &= \Phi_t K_{t-1} B_1 \bar{\mu}_{t-1} + \Phi_t (I - K_{t-1} B_1) Y_{t-1} \\ \bar{\Sigma}_t &= (B_1 K_t B_1)^{-1} \end{aligned} \quad (5.62)$$

The matrix  $K_t$  is updated via equation (5.61), or updating its inverse in the following form makes the computation faster, that is

$$\begin{aligned} K_t^{-1} &= B_1 D_t^{-\top} D_t^{-1} B_1 + B_1 \Phi_t (B_1^{-1} - K_{t-1}) \Phi_t^\top B_1 + B_1, \\ \bar{\Sigma}_t &= D_t^{-\top} D_t^{-1} + \Phi_t (B_1^{-1} - K_{t-1}) \Phi_t^\top + B_1^{-1} \end{aligned}$$

and  $K_1 = B_1^{-1} - A_1^{-1} = \begin{bmatrix} \frac{\sigma^4}{\sigma^2 + L_x^2} & 0 \\ 0 & \frac{\tau^4}{\tau^2 + L_u^2} \end{bmatrix}$ . For calculation details, readers can refer to Appendix B.2.

### 5.5.3 The Estimation Distribution

Because of the joint distribution (5.58), one can find the best estimation with a given  $\theta$  by

$$X_{1:t} | Y_{1:t}, \theta \sim N(L^{-\top} W, L^{-\top} L^{-1}),$$

thus

$$\hat{X}_{1:t} = L^{-\top} (W + Z),$$

where  $Z \sim N(0, I(\sigma, \tau))$ .

For  $X_t$ , the joint distribution with  $Y_{1:t}$  updated to time  $t$  is

$$X_t, Y_{1:t} \mid \theta \sim N\left(0, \begin{bmatrix} C_t^\top (A_t - B_t)^{-1} C_t & C_t^\top (A_t - B_t)^{-1} \\ (A_t - B_t)^{-1} C_t & (I - A_t^{-1} B_t)^{-1} B_t^{-1} \end{bmatrix}\right),$$

where  $C_t^\top = \begin{bmatrix} 0 & \cdots & 0 & 1 & 0 \\ 0 & \cdots & 0 & 0 & 1 \end{bmatrix}$ . Thus,

$$X_t \mid Y_{1:t}, \theta \sim N\left(\mu_t^{(X)}, \Sigma_t^{(X)}\right),$$

where

$$\begin{aligned} \mu_t^{(X)} &= C_t^\top A^{-1} B Y = C_t^\top L^{-\top} W, \\ \Sigma_t^{(X)} &= C_t^\top A^{-1} C_t = U_t^\top U_t, \end{aligned}$$

and  $U_t = L^{-1} C_t$ . The recursive updating formula is

$$\mu_t^{(X)} = K_t B_1 \bar{\mu}_t + (I - B_1 K_t) Y_t \quad (5.63)$$

$$\Sigma_t^{(X)} = B_1^{-1} - K_t. \quad (5.64)$$

#### 5.5.4 Prior Distribution for Parameter

The well known Hierarchical Linear Model, where the parameters vary at more than one level, was firstly introduced by Lindley and Smith (1972); Smith (1973). Hierarchical Model can be used on data with many levels, although 2-level models are the most common ones. The state-space model in equations (5.1) and (5.2) is one of Hierarchical Linear Model if  $G_t$  and  $F_t$  are linear, and non-linear model if  $G_t$  and  $F_t$  are non-linear processes. Researchers have made a few discussions and work on these both linear and non-linear models. In this section, we only discuss on the prior for parameters in these models.

Various informative and non-informative prior distributions have been suggested for scale parameters in hierarchical models. Gelman *et al.* (2006) give a discussion on prior distributions for variance parameters in hierarchical models. General considerations include using invariance (Jeffries, 1961), maximum entropy (Jaynes, 1983) and agreement with classical estimators (Box and Tiao, 2011). Regarding informative priors, the author suggests to distinguish them into three categories: (i) is traditional informative prior. A prior distribution giving numerical information is crucial to statistical modeling and it can be found from a literature review, an earlier data analysis

or the property of the model itself. (ii) is weakly informative prior. This genre prior is not supplying any controversial information but are strong enough to pull the data away from inappropriate inferences that are consistent with the likelihood. Some examples and brief discussions of weakly informative priors for logistic regression models are given in (Gelman *et al.*, 2008). (iii) is uniform prior, which allows the information from the likelihood to be interpreted probabilistically.

Stroud and Bengtsson (2007) discuss a model with different structures in the errors. The two errors  $\omega_t$  and  $\varepsilon_t$  are assumed normally distributed as

$$\begin{aligned}\omega_t &\sim N(0, \alpha Q), \\ \varepsilon_t &\sim N(0, \alpha R),\end{aligned}$$

where the two matrices  $R$  and  $Q$  are known and  $\alpha$  is an unknown scale factor to be estimated. (Note that a perfect model is obtained by setting  $Q = 0$ .) Therefore, the density of the Gaussian state-space model becomes

$$\begin{aligned}p(y_t | x_t, \alpha) &= N(F(x_t), \alpha R), \\ p(x_t | x_{t-1}, \alpha) &= N(G(x_{t-1}), \alpha Q).\end{aligned}$$

The parameter  $\alpha$  is assumed *Inverse Gamma* distribution.

For the priors of all the parameters in OU-process, shown in equation (5.52) and (5.56), firstly we should understand what meanings of these parameters are standing for. The reciprocal of  $\gamma$  is typical velocity falling in the reasonable range of 0.1 to 100  $m/s$ .  $\xi$  is the error occurs in transition process,  $\sigma$  and  $\tau$  are errors in the forward map for position and velocity respectively. Generally, the error is a positive finite number. Considering prior distributions for these parameters, before looking at the data, we have an idea of ranges where these parameters are falling in. Conversely, we do not have any assumptions about the true value of  $\lambda$ , which means it could be anywhere. According to this assumption, the prior distributions are

$$\begin{aligned}\gamma &\sim IG(10, 0.5), \\ \xi^2 &\sim IG(5, 2.5), \\ \sigma^2 &\sim IG(5, 2.5),\end{aligned}$$

where  $IG(\alpha, \beta)$  represents the *Inverse Gamma* distribution with two parameters  $\alpha$  and  $\beta$ .

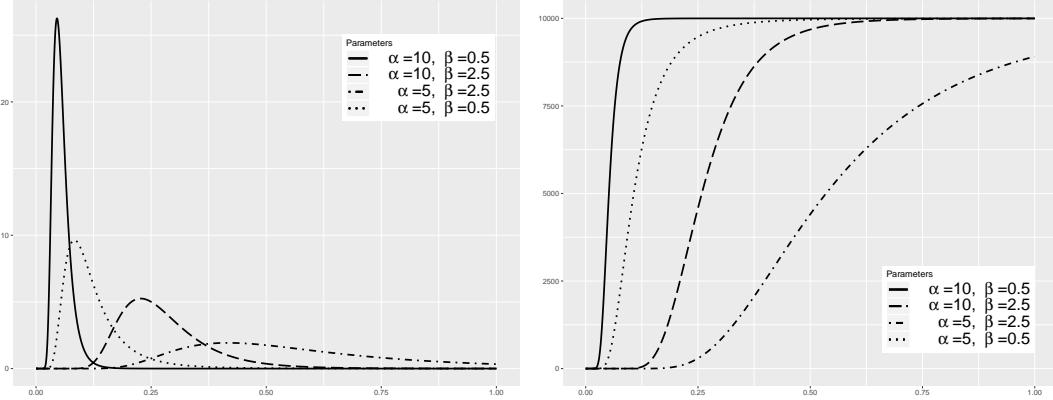


Figure 5.9: Probability density function and cumulative distribution function of *Inverse Gamma* with two parameters  $\alpha$  and  $\beta$ .

### 5.5.5 Efficiency of Delayed-Acceptance Metropolis-Hastings Algorithm

We have discussed the efficiency of Metropolis-Hastings (MH) algorithm and how it is affected by the step size. To explain it explicitly, here we give an example comparing Eff, EffUT, ESS and ESSUT, which are calculated by using the same dataset and running 10 000 iterations of DA MH. We are taking a sequence from 0.1 to 4 with equal-space of 0.3, so that  $s = \{0.1, \dots, 4\}$ , and to solve criterion formula with each of the value. Table 5.1 and figure 5.10 show the compares the results of the calculation.

The best step size found by Eff is 1, which is as the same as that found by ESS. By using  $s = 1$  and running 1 000 iterations, the DA MH takes 36.35 seconds to get the Markov chain for  $\theta$  and the acceptance rates  $\alpha_1$  for approximating  $\hat{\pi}(\cdot)$  and  $\alpha_2$  for estimating the posterior distribution  $\pi(\cdot)$  are 0.3097 and 0.8324 respectively. By using EffUT and ESSUT, the best step size is 2.5, which is bigger. One of the advantages of using this step size is the significant decreasing of the computation time to 5.10 seconds. It is because the surrogate  $\hat{\pi}(\cdot)$  takes bad proposals out and only good ones are accepted to pass to the next level. It can be seen from the lower rates  $\alpha_1$  in table 5.1.

On the surface, a bigger step size causes lower acceptance rates  $\alpha_1$  and it might not be a smart choice. However, on the other hand, one should notice the less time cost. To make it sensible, we are running the DA MH with different step sizes, as presented in table 5.1, for the same (or similar) amount of time. Because of the bigger step size takes less time than smaller one, so we achieve a longer chain. To be more clear, we take 1 000 samples out from a longer chain, such as 8 500, and calculate Eff, EffUT,

Table 5.1: An example of Eff, EffUT, ESS and ESSUT found by running 10 000 iterations with same data. The computation time is measured in seconds  $s$ .

	Values	Time	Step Size	$\alpha_1$	$\alpha_2$
Eff	0.0515	36.35	1.0	0.3097	0.8324
EffUT	0.0031	5.10	2.5	0.0360	0.7861
ESS	501.4248	36.35	1.0	0.3097	0.8324
ESSUT	29.8912	5.10	2.5	0.0360	0.7861

ESS and ESSUT separately using the embedded function `IAT`, (Christen *et al.*, 2010), and `ESS` of the package `LaplaceDemon` in *R* and the above formulas . As we can see from the outcomes, by running the similar amount of time, the Markov chain using a bigger step size has a higher efficiency and effective sample size in unit time. More intuitively, the advantage of using larger step size is the sampling algorithm generates more representative samples per second. Figure B.1 is comparing different  $\theta$  chains found by using different step sizes but running the same amount of time. As we can see that  $\theta$  with the optimal step size has a lower correlated relationship.

Table 5.2: Comparing Eff, EffUT, ESS and ESSUT values using different step size. The 1000\* means taking 1 000 samples from a longer chain, like 1 000 out of 5 000 sample chain. The computation time is measured in seconds  $s$ .

Step Size	Length	Time	Eff	EffUT	ESS	ESSUT
1.0	1 000	3.48	0.0619	0.0178	69.4549	19.9583
1.3	1 400	3.40	0.0547	0.0161	75.3706	22.1678
	1 000*	3.40	0.0813	0.0239	72.5370	21.3344
2.2	5 000	3.31	0.0201	0.0061	96.6623	29.2031
	1 000*	3.31	0.0941	0.0284	94.2254	28.4669
2.5	7 000	3.62	0.0161	0.0044	112.3134	31.0258
	1 000*	3.62	<b>0.1095</b>	<b>0.0302</b>	<b>113.4063</b>	<b>31.3277</b>

### 5.5.6 A Sliding Window State and Parameter Estimation Approach

The length of data used in the algorithm really affects the computation time. The forecast distribution  $p(Y_t | Y_{1:t-1}, \theta)$  and estimation distribution  $p(X_t | Y_{1:t}, \theta)$  require

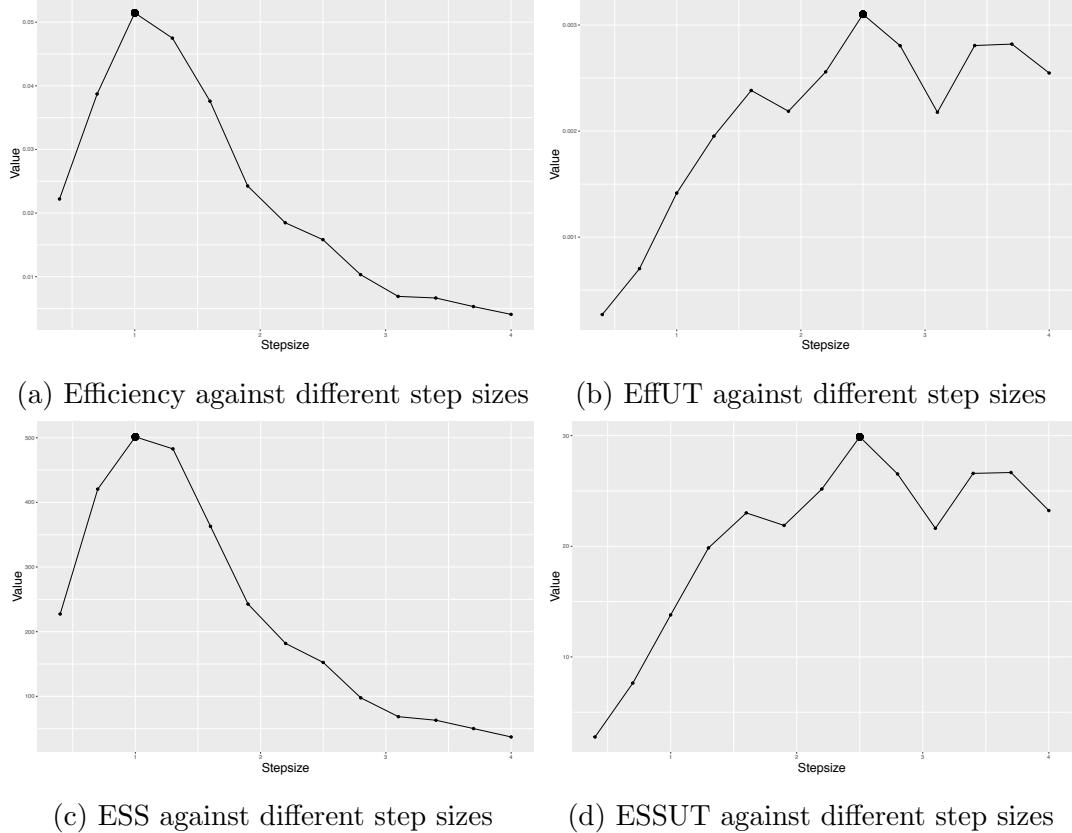


Figure 5.10: Influences of different step sizes on sampling efficiency (Eff), efficiency in unit time (EffUT), effective sample size (ESS) and effective sample size in unit time (ESSUT) found by using the same data

finding the inverse of the covariance  $\Sigma_{YY}^{(t+1)}$ , however, which is time consuming if the sample size is big to generate a large sparse matrix. For a moving vehicle, one is more willing to get the estimation and moving status instantly rather than being delayed. Therefore, a compromise solution is using fixed-length sliding window sequential filtering. A fixed-lag sequential parameter learning method was proposed by Polson *et al.* (2008) and named as *Practical Filtering*. The authors rely on the approximation of

$$p(x_{0:n-L}, \theta | y_{0:n-1}) \approx p(x_{0:n-L}, \theta | y_{0:n})$$

for large  $L$ . The new observations coming after the  $n$ th data has little influence on  $x_{0:n-L}$ .

Being inspired, we are not using the first 0 to  $n - 1$  date and ignoring the latest  $n$ th, but using all the latest with truncating the first few history ones. Suppose we are given a fixed-length  $L$ , up to time  $t$ , which should be greater than  $L$ , we are estimating  $x_t$  by using all the retrospective observations to the point at  $t - L + 1$ . In another

word, the estimation distribution for the current state is

$$p(X_t | Y_{t-L+1:t}, \theta), \quad (5.65)$$

where  $t > L$ . We name this method *Sliding Window Sequential Parameter Learning Filter*.

The next question is how to choose an appropriate  $L$ . The length of data used in MH and DA MH algorithms has an influence on the efficiency and accuracy of parameter learning and state estimation. Being tested on real data set, there is no doubt that the more data be in use, the more accurate the estimation is, and lower efficient is in computation. In table B.4, one can see the pattern of parameters  $\gamma, \xi, \tau$  follow the same trend with the choice of  $L$  and  $\sigma$  increases when  $L$  decreases. Since estimation bias is inevitable, we are indeed to keep the bias as small as possible, and in the meantime, the higher efficiency and larger effective sample size are bonus items. In figure 5.11, we can see that the efficiency and effective sample size is not varying along the sample size used in sampling algorithm, but in unit time, they are decreasing rapidly as data size increases. In addition, from a practical point of view, the observation error  $\sigma$  should be kept at a reasonable level, let's say  $50\text{cm}$ , and the computation time should be as less as possible. To reach that level,  $L = 100$  is an appropriate choice. For a one-dimensional linear model,  $L$  can be chosen larger and that does not change too much. If the data up to time  $t$  is less than or equal to the chosen  $L$ , the whole data set is used in learning  $\theta$  and estimating  $X_t$ .

For the true posterior, the algorithm requires a cheap estimation  $\hat{\pi}(\cdot)$ , which is found by one-variable-at-a-time Metropolis-Hastings algorithm. The advantage is getting a precise estimation of the parameter structure, and disadvantage is, obviously, lower efficiency. Luckily, we find that it is not necessary to run this MH every time when estimate a new state from  $x_{t-1}$  to  $x_t$ . In fact, in the DA MH process, the cheap  $\hat{\pi}$  does not vary too much in the filtering process with new data coming into the dataset. We may use this property in the algorithm. At first, we use all available data from 1 to  $t$  with length up to  $L$  to learn the structure of  $\theta$  and find out the cheap approximation  $\hat{\pi}$ . Then, use DA MH to estimate the true posterior  $\pi$  for  $\theta$  and  $x_t$ . After that, extend dataset to  $1 : t + 1$  if  $t \leq L$  or shift the data window to  $2 : t + 1$  if  $t > L$  and run DA MH again to estimate  $\theta$  and  $x_{t+1}$ . From figures B.3 and B.4, we can see that the main features and parameters in the estimating process between using batch and sliding window methods have not significant differences.

To avoid estimation bias in the algorithm, we are introducing *threshold* and *cut off* processes. *threshold* means when a bias occurs in the algorithm, the cheap  $\hat{\pi}$  may not

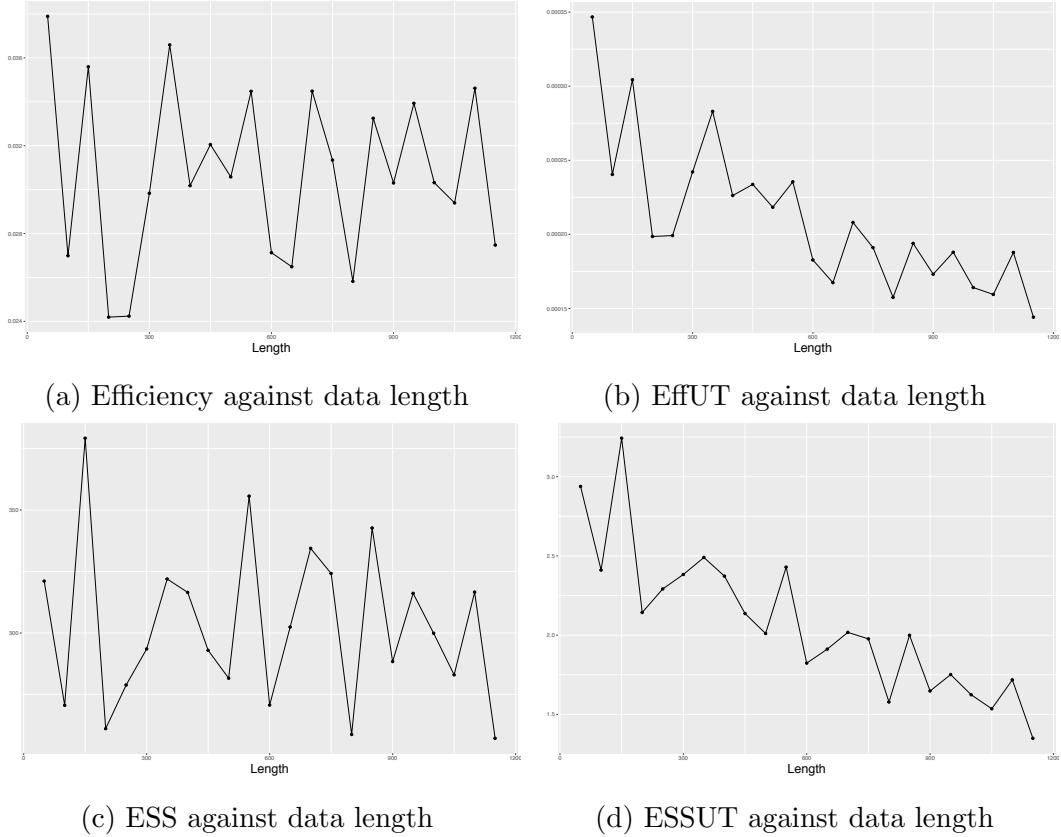
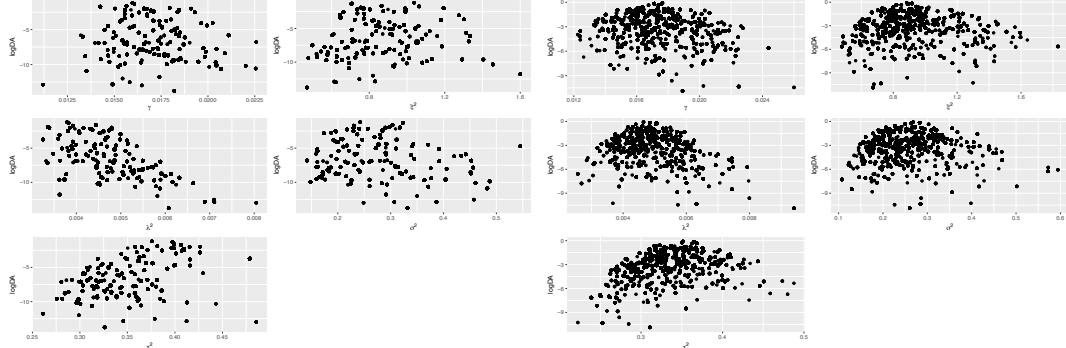


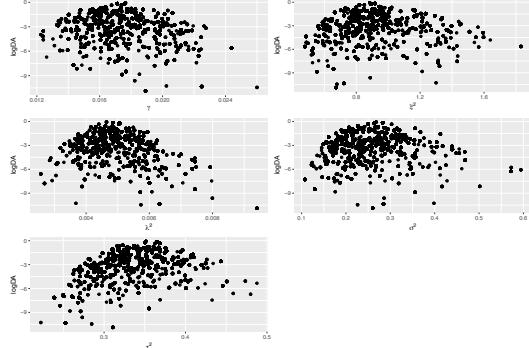
Figure 5.11: Comparison of efficiency (Eff), efficiency in unit time (EffUT), effective sample size (ESS) and effective sample size in unit time (ESSUT) against the different length of data. Increasing data length does not significantly improve the efficiency and ESSUT.

be appropriate and a new one is needed. Thus, we have to update  $\hat{\pi}$  with a latest data we have. A *cut off* process stops the algorithm when a large  $\Delta_t$  happens. A large time gap indicates the vehicle stops at some time point and it causes irregularity and bias. A smart way is stopping the process and waiting for new data coming in. By running testings on real data, the *threshold* is chosen  $\alpha_2 < 0.7$  and *cut off* is  $\Delta_t \geq 300$  seconds. These two values are on researchers' choice. From figures 5.12 and 5.13, we can see that by using the *threshold*, we are efficiently avoiding bias and getting more effective samples.

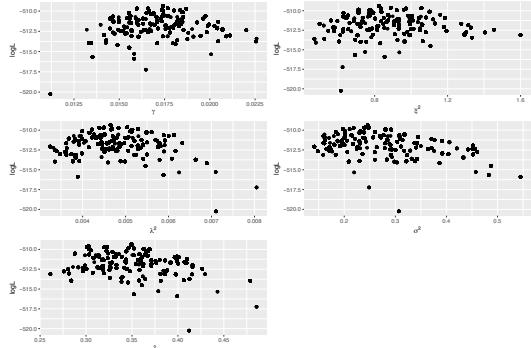
So far, the complete algorithm is summarized in the following Algorithm 5.2:



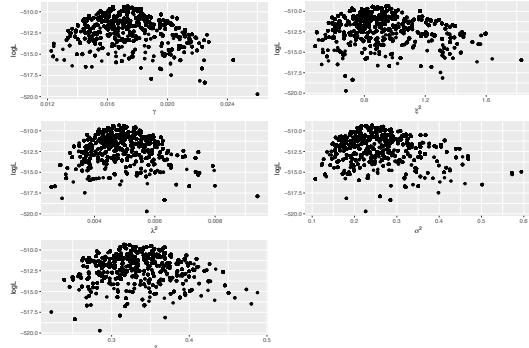
(a)  $\ln DA$  surfaces of not-updating-mean



(b)  $\ln DA$  surfaces of updating-mean



(c)  $\ln L$  surfaces of not-updating-mean



(d)  $\ln L$  surfaces of updating-mean

Figure 5.12: Comparison  $\ln DA$  and  $\ln L$  surfaces between not-updating-mean and updating-mean methods. It is obviously that the updating-mean method has dense log-surfaces indicating more effective samples.

### 5.5.7 Implementation

To implement the Algorithm 5.2, firstly we should get an idea of how the hyper parameter space looks like by running step 2 of the algorithm with some observed data. By setting  $L = 100$  and running 5 000 iterations, we can find the whole  $\theta$  samples in 59 seconds. For each parameter of  $\theta$ , we take 1 000 sub-samples out of 5 000 as new sequences. The new  $\theta^*$  is representative for the hyper parameter space. Then, the traces and correlation is derived from  $\theta^*$ . Meanwhile, the acceptance rates for each parameter are  $\alpha_\gamma = 0.453, \alpha_{\xi^2} = 0.433, \alpha_{\lambda^2} = 0.435, \alpha_{\sigma^2} = 0.414, \alpha_{\tau^2} = 0.4490$  respectively. Hence, the structure of  $\hat{\theta} \sim N(m_t, C_t)$  is achieved. That can be seen in figure 5.14.

Since a cheap surrogate  $\hat{\pi}(\cdot)$  for the true  $\pi(\cdot)$  is found in step 2, it is time to move to the next step. Algorithm 5.2 takes fixed  $L$  length data from  $Y_{1:L}$  to  $Y_{t-L+1:t}$  until an irregular large time lag meets the *cutting-off* criterion. In the implementation, the

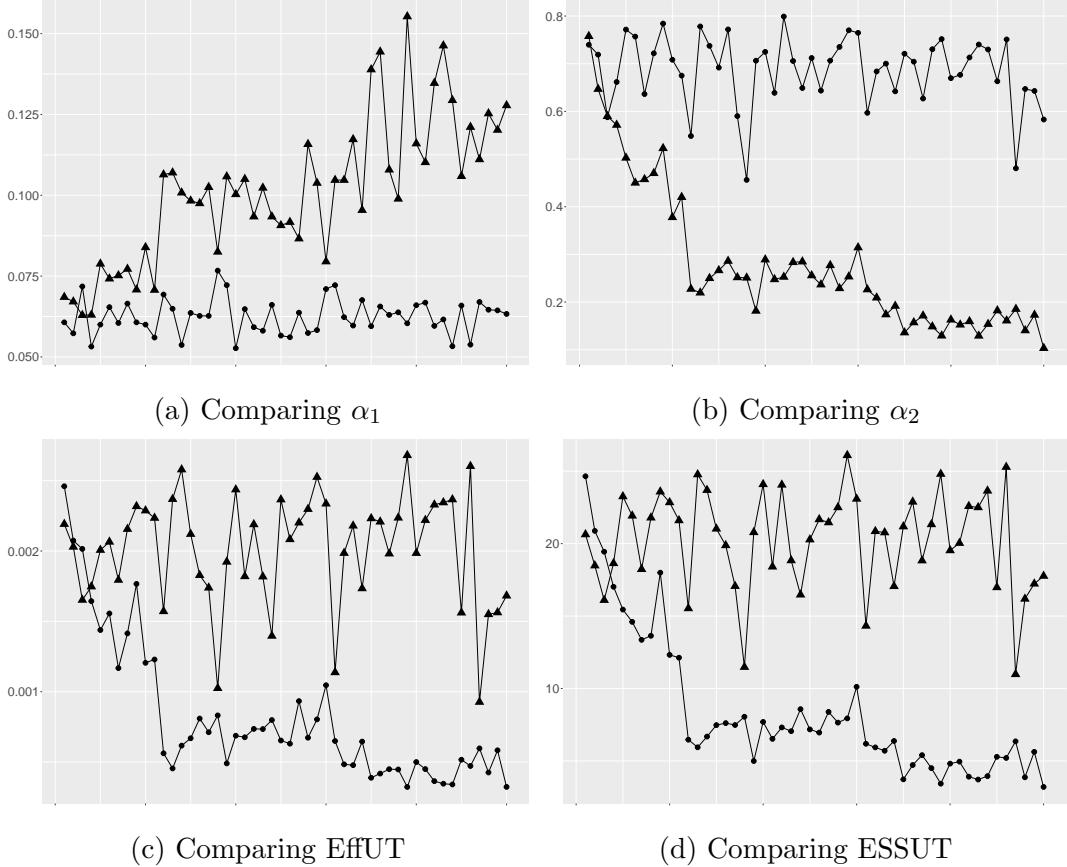


Figure 5.13: Comparison of acceptance rates  $\alpha_1$ ,  $\alpha_2$ , EffUT and ESSUT between not-updating-mean and updating-mean methods. Black solid dots  $\bullet$  indicate values obtained from not-updating-mean method and black solid triangular  $\blacktriangle$  indicate values obtained from updating-mean method. The acceptance rates of the updating-mean method are more stable and effective samples are larger in unit computation time.

first *cutting-off* occurs at the 648th data point. The first estimated  $\hat{X}_{1:L}$  was found by the batch method and  $\hat{X}_{L+1}$  to  $\hat{X}_t$  were found sequentially around 9 seconds with 10 000 iterations each time.



Figure 5.14: Visualization of the parameters correlation matrix, which is found in learning phase.

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**Algorithm 5.2:** Sliding Window MCMC

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1 Initialization: Set up  $L$ , *threshold* and *cutting-off* criteria.

2 Learning process: Estimate  $\theta$  with  $p(\theta | Y_{1:\min\{t,L\}}) \propto p(Y_{1:\min\{t,L\}} | \theta) p(\theta)$  by one-variable-at-a-time Random Walk Metropolis-Hastings algorithm gaining the target acceptance rates and find out the structure of  $\theta \sim N(\mu, \Sigma)$  and the approximation  $\hat{\pi}(\cdot)$ .

3 Estimate  $X_{\max\{1,t-L+1\}:\min\{t,L\}}$  with  $Y_{\max\{1,t-L+1\}:\min\{t,L\}}$ : **for**  $i$  from 1 to  $N$  **do**

4     Propose  $\theta_i^*$  from  $N(\theta_i | \mu, \Sigma)$ , accept it with probability  

$$\alpha_1 = \min \left\{ 1, \frac{\hat{\pi}(\theta_i^*) q(\theta_i, \theta_i^*)}{\hat{\pi}(\theta_i) q(\theta_i^*, \theta_i)} \right\}$$
 and go to next step; otherwise go to step 4.

5     Accept  $\theta_i^*$  with probability  $\alpha_2 = \min \left\{ 1, \frac{\pi(\theta_i^*) \hat{\pi}(\theta_i)}{\pi(\theta_i) \hat{\pi}(\theta_i^*)} \right\}$  and go to next step;  
otherwise go to step 4.

6     Calculate  $\mu_i^{(t)}, \Sigma_i^{(t)}$  for  $X_t$  and  $\mu_i^{(t+s)}, \Sigma_i^{(t+s)}$  for  $X_{t+s}$ .

7 **end**

8 Calculate  $\mu_X^{(t)} = \frac{1}{N} \sum_i \mu_i^{(t)}$ ,  
 $\text{Var}[X^{(t)}] = \frac{1}{N} \sum_i (\mu_i^{(t)} \mu_i^{(t)\top} + \Sigma_i) - \frac{1}{N^2} \left( \sum_i \mu_i^{(t)} \right) \left( \sum_i \mu_i^{(t)} \right)^\top$  and  $\mu_X^{(t+s)}$ ,  
 $\text{Var}[X^{(t+s)}]$  with the same formula.

9 Check *threshold* and *cutting-off* criteria. **if** *threshold* is TRUE **then**

10     Update  $\theta \sim N(\mu, \Sigma)$

11 **else if** *cutting-off* is TRUE **then**

12     Stop process.

13 **else**

14     Go to next step.

15 **end**

16 Shift the window by setting  $t = t + 1$  and go back to step 3.

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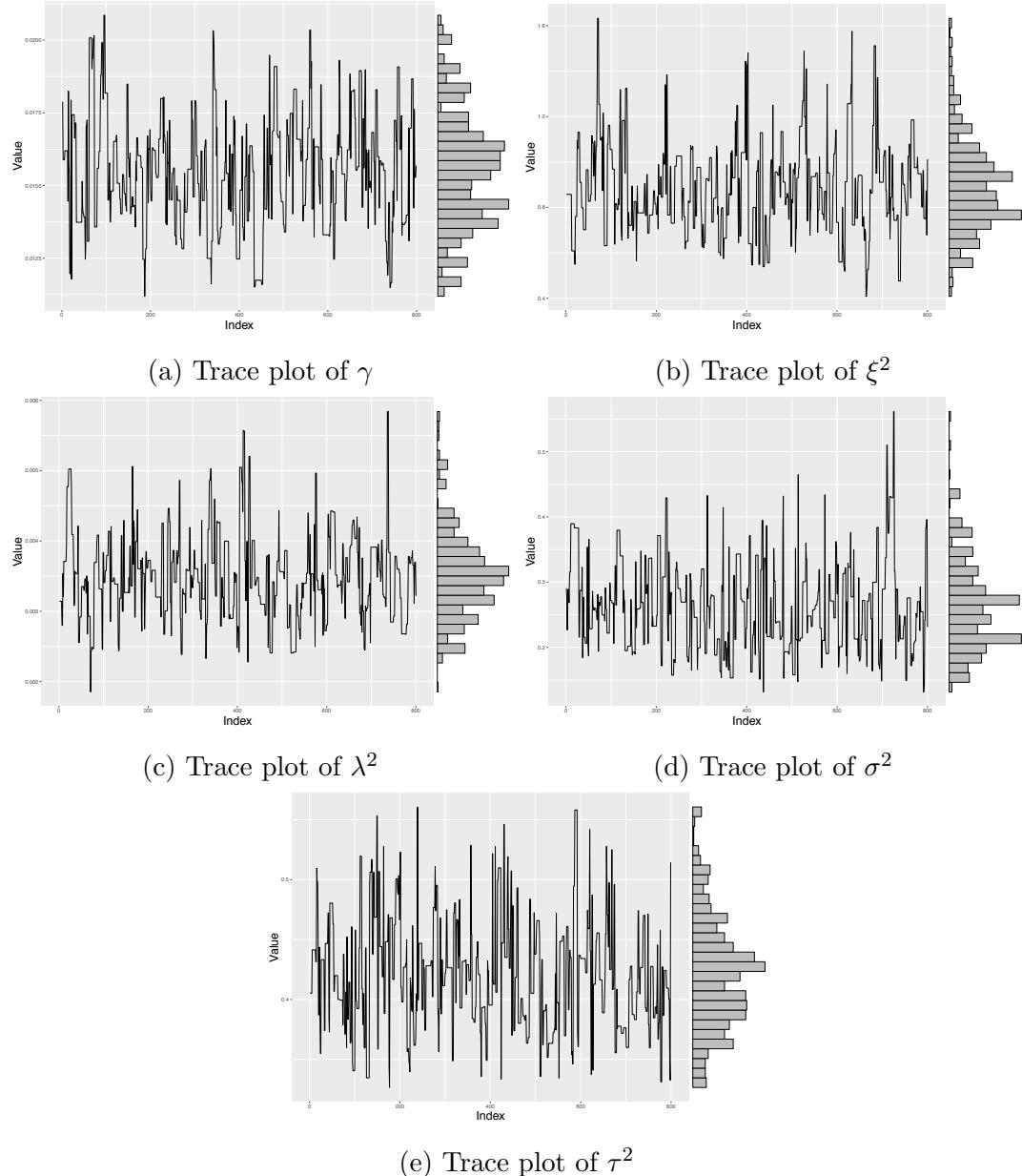


Figure 5.15: Trace plots of  $\theta$  from learning phase after taking 1 000 burn-in samples out from 5 000.

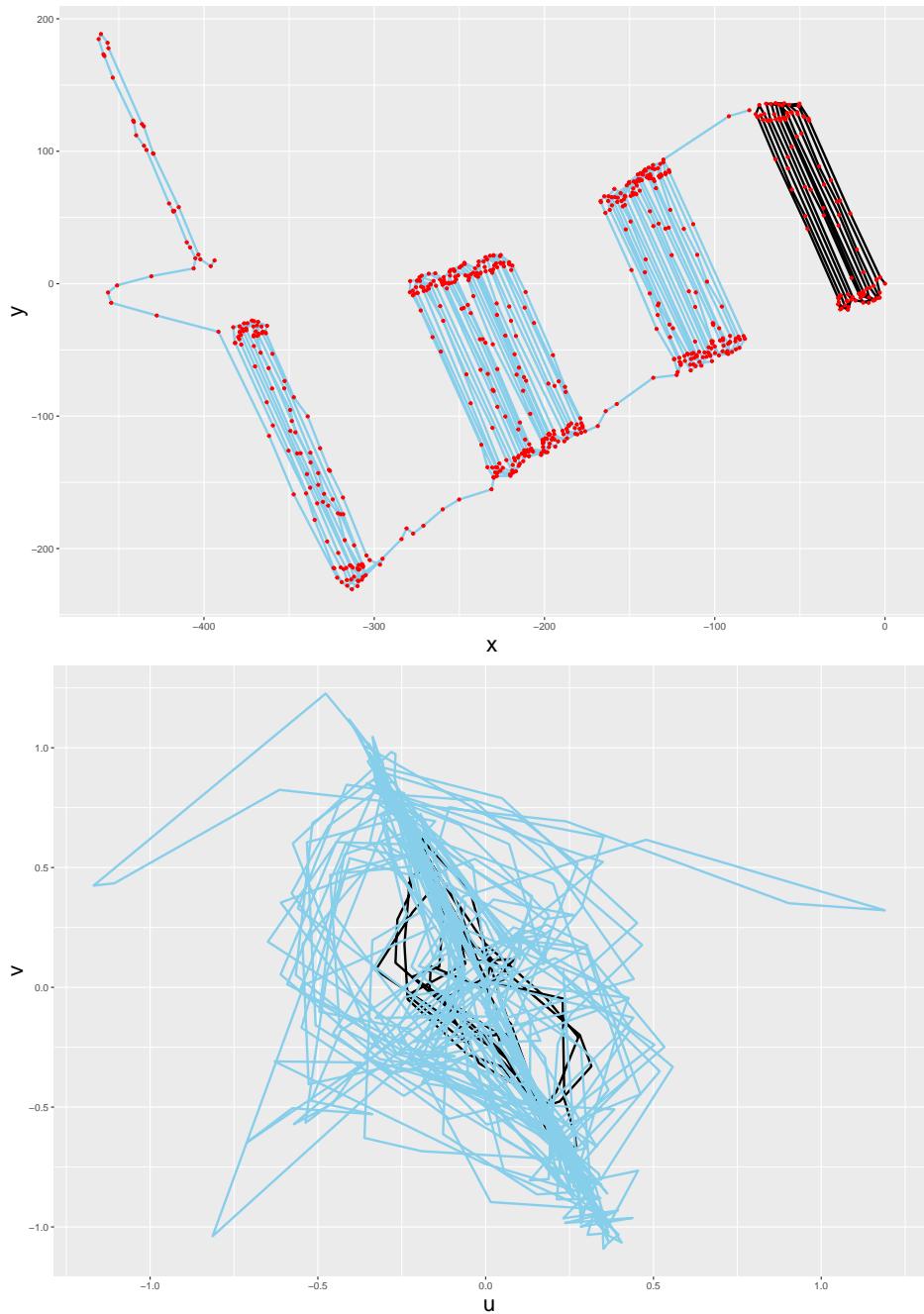


Figure 5.16: Estimations of  $X$  and  $Y$  found by combined batch and sequential methods. The black line is the estimation by batch method and the blue line is the sequential MCMC filtering estimation. Red dots are the measurements.

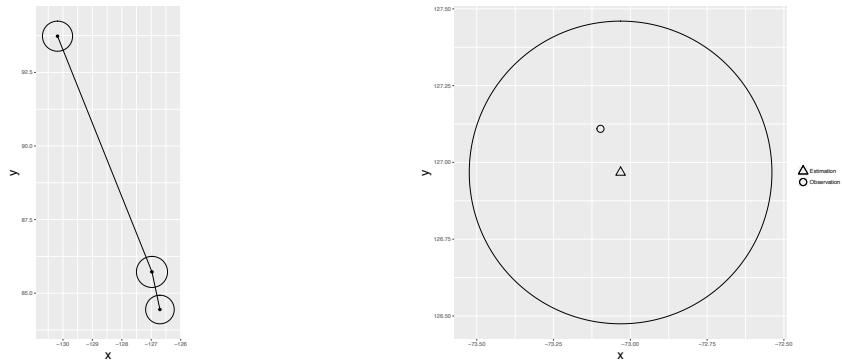


Figure 5.17: Zoom in on estimations. For each estimation  $\hat{X}_i (i = 1, \dots, t)$ , there is a error circle around it.

## 5.6 Discussion and Future Work

In this chapter, we are using the a self-tuning one-variable-at-a-time Metropolis-Hastings Random Walk to learn the parameter hyper space for a linear state-space model. Starting from the joint covariance and distribution of  $X$  and  $Y$ , we have a recursive way to update the mean and covariance sequentially. After getting the cheap approximation posterior distribution, DA MH algorithm accelerates the estimating process. The advantage of this algorithm is that it is easily to understand and implement in practice. By contrast, Particle Learning algorithm is highly efficient, however, the sufficient statistics are not available at all time .

Some future work can be done on inferring state from precious movement with other kinetic information, not just with diffusive velocity. Besides, I am more interested in increasing the efficiency and accuracy of MCMC method.



# Chapter 6

## Future Work

In this thesis, two main practical algorithms are proposed: the adaptive V-spline and the adaptive sequential MCMC algorithm. Being honest, there are a few flaws in these two algorithms and future work remains to be done to improve their performances.

### Gradient Boosting V-Spline

V-spline is an advanced smoothing spline algorithm returning least true mean squared errors. However, to implement this algorithm on-line needs feasible solutions. One of them probably is combining spline method and gradient boosting algorithm.

In machine learning application, it is best to build a non-parametric regression or classification model from the data itself. A connection between the statistical framework and machine learning is the gradient-descent based formulation of boosting methods, which was derived by (Freund and Schapire, 1995), (Friedman, 2001). The gradient boosting algorithm is a powerful machine-learning technique that has shown considerable success in a wide range of practical applications, particularly in machine learning competitions on *Kaggle*.

The motivation of gradient boosting algorithms is combining weak learners together as a strong leaner, which keeps minimizing the target loss function. It has highly customizable application to meet particular needs, like being learned with respect to different loss functions. For example, for a continuous response  $y \in R$ , the loss function can be chosen as a Gaussian  $L_2$  loss function. Hence, the squared error  $L_2$  loss function is

$$L_2(y, f(t)) = \frac{1}{2} (y - f(t))^2,$$

and the best trained  $f^*$  is

$$f^* = \arg_f \min E_{t,y}[L_2(y, f)].$$

To find  $f^*$ , it is reducing the loss  $\tilde{y}_i = y_i - F_{m-1}(t_i)$  recursively. Consequently, the

$$f_m(t) = f_{m-1}(t) + \rho_m h(t, \alpha_m),$$

is the sum of some basic learners  $h_m(t, \alpha)$ .  $m = 1, \dots, M$  determines the complexity of the solution.

On-line boosting algorithms are given by (Babenko *et al.*, 2009) and (Beygelzimer *et al.*, 2015). It is assumed that the loss over the entire training data can be expressed as a sum of the loss for each point  $t_i$ , that is  $L(f(t, y)) = \sum_i L(f(t_i, y_i))$ . Instead of computing the gradient of the entire loss, the gradient is computed with respect to just one data point. Furthermore, by adding additional regularization term will help to smooth the final learned weights to avoid over-fitting in a penalized regression problem (Chen and Guestrin, 2016).

Accordingly, the V-spline  $f^*(t)$  is a sum of several weak learners  $f_m(t)$ , each of which has  $2N$  parameters  $\theta_m = \{\theta_m^{(1)}, \dots, \theta_m^{(2N)}\}$ . The optimal  $\theta^*$  is found by

$$\theta^* = \sum_{m=0}^M \theta_m,$$

where  $\theta_m$  is computed via  $\theta_m = -\rho_m \frac{\partial L(\theta)}{\partial \theta}$ .

As a result, after  $M$  iterations,  $\theta^*$  is convergence and  $f^*(t, y, \theta^*)$  is obtained.

## Non-trivial V-Spline with Correlated Errors

In Chapter 3, the Bayes estimate of V-spline with correlated errors is given. The extended GCV serves to find the optimal parameters for the estimate. Whereas, the extended GCV is only applicable for trivial V-spline, where  $\lambda(t)$  is constant.

In (Opsomer *et al.*, 2001) and (Wang, 1998), the authors present a few extensions of the generalized maximum likelihood (GML), generalized cross-validation (GCV) and unbiased risk (UBR) methods to find optimal parameters for smoothing spline ANOVA models when observations are correlated. These algorithms in applied on conventional polynomial smoothing spline, but not on V-spline. Suppose the errors of the observations  $y$  and  $v$  are  $\varepsilon_y \sim N(0, \sigma^2 W^{-1})$  and  $\varepsilon_v \sim N(0, \tau^2 U^{-1})$  with unknown parameters  $\sigma^2$  and  $\tau^2$ , I hope to find general solutions, similarly to GML, GCV and UBR, to tune the parameters for V-spline returning least true mean squared errors.

## Informative Proposals

In Chapter 5, the proposed adaptive MCMC algorithm draws samples of  $\theta = \{\gamma, \xi^2, \lambda^2, \sigma^2, \tau^2\}$  from  $N(m, C)$ , where the information of  $m$  and  $C$  are learned from a self-tuning learning phase. For each  $\theta^{(i)}$ , it generates a paired mean and variance  $\{\mu_t^{(i)}, \Sigma_t^{(i)}\}$  for mixture Gaussian  $x_t$ .

In the sampling step of real data application, the mechanic boom status is not incorporated, which may provide useful information. Like the penalty parameter  $\lambda$  being classified by  $\lambda_d$  and  $\lambda_u$  according to boom status, the MCMC sampler may use this information to propose  $\theta$  with different strategies, such as different step sizes, different  $ms$  and  $Cs$ . In this way, the parameter  $\theta$  is classified by  $\theta_u$  and  $\theta_d$ .

(not finished yet)

## Grid-based MCMC

In several references, Grid-based methods have been proved that it provides an optimal recursion of the filtered density  $p(x_t | y_{1:t})$  if the state-space is discrete and consists of a finite number of states (Ristic *et al.*, 2004), (Stroud *et al.*, 2016), (Arulampalam *et al.*, 2002) and (Hartmann *et al.*, 2016).

In the application of real time series dataset, the model is supposed as an OU-process containing five unknown parameters. With the idea of grid-based algorithm, the 5-dimension parameter space  $\mathbb{R}^5$  can be initialized by spanning  $\theta_0^{(i)}$  with equal weights  $w_0 = \{\frac{1}{N}, \frac{1}{N}, \frac{1}{N}, \frac{1}{N}, \frac{1}{N}\}$  at time  $t = 0$ , where  $i = 1, \dots, N$ . When a new observation  $Y_t = \{y_t, v_t\}$  comes into the system, the weights for each parameter in each subspace are updated via  $w_t \propto p(Y_t | \theta, Y_{1:t-1})w_{t-1}$ .

However, the grid-based MCMC may not be practical for a higher  $n$ -dimensional space, which requires  $O(N^n)$  computation cost per MCMC step.

## Parallel MCMC

Parallel computing is a type of computation in which many calculations or the execution of processes are carried out simultaneously on multi-core processors (Asanovic *et al.*, 2006). A master process controls the strategy on how to split large, expensive computation into smaller slave processes and solved concurrently on each separate processor (Almasi and Gottlieb, 1994). After computing, slave processes pass results back to the master process, in which the final result is generated.

Parallel MCMC is using this technology to deploy the computation and run samplers on multi-core CPU. Approaches for parallel MCMC are either by implementing parallelization within a single chain or by running multiple chains (Wu *et al.*, 2012). It is useful for computing complex Bayesian models, which do not only lead to a dramatic speedup in computing but can also be used to optimize model parameters in complex Bayesian models.

A simple parallel Monte Carlo estimation of  $E[p(\theta)]$  proceeds in the following way (Kontoghiorghe, 2005). Suppose there amount to  $k$  CPU cores to generate  $N$  samples. Thus, on each CPU there are  $m = N/k$  samples on average. A master process passes  $m$  to each slave process  $i$ ,  $i = 1, \dots, k$ . At each slave process, it generates  $m$  samples for  $\theta_i^{(m)}$  and passes middle-result  $S_i$  back to the master process. At last, the master process computes the final result by

$$E[p(\theta)] = \frac{\sum_i S_i}{N}.$$

Therefore, parallel MCMC is using MCMC sampler scheme to draw samples on multi-cores simultaneously. A naive yet natural approach to parallel MCMC is simply to generate several independent Markov chains on different processors and then combine the results appropriately (Bradford and Thomas, 1996) (Gelman and Rubin, 1992). Or, alternatively, develop parallelism within a single chain. Suppose there are  $k$  CPU cores. Give initial values  $\theta_i^{(0)}$  for each core. Concurrently update  $\theta$  chains by a predetermined MCMC sampler with  $p(\theta | y_{1:t})$  on each slave process. Computes summary statistics for the updated  $\theta_i^{(0:N)}$  and passes back to the master process. Finally, achieve a sequence of  $\theta$  of length  $kN$  (Wu *et al.*, 2012).

A further weighted parallel MCMC and parallelization approach to the Gibbs sampler is proposed by (VanDerwerken and Schmidler, 2013).

Consequently, the parallel MCMC is a potential alternative approach of sliding window MCMC in Chapter 5 to improve the computation speed in high dimensional space.

# Chapter 7

## Summary

Inference and characterization of planar trajectories have been confusing researchers for decades. Precise and efficient algorithms are highly demanded in all kinds of applications. In this thesis, an off-line method V-spline is proposed to reconstruct the whole trajectory and an on-line adaptive MCMC algorithm is used to update and track unknown state and parameter instantly.

In Chapter 2, the proposed V-spline is built up by new basis functions consisting of Hermite spline. For  $n$  paired time series data  $\{t_i, y_i, v_i\}_{i=1}^n$ , the amount of basis functions is  $2n$ . In the new objective function (2.5), V-spline incorporates both location and velocity information but penalizes excessive accelerations. It is not only minimizing the squared residuals of  $|y_i - f(t_i)|^2$  but also reducing the squared residuals of  $|v_i - f'(t_i)|^2$ , for  $i = 1, \dots, n$ , with a new parameter  $\gamma$ .

In the objective function of a conventional smoothing spline, the penalty parameter  $\lambda$  is one single constant that controls the trade-off between interpolations ( $\lambda \rightarrow 0$ ) and a straight line ( $\lambda \rightarrow \infty$ ). Instead, the penalty parameter  $\lambda(t)$  of a V-spline is a function, which is varying at different intervals. In fact, one can consider it a piecewise constant  $\lambda(t_i) = \lambda_i$  in intervals  $[t_i, t_{i+1}]$  for  $i = 1, \dots, n-1$ . Hence, in V-spline objective function, there are overall  $n$  parameters, including  $n-1$   $\lambda$ s and  $\gamma$ , to be estimated. Additionally, to handle unexpected curvatures in the reconstruction, an adjusted penalty term  $\frac{(\Delta t_i)^3}{(\Delta d_i)^2}$  is used to adapt to more complicated curvature status. The idea behind this term is either velocity and acceleration goes to zero, the penalty  $\lambda$  should be large enough to enforce a straight line.

It is proved that with improper priors, smoothing splines are corresponding to Bayes estimates, particularly, can be interpreted by Gaussian process regression in a reproducing kernel Hilbert space. This interesting property can be used in more flexible

and general applications. Similarly, if the V-spline is equipped with an appropriate inner product (3.13) and keep  $\lambda$  constant, it is corresponding to the posterior mean of the Bayes estimates in a particular reproducing kernel Hilbert space  $\mathcal{C}_{\text{p.w.}}^{(2)}[0, 1]$ , in which the second derivatives are piecewise continuous. This result is discussed in Chapter 3. Recall the property of V-splines that only if  $\lambda(t)$  is constant and  $\gamma = 0$  would the second derivatives be continuous in the entire interval. Otherwise, the second derivatives may not be continuous at joint knots but are linear in each interval. That is piecewise continuous. Therefore, this kind of V-splines is named trivial V-splines. In contrast, a non-trivial V-spline has a penalty function  $\lambda(t)$ .

Furthermore, generic smoothing splines are always involving independent errors. Extended research is considering using correlated errors or correlated observations, that are more common in real life applications. In Chapter 3, it is proved by numerical simulation that the V-spline and its Bayes estimate return the same results even if the errors in observed  $y$  and  $v$  are correlated.

To find the best parameters, an extended leave-one-out cross-validation technique is proposed to find all the smoothing parameters of interest in Chapter 2. This method is using observed data itself to tune the parameters at the optimal level. Accordingly, V-spline is a data-driven nonparametric regression solution to handle paired time series data consisting position and velocity information. However, for data with correlated errors, the generalized cross-validation algorithm is more effective. Being modified a generic GCV, in Chapter 3, an extended GCV is used for finding the optimal parameters for V-spline and its Bayes estimate containing correlated errors. Suppose the solution of a V-spline and its first derivative are in the form of  $f = S(\lambda, \gamma)y + \gamma T(\lambda, \gamma)v$  and  $f' = U(\lambda, \gamma)y + \gamma V(\lambda, \gamma)v$ , the GCV is calculating the trace of matrices  $S$ ,  $T$ ,  $U$  and  $V$ . It is much faster than calculating the sum of the single element in each matrix in LOOCV.

Simulation studies are given to compare the performances of V-spline and other methods, such as Wavelet algorithms and penalized B-spline, in Chapter 2. It is obvious that all algorithms are very competitive on reconstructing trajectories with respect to mean squared errors, but only the proposed V-spline returns the least true mean squared errors. That means the V-spline performs better and closer to the true singles. At the end of that chapter, a real data example are presented to demonstrate the effectiveness of V-spline. Being applied to a real GPS dataset, the parameter  $\lambda$  is classified by  $\lambda_u$  and  $\lambda_d$  representing for two operating status of a mechanic boom.  $\lambda_u$  is a set of  $\{\lambda_i\}$  in the intervals where the boom is not operating and, in contrast,  $\lambda_d$

is a set of  $\{\lambda_i\}$  in the intervals where the boom is operating. The reconstruction from V-spline can be treated as the real trajectory of a moving vehicle with confidence.

Without loss of generality,  $\lambda(t)$  can be classified into more groups to adapt to complex maneuver system and V-spline is flexible to be applied on higher dimensional cases.

However, subject to the property that smoothing splines require the solution of a global problem that involves the entire set of points to be interpolated, it might not be suitable for on-line estimation. Hence, Chapter 4 is the content of an overview of existing filtering and estimation algorithms. Some popular algorithms, such as Particle filter, are concentrating on inferring the unknown state but assuming the parameters are known. Moreover, the sample impoverishment has never been solved properly. Liu and West's filter is trying to kill particle degeneracy by incorporating with a shrinkage kernel. Meanwhile, it estimates the unknown parameters simultaneously. Storvik filter and Particle learning algorithms are marginalizing out the parameters through sufficient statistics and achieving a better estimation than Liu and West's filter. In some way, they are advanced algorithms but not practicable any time. In most situations, sufficient statistics are not available or hard to find. A more flexible and easy-implement method is in demand.

As a result, an adaptive sequential MCMC algorithm is proposed in Chapter 5. Similarly, with V-spline, the adaptive sequential MCMC is dealing with paired time series dataset including both position and velocity information.

In the case of a linear state-space model and starting with a joint distribution over state  $x$ , observation  $y$  and parameter  $\theta$ , an MCMC sampler is implemented with two phases. In the learning phase, a self-tuning sampler is utilizing one-variable-at-a-time random walk Metropolis-Hastings (MH) algorithm to learn the parameter mean and covariance structure by aiming at a target acceptance rate. After exploring the parameter space, the information is used in the subsequent phase — the estimation phase — to inform the proposed mechanism and is also used in a delayed-acceptance algorithm.

Suppose the mean and covariance matrix of  $\theta$  are  $m$  and  $C = L^\top L$  respectively, where  $L$  is its Cholesky decomposition. Then the proposal  $\theta^* = \theta + \epsilon LZ$  and  $Z \sim N(0, I)$ ,  $\epsilon$  is the step size. The effect of  $L$  is to reduce the correlation of proposals and move to the next step on purpose. The step size  $\epsilon$  makes the proposal process more efficient. Rather than focusing on the criteria of efficiency (Eff) and effective sample size (ESS), the Eff in unit time (EffUT) and ESS in unit time (ESSUT) should be

the new criteria to determine the optimal step size. By running the same amount of time, the optimal step size found by EffUT and ESSUT generates more effective and representative samples.

Further, the delayed-acceptance algorithm is using a cheap surrogate  $p(\theta | m, C)$  to the true posterior  $p(\theta | y)$  in the first line of defense to keep not-good samples outside. Only good proposals would pass the first line and move forward to the additional expensive calculation. This strategy greatly improves sampling efficiency.

Information on the resulting state of the system is indicated by a Gaussian mixture. For each sample of  $\theta^{(i)}$ , it matches an  $x \sim N(\mu^{(i)}, \sigma^{(i)})$ . Consequently, the final estimation of  $x$  is given by a set of the Gaussian mixture.

In the on-line mode, the algorithm is adaptive and uses a sliding window approach by cutting off historical data to accelerate sampling speed and to maintain appropriate acceptance. In a simple one parameter simulation in Chapter 4, the proposed adaptive MCMC shows a stable feature comparing with other filtering methods. And in Chapter 5, this algorithm shows an advantage in estimating irregularly sampled time series data.

At the end of Chapter 5, the proposed algorithm is applied to combined state and parameter estimation in the case of irregularly sampled GPS time series data. Suppose it is a four-dimensional linear Ornstein-Uhlenbeck (OU) process containing  $z = \{x, u, y, v\}$  with respects to  $\{x, u\}$  on  $X$ -axis and  $\{y, v\}$  on  $Y$ -axis, the parameter space is in 5 dimensions, that is  $\theta = \{\gamma, \xi^2, \lambda^2, \sigma^2, \tau^2\}$ . The proposed algorithm efficiently infers the state  $z_t$  through time  $t$  within acceptable errors. Not limited, it also predicts the upcoming states simultaneously.

As a conclusion, the proposed algorithms in this thesis are contributing to related areas, nevertheless, are not perfect. The V-spline may not be appropriate for on-line estimation and the sliding window adaptive MCMC algorithm is not using the entire data set that might lose some information. Future work and deeper research are required to improve their performances.

# Appendices



# Appendix A

## Proofs And Figures of V-Spline Theorems

### A.1 Penalty Matrix in (2.12)

The  $i$ -th  $\Omega^{(i)}$  is a  $2n \times 2n$  bandwidth four symmetric matrix and its non-zero elements on the upper triangular are

$$\Omega_{2i-1,2i-1}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{00}^{(i)}(t)}{dt^2} \frac{d^2 h_{00}^{(i)}(t)}{dt^2} dt = \frac{12}{\Delta_i^3} \quad (\text{A.1.1})$$

$$\Omega_{2i-1,2i}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{00}^{(i)}(t)}{dt^2} \frac{d^2 h_{10}^{(i)}(t)}{dt^2} dt = \frac{6}{\Delta_i^2} \quad (\text{A.1.2})$$

$$\Omega_{2i-1,2i+1}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{00}^{(i)}(t)}{dt^2} \frac{d^2 h_{01}^{(i)}(t)}{dt^2} dt = \frac{-12}{\Delta_i^3} \quad (\text{A.1.3})$$

$$\Omega_{2i-1,2i+2}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{00}^{(i)}(t)}{dt^2} \frac{d^2 h_{11}^{(i)}(t)}{dt^2} dt = \frac{6}{\Delta_i^2} \quad (\text{A.1.4})$$

$$\Omega_{2i,2i}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{10}^{(i)}(t)}{dt^2} \frac{d^2 h_{10}^{(i)}(t)}{dt^2} dt = \frac{4}{\Delta_i} \quad (\text{A.1.5})$$

$$\Omega_{2i,2i+1}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{10}^{(i)}(t)}{dt^2} \frac{d^2 h_{01}^{(i)}(t)}{dt^2} dt = \frac{-6}{\Delta_i^2} \quad (\text{A.1.6})$$

$$\Omega_{2i,2i+2}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{10}^{(i)}(t)}{dt^2} \frac{d^2 h_{11}^{(i)}(t)}{dt^2} dt = \frac{2}{\Delta_i} \quad (\text{A.1.7})$$

$$\Omega_{2i+1,2i+1}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{01}^{(i)}(t)}{dt^2} \frac{d^2 h_{01}^{(i)}(t)}{dt^2} dt = \frac{12}{\Delta_i^3} \quad (\text{A.1.8})$$

$$\Omega_{2i+1,2i+2}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{01}^{(i)}(t)}{dt^2} \frac{d^2 h_{11}^{(i)}(t)}{dt^2} dt = \frac{-6}{\Delta_i^2} \quad (\text{A.1.9})$$

$$\Omega_{2i+2,2i+2}^{(i)} = \int_{t_i}^{t_{i+1}} \frac{d^2 h_{11}^{(i)}(t)}{dt^2} \frac{d^2 h_{11}^{(i)}(t)}{dt^2} dt = \frac{4}{\Delta_i} \quad (\text{A.1.10})$$

where  $\Delta_i = t_{i+1} - t_i$  and  $i = 1, 2, \dots, n - 1$ . Then

$$\Omega = \sum_{i=1}^{n-1} \lambda_i \Omega^{(i)}$$

## A.2 Proof of Theorem 1

*Proof.* If  $g : [a, b] \mapsto \mathbb{R}$  is a proposed minimizer, construct a cubic spline  $f(t)$  that agrees with  $g(t)$  and its first derivatives at  $t_1, \dots, t_n$ , and is component-wise linear on  $[a, t_1]$  and  $[t_n, b]$ . Let  $h(t) = g(t) - f(t)$ . Then, for  $i = 1, \dots, n - 1$ ,

$$\begin{aligned} \int_{t_i}^{t_{i+1}} f''(t)h''(t)dt &= f''(t)h'(t) \Big|_{t_i}^{t_{i+1}} - \int_{t_i}^{t_{i+1}} f'''(t)h'(t)dt \\ &= 0 - f'''(t_i^+) \int_{t_i}^{t_{i+1}} h'(t)dt \\ &= -f'''(t_i^+) (h(t_{i+1}) - h(t_i)) \\ &= 0. \end{aligned}$$

Additionally,  $\int_a^{t_1} f''(t)h''(t)dt = \int_{t_n}^b f''(t)h''(t)dt = 0$ , since  $f(t)$  is assumed linear outside the knots. Thus, for  $i = 0, \dots, n$ ,

$$\begin{aligned} \int_{t_i}^{t_{i+1}} |g''(t)|^2 dt &= \int_{t_i}^{t_{i+1}} |f''(t) + h''(t)|^2 dt \\ &= \int_{t_i}^{t_{i+1}} |f''(t)|^2 dt + 2 \int_{t_i}^{t_{i+1}} f''(t)h''(t)dt + \int_{t_i}^{t_{i+1}} |h''(t)|^2 dt \\ &= \int_{t_i}^{t_{i+1}} |f''(t)|^2 dt + \int_{t_i}^{t_{i+1}} |h''(t)|^2 dt \\ &\geq \int_{t_i}^{t_{i+1}} |f''(t)|^2 dt. \end{aligned}$$

The result  $J[f] \leq J[g]$  follows since  $\lambda_i > 0$ .

Furthermore, equality of the curvature penalty term only holds if  $g(t) = f(t)$ . On  $[t_1, t_n]$ , we require  $h''(t) = 0$  but since  $h(t_i) = h'(t_i) = 0$  for  $i = 1, \dots, n$ , this means  $h(t) = 0$ . Meanwhile on  $[a, t_1]$  and  $[t_n, b]$ ,  $f''(t) = 0$  so that equality requires  $g''(t) = 0$ . Since  $f(t)$  agrees with  $g(t)$  and its first derivatives at  $t_1$  and  $t_n$ , equality is forced on both intervals.  $\square$

## A.3 Proof of Theorem 2

To prove Theorem 2, we are introducing a lemma given by (Peng, 1983) in the first place.

**Lemma A.3.1.** Functions  $N_1(t), N_2(t), \dots, N_n(t)$  on interval  $[a, b]$ , if they are linear dependent, the necessary and sufficient condition is for any  $c_1, c_2, \dots, c_n \in [a, b]$ , the determinant  $D(c_1, c_2, \dots, c_n) = 0$ ; if they are linear independent, the necessary and sufficient condition is that there exist  $c_1, c_2, \dots, c_n \in [a, b]$ , so that the determinant  $D(c_1, c_2, \dots, c_n) \neq 0$ , where

$$D(c_1, c_2, \dots, c_n) = \begin{vmatrix} N_1(c_1) & N_1(c_2) & \cdots & N_1(c_n) \\ N_2(c_1) & N_2(c_2) & \cdots & N_2(c_n) \\ \vdots & \vdots & \ddots & \vdots \\ N_n(c_1) & N_n(c_2) & \cdots & N_n(c_n) \end{vmatrix}$$

In the following, we are proving Theorem 2 with the help of Lemma A.3.1.

*Proof.* It is obvious that these basis functions are continuous on subinterval  $[t_i, t_{i+1}]$ , where  $i = 1, \dots, n - 1$ . We will prove that these basis functions are independent at first.

Given  $2n$  basis functions and  $n$  knots, we choose  $t_1, \frac{t_1+t_2}{2}, t_2, \frac{t_2+t_3}{2}, \dots, t_{n-1}, \frac{t_{n-1}+t_n}{3}, \frac{2(t_{n-1}+t_n)}{3}, t_n$  as new  $2n$  knots, and denoted by  $c_1, c_2, \dots, c_{2n}$ . Then the determinant is

$$D(c_1, c_2, \dots, c_{2n}) = \begin{bmatrix} N_1(c_1) & N_1(c_2) & \cdots & N_1(c_{2n}) \\ N_2(c_1) & N_2(c_2) & \cdots & N_2(c_{2n}) \\ \vdots & \vdots & \ddots & \vdots \\ N_{2n}(c_1) & N_{2n}(c_2) & \cdots & N_{2n}(c_{2n}) \end{bmatrix} \quad (\text{A.3.1})$$

where the non-zero elements of matrix  $D$  are

$$\begin{aligned} N_1(t_1) &= 1 & N_1\left(\frac{t_1+t_2}{2}\right) &= a_{12} & N_2(t_1) &= 0 \\ N_2\left(\frac{t_1+t_2}{2}\right) &= a_{22} & N_{2i+1}\left(\frac{t_i+t_{i+1}}{2}\right) &= a_{2i+1,2i} & N_{2i+1}(t_{i+1}) &= 1 \\ N_{2i+1}\left(\frac{t_{i+1}+t_{i+2}}{2}\right) &= a_{2i+1,2i+2} & N_{2i+2}\left(\frac{t_i+t_{i+1}}{2}\right) &= a_{2i+2,2i} & N_{2i+2}\left(\frac{t_{i+1}+t_{i+2}}{2}\right) &= a_{2i+2,2i+2} \\ N_{2n-1}(t_{2n-1}) &= 0 & N_{2n-1}\left(\frac{t_{2n-1}+t_{2n}}{3}\right) &= a_{2n-1,2n-2} & N_{2n-1}\left(\frac{2(t_{2n-1}+t_{2n})}{3}\right) &= a_{2n-1,2n-1} \\ N_{2n-1}(t_{2n}) &= 1 & N_{2n}\left(\frac{t_{2n-1}+t_{2n}}{3}\right) &= a_{2n,2n-2} & N_{2n}\left(\frac{2(t_{2n-1}+t_{2n})}{3}\right) &= a_{2n,2n-1} \\ N_{2n}(t_{2n}) &= 0 & & & & \end{aligned}$$

where  $i = 1, \dots, n - 1$ . By decomposing determinant  $D$  in the following way, it will

give us

$$\begin{aligned}
\det D &= \begin{vmatrix} 1 & a_{12} & 0 & 0 & \cdots & 0 & 0 \\ 0 & a_{22} & 0 & 0 & \cdots & 0 & 0 \\ 0 & a_{32} & 1 & a_{34} & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & \cdots & a_{2n-1,2n-1} & 1 \\ 0 & 0 & 0 & 0 & \cdots & a_{2n,2n-1} & 0 \end{vmatrix} = \begin{vmatrix} a_{22} & 0 & 0 & \cdots & 0 & 0 \\ a_{32} & 1 & a_{34} & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & a_{2n-1,2n-1} & 1 \\ 0 & 0 & 0 & \cdots & a_{2n,2n-1} & 0 \end{vmatrix} \\
&= a_{22} \begin{vmatrix} 1 & a_{34} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & a_{2n-1,2n-1} & 1 \\ 0 & 0 & \cdots & a_{2n,2n-1} & 0 \end{vmatrix} \cdots = a_{22}a_{44} \cdots a_{2n-4,2n-4} \begin{vmatrix} a_{2n-2,2n-2} & a_{2n-2,2n-1} & 0 \\ a_{2n-1,2n-2} & a_{2n-1,2n-1} & 1 \\ a_{2n,2n-2} & a_{2n,2n-1} & 0 \end{vmatrix} \\
&= a_{22}a_{44} \cdots a_{2n-4,2n-4}(a_{2n-2,2n-1}a_{2n,2n-2} - a_{2n,2n-1}a_{2n-2,2n-2}) \neq 0.
\end{aligned}$$

With the conclusion of Lemma A.3.1,  $N_1(t), \dots, N_{2n}(t)$  are linearly independent on the entire interval  $[t_1, t_n]$ .

Secondly, we will prove that basis functions represent any cubic function on each interval  $[t_i, t_{i+1}]$ . Due to the definition of cubic spline, on interval  $[t_i, t_{i+1}]$ , a cubic spline  $g(t)$  can be written in the form of

$$g(t) = d_i(t - t_i)^3 + c_i(t - t_i)^2 + b_i(t - t_i) + a_i, \text{ for } t_i \leq t \leq t_{i+1} \quad (\text{A.3.2})$$

For any  $f(t)$  on  $[t_1, t_n]$ , it can be represented as  $f(t) = \sum_{k=1}^{2n} \theta_k N_k(t)$ . Then for  $\forall t \in [t_i, t_{i+1}], i = 1, \dots, n-1$ , we have

$$f(t) = \begin{cases} \theta_{2i-1} N_{2i-1}(t) + \theta_{2i} N_{2i}(t) + \theta_{2i+1} N_{2i+1}(t) + \theta_{2i+2} N_{2i+3}(t), & t_i \leq t \leq t_{i+1} \\ 0, & \text{otherwise} \end{cases}$$

Hence,

$$\begin{aligned}
f(t) &= \theta_{2i-1} \left( 2 \left( \frac{t - t_i}{t_{i+1} - t_i} \right)^3 - 3 \left( \frac{t - t_i}{t_{i+1} - t_i} \right)^2 + 1 \right) + \theta_{2i} \left( \frac{(t - t_i)^3}{(t_{i+1} - t_i)^2} - 2 \frac{(t - t_i)^2}{t_{i+1} - t_i} + (t - t_i) \right) \\
&\quad + \theta_{2i+1} \left( -2 \left( \frac{t - t_i}{t_{i+1} - t_i} \right)^3 + 3 \left( \frac{t - t_i}{t_{i+1} - t_i} \right)^2 \right) + \theta_{2i+2} \left( \frac{(t - t_i)^3}{(t_{i+1} - t_i)^2} - \frac{(t - t_i)^2}{t_{i+1} - t_i} \right).
\end{aligned}$$

After rearranging, we have

$$\begin{aligned}
f(t) &= \left( \frac{2\theta_{2i-1}}{(t_{i+1} - t_i)^3} + \frac{\theta_{2i}}{(t_{i+1} - t_i)^2} - \frac{2\theta_{2i+1}}{(t_{i+1} - t_i)^3} + \frac{\theta_{2i+2}}{(t_{i+1} - t_i)^2} \right) (t - t_i)^3 \\
&\quad + \left( -\frac{3\theta_{2i-1}}{(t_{i+1} - t_i)^2} - \frac{2\theta_{2i}}{(t_{i+1} - t_i)} + \frac{3\theta_{2i+1}}{(t_{i+1} - t_i)^2} - \frac{\theta_{2i+2}}{(t_{i+1} - t_i)} \right) (t - t_i)^2 \\
&\quad + \theta_{2i}(t - t_i) + \theta_{2i-1},
\end{aligned}$$

where coefficients are

$$\begin{cases} \theta_{2i-1} = a_i \\ \theta_{2i} = b_i \\ -\frac{3\theta_{2i-1}}{(t_{i+1}-t_i)^2} - \frac{2\theta_{2i}}{(t_{i+1}-t_i)} + \frac{3\theta_{2i+1}}{(t_{i+1}-t_i)^2} - \frac{\theta_{2i+2}}{(t_{i+1}-t_i)} = c_i \\ \frac{2\theta_{2i-1}}{(t_{i+1}-t_i)^3} + \frac{\theta_{2i}}{(t_{i+1}-t_i)^2} - \frac{2\theta_{2i+1}}{(t_{i+1}-t_i)^3} + \frac{\theta_{2i+2}}{(t_{i+1}-t_i)^2} = d_i \end{cases}$$

The results can always be solved for  $\theta_{2i-1}, \theta_{2i}, \theta_{2i+1}, \theta_{2i+2}$  in terms of  $a_i, b_i, c_i, d_i$  on interval  $[t_i, t_{i+1}]$ . So cubic spline on each interval can be represented by basis functions.

Finally, we will prove basis functions are continuous on  $[t_1, t_n]$ . For any knot  $t_i$ , where  $t_1 < t_i < t_n$ , it is known that  $f(t_i) = \theta_{2i-1}$ . Moreover,

$$\begin{aligned} \lim_{t \rightarrow t_i^+} f(t) &= \lim_{t \rightarrow t_i^+} (\theta_{2i-1} N_{2i-1}(t) + \theta_{2i} N_{2i}(t) + \theta_{2i+1} N_{2i+1}(t) + \theta_{2i+2} N_{2i+3}(t)) = \theta_{2i-1}, \\ \lim_{t \rightarrow t_i^-} f(t) &= \lim_{t \rightarrow t_i^-} (\theta_{2i-1} N_{2i-1}(t) + \theta_{2i} N_{2i}(t) + \theta_{2i+1} N_{2i+1}(t) + \theta_{2i+2} N_{2i+3}(t)) = \theta_{2i-1}. \end{aligned}$$

As a result,

$$\lim_{t \rightarrow t_i^+} f(t) = \lim_{t \rightarrow t_i^-} f(t) = f(t),$$

$f(t)$  is continuous at joint knots, and then continuous on whole interval  $[t_1, t_n]$ .

Consequently,  $f(t)$  is a continuous cubic spline represented by basis functions  $N_1(t), \dots, N_{2n}(t)$  on the entire interval  $[t_1, t_n]$ .  $\square$

## A.4 Proof of Corollary 1

*Proof.* By setting  $\gamma \rightarrow 0$ , the velocity information  $v$  is taken away. The degrees of freedom of parameters decreases from  $2n$  to  $n$ . Hence, there exists an  $n \times 2n$  matrix  $Q_\lambda$  restricting  $n$  degrees of freedom of  $\hat{\theta}$  and satisfying  $Q_\lambda \hat{\theta} = 0$ .

It is easily seen that the matrices  $B$  and  $C$  have the following property:

$$\begin{aligned} BB^\top &= CC^\top = I_n, \\ C^\top CB^\top &= B^\top BC^\top = 0. \end{aligned}$$

Denoting  $G = B^\top B + \gamma C^\top C + n\Omega_\lambda$  and giving  $\hat{\theta} = (B^\top B + \gamma C^\top C + n\Omega_\lambda)^{-1}(B^\top y + \gamma C^\top v)$ , we will have  $G\hat{\theta} = B^\top y + \gamma C^\top v$  and

$$\begin{aligned} BG\hat{\theta} &= y + \gamma BC^\top v \\ CG\hat{\theta} &= CB^\top y + \gamma v. \end{aligned}$$

Therefore,  $C^\top CG\hat{\theta} = C^\top(CB^\top y + \gamma v) = \gamma C^\top v$ . If by setting  $\gamma = 0$ , then we will have  $Q_\lambda = C^\top CG$ , which consists of the even rows of  $\Omega_\lambda$ .

By integrating by parts and using properties of the basis functions at the knots, one can get the even rows of  $\Omega^{(i)}$ , which are

$$\begin{aligned}\Omega_{2i,2i-1}^{(i)} &= N''_{2i-1}(t_i^-) - N''_{2i-1}(t_i^+) \\ \Omega_{2i,2i}^{(i)} &= N''_{2i}(t_i^-) - N''_{2i}(t_i^+) \\ \Omega_{2i,2i+1}^{(i)} &= N''_{2i+1}(t_i^-) - N''_{2i+1}(t_i^+) \\ \Omega_{2i,2i+2}^{(i)} &= N''_{2i+2}(t_i^-) - N''_{2i+2}(t_i^+) \\ \Omega_{2i+2,2i-1}^{(i)} &= N''_{2i-1}(t_{i+1}^-) - N''_{2i-1}(t_{i+1}^+) \\ \Omega_{2i+2,2i}^{(i)} &= N''_{2i}(t_{i+1}^-) - N''_{2i}(t_{i+1}^+) \\ \Omega_{2i+2,2i+1}^{(i)} &= N''_{2i+1}(t_{i+1}^-) - N''_{2i+1}(t_{i+1}^+) \\ \Omega_{2i+2,2i+2}^{(i)} &= N''_{2i+2}(t_{i+1}^-) - N''_{2i+2}(t_{i+1}^+)\end{aligned}$$

Thus

$$Q_\lambda = nC^\top C\Omega_\lambda = nC^\top C \sum_i \lambda_i \Omega^{(i)}.$$

Consequently, if and only if  $\lambda$  is constant,  $Q_\lambda \hat{\theta} = -\lambda(f''(t_i^+) - f''(t_i^-)) = 0$ , for  $i = 1, \dots, n$ , otherwise  $Q_\lambda \theta = 0$  is true but does not represent  $f''(t_i^+) - f''(t_i^-)$ .

As a result,  $f''(t)$  is continuous at joint knots  $t_i$  if  $\lambda(t)$  is constant and  $\gamma = 0$ .

□

## A.5 Proof of Lemma 2

*Proof.* For any smooth curve  $f$  with  $\mathbf{y}^*$ , we have

$$\begin{aligned}& \frac{1}{n} \sum_{j=1}^n (y_j^* - f(t_j))^2 + \frac{\gamma}{n} \sum_{j=1}^n (v_j^* - f'(t_j))^2 + \sum_{j=1}^n \lambda_j \int_{t_j}^{t_{j+1}} f''^2 dt \\ & \geq \frac{1}{n} \sum_{j \neq i} (y_j^* - f(t_j))^2 + \frac{\gamma}{n} \sum_{j \neq i} (v_j^* - f'(t_j))^2 + \sum_{j=1}^n \lambda_j \int_{t_j}^{t_{j+1}} f''^2 dt \\ & \geq \frac{1}{n} \sum_{j \neq i} (y_j^* - \hat{f}^{(-i)}(t_j))^2 + \frac{\gamma}{n} \sum_{j \neq i} (v_j^* - \hat{f}'^{(-i)}(t_j))^2 + \sum_{j=1}^n \lambda_j \int_{t_j}^{t_{j+1}} (\hat{f}''^{(-i)})^2 dt \\ & = \frac{1}{n} \sum_{j=1}^n (y_j^* - \hat{f}^{(-i)}(t_j))^2 + \frac{\gamma}{n} \sum_{j=1}^n (v_j^* - \hat{f}'^{(-i)}(t_j))^2 + \sum_{j=1}^n \lambda_j \int_{t_j}^{t_{j+1}} (\hat{f}''^{(-i)})^2 dt\end{aligned}$$

by the definition of  $\hat{\mathbf{f}}^{(-i)}$ ,  $\hat{\mathbf{f}}'^{(-i)}$  and the fact that  $y_i^* = \hat{f}^{(-i)}(t_i)$ ,  $v_i^* = \hat{f}'^{(-i)}(t_i)$ . It follows that  $\hat{f}^{(-i)}$  is the minimizer of the objective function (2.5), so that

$$\begin{aligned}\hat{\mathbf{f}}^{(-i)} &= S\mathbf{y}^* + \gamma T\mathbf{v}^* \\ \hat{\mathbf{f}}'^{(-i)} &= U\mathbf{y}^* + \gamma V\mathbf{v}^*\end{aligned}$$

as required.  $\square$

## A.6 Proof of Theorem 3

*Proof.*

$$\begin{aligned}\hat{f}^{(-i)}(t_i) - y_i &= \sum_{j=1}^n S_{ij}y_j^* + \gamma \sum_{j=1}^n T_{ij}v_j^* - y_i^* \\ &= \sum_{j \neq i}^n S_{ij}y_j + \gamma \sum_{j \neq i}^n T_{ij}v_j + S_{ii}\hat{f}^{(-i)}(t_i) + \gamma T_{ii}\hat{f}'^{(-i)}(t_i) - y_i \\ &= \sum_{j=1}^n S_{ij}y_j + \gamma \sum_{j=1}^n T_{ij}v_j + S_{ii}(\hat{f}^{(-i)}(t_i) - y_i) + \gamma T_{ii}(\hat{f}'^{(-i)}(t_i) - v_i) - y_i \\ &= (\hat{f}(t_i) - y_i) + S_{ii}(\hat{f}^{(-i)}(t_i) - y_i) + \gamma T_{ii}(\hat{f}'^{(-i)}(t_i) - v_i).\end{aligned}\tag{A.6.1}$$

Additionally,

$$\begin{aligned}\hat{f}'^{(-i)}(t_i) - v_i &= \sum_{j=1}^n U_{ij}y_j^* + \gamma \sum_{j=1}^n V_{ij}v_j^* - v_i^* \\ &= \sum_{j \neq i}^n U_{ij}y_j + \gamma \sum_{j \neq i}^n V_{ij}v_j + U_{ii}\hat{f}^{(-i)}(t_i) + \gamma V_{ii}\hat{f}'^{(-i)}(t_i) - v_i \\ &= \sum_{j=1}^n U_{ij}y_j + \gamma \sum_{j=1}^n V_{ij}v_j + U_{ii}(\hat{f}^{(-i)}(t_i) - y_i) + \gamma V_{ii}(\hat{f}'^{(-i)}(t_i) - v_i) - v_i \\ &= (\hat{f}'(t_i) - v_i) + U_{ii}(\hat{f}^{(-i)}(t_i) - y_i) + \gamma V_{ii}(\hat{f}'^{(-i)}(t_i) - v_i).\end{aligned}\tag{A.6.2}$$

Thus

$$\hat{f}'^{(-i)}(t_i) - v_i = \frac{\hat{f}'(t_i) - v_i}{1 - \gamma V_{ii}} + \frac{U_{ii}(\hat{f}^{(-i)}(t_i) - y_i)}{1 - \gamma V_{ii}}.\tag{A.6.3}$$

By substituting equation (A.6.3) to (A.6.1), we get

$$\hat{f}^{(-i)}(t_i) - y_i = \frac{\hat{f}(t_i) - y_i + \gamma \frac{T_{ii}}{1 - \gamma V_{ii}} (\hat{f}'(t_i) - v_i)}{1 - S_{ii} - \gamma \frac{T_{ii}}{1 - \gamma V_{ii}} U_{ii}}.$$

Consequently,

$$CV(\lambda, \gamma) = \frac{1}{n} \sum_{i=1}^n \left( \frac{\hat{f}(t_i) - y_i + \gamma \frac{T_{ii}}{1-\gamma V_{ii}} (\hat{f}'(t_i) - v_i)}{1 - S_{ii} - \gamma \frac{T_{ii}}{1-\gamma V_{ii}} U_{ii}} \right)^2.$$

□

## A.7 Reconstructions at SNR=3

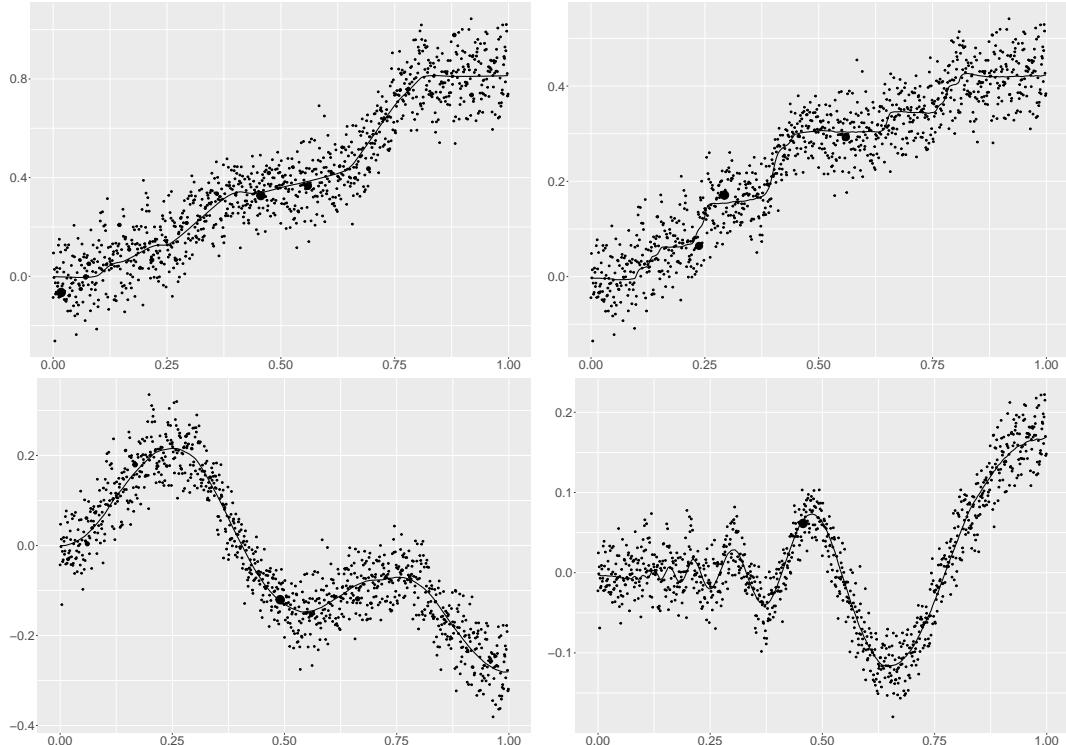
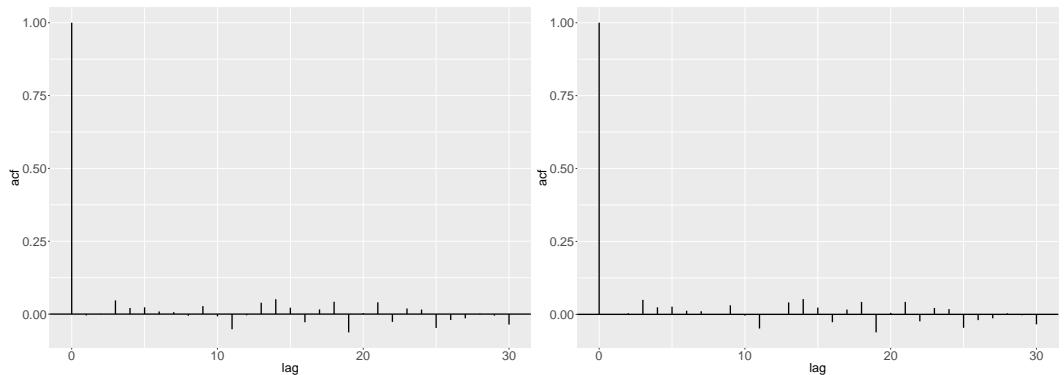
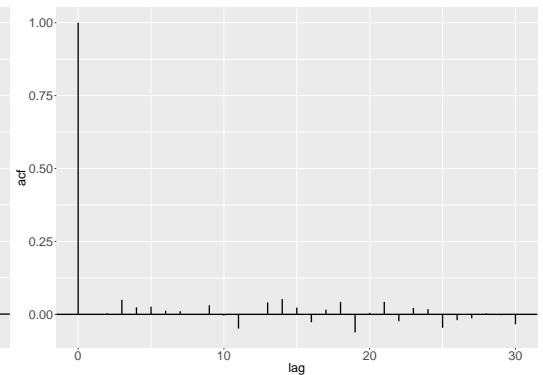


Figure A.1: Reconstructions of generated *Blocks*, *Bumps*, *HeaviSine* and *Doppler* functions by V-spline at SNR=3. The penalty values  $\lambda(t)$  in V-spline are projected into reconstructions. The black dots are the measurements. The bigger black dots indicate the larger penalty values.

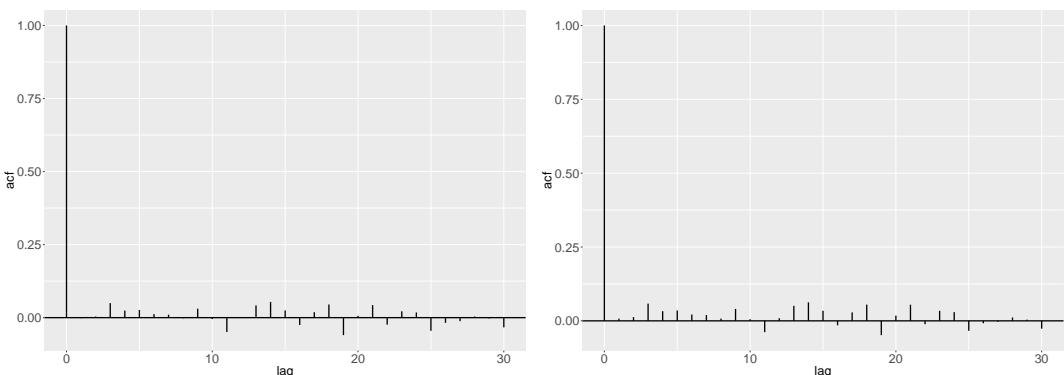
## A.8 Residual Analysis of Simulations



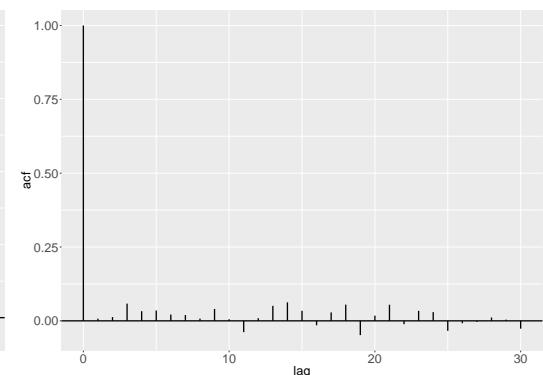
(a) ACF of residuals from *Blocks*



(b) ACF of residuals from *Bumps*



(c) ACF of residuals from *HeaviSine*



(d) ACF of residuals from *Doppler*

Figure A.2: ACF of residuals at SNR level of 7.

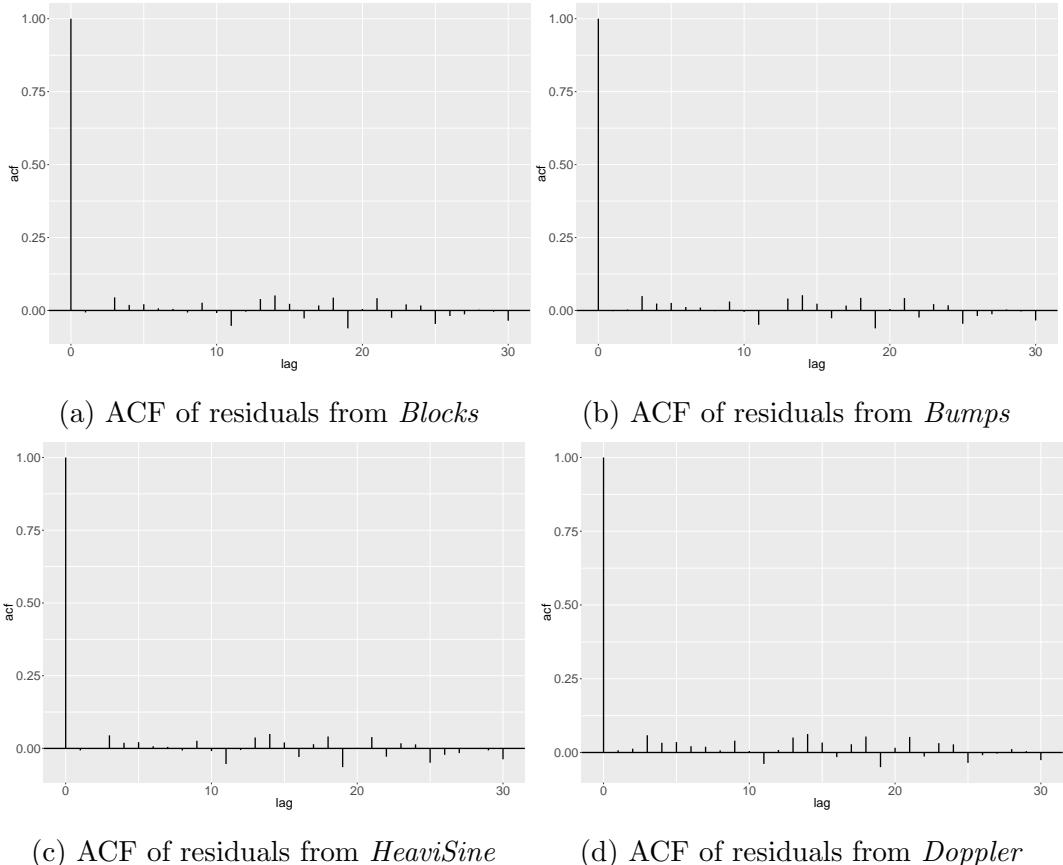


Figure A.3: ACF of residuals at SNR level of 3.



(a) residuals of  $x$



(b) residuals of  $y$

Figure A.4: Residuals of 2-dimensional real data reconstruction

# Appendix B

## Calculations And Figures of Adaptive Sequential MCMC

### B.1 Linear Simulation Calculations

#### The Forecast Distribution

Calculating the log-posterior of parameters requires finding out the forecast distribution of  $p(y_{1:t} | y_{1:t-1}, \theta)$ . A general way is using the joint distribution of  $y_t$  and  $y_{1:t-1}$ , which is  $p(y_{1:t} | \theta) \sim N(0, \Sigma_{YY})$  and following the procedure in Section 5.2.2 to work out the inverse matrix of a multivariate normal distribution. For example, one may find the inverse of the covariance matrix

$$\Sigma_{YY}^{-1} = B(I - A^{-1}B) = \frac{1}{\sigma^4} (\sigma^2 I - A^{-1}) \triangleq \frac{1}{\sigma^4} \begin{bmatrix} Z_t & b_t \\ b_t^\top & K_t \end{bmatrix}.$$

Therefore, the original form of this covariance is

$$\Sigma_{YY} = \sigma^4 \begin{bmatrix} (Z - bK^{-1}b^\top)^{-1} & -Z^{-1}b(K - b^\top Z^{-1}b)^{-1} \\ -K^{-1}b^\top(Z - bK^{-1}b^\top)^{-1} & (K - b^\top Z^{-1}b)^{-1} \end{bmatrix}.$$

For sake of simplicity, here we are using  $Z$  to represent the  $t \times t$  matrix  $Z_t$ ,  $b$  to represent the  $t \times 1$  vector  $b_t$  and  $K$  to represent the  $1 \times 1$  constant  $K_t$ . By denoting  $C_t^\top = [0 \ \dots \ 0 \ 1]$  and post-multiplying  $\Sigma_{YY}^{-1}$ , it gives us

$$\Sigma_{YY}^{-1} C_t = \frac{1}{\sigma^4} (\sigma^2 I - A^{-1}) C_t = \frac{1}{\sigma^4} \begin{bmatrix} b_t \\ K_t \end{bmatrix}. \quad (\text{B.1.1})$$

By using the formula, one can find a recursive way to update  $K_t$  and  $b_{t-1}$ , which are

$$K_t = \frac{\sigma^4}{\tau^2 + \sigma^2 + \phi^2(\sigma^2 - K_{t-1})}, \quad (\text{B.1.2})$$

$$b_t = \begin{bmatrix} \frac{b_{t-1}\phi K_t}{\sigma^2} \\ \frac{K_t(\sigma^2 + \tau^2) - \sigma^4}{\phi\sigma^2} \end{bmatrix}. \quad (\text{B.1.3})$$

With the above formula, the recursive way of updating the mean and covariance are

$$\bar{\mu}_t = \frac{\phi}{\sigma^2} K_{t-1} \bar{\mu}_{t-1} + \phi \left( 1 - \frac{K_{t-1}}{\sigma^2} \right) y_{t-1}, \quad (\text{B.1.4})$$

$$\bar{\Sigma}_t = \sigma^4 K_t^{-1}, \quad (\text{B.1.5})$$

where  $K_1 = \frac{\sigma^4}{\sigma^2 + \tau^2 + L^2\phi^2}$ . For calculation details, readers can refer to Appendix B.1.

By using the formula again, one term of equation (5.30) becomes

$$A_t^{-1}C_t = \left( I - \frac{M_t^{-1}u_t u_t^\top}{1 + u_t^\top M_t^{-1}u_t} \right) M_t^{-1}C_t, \quad (\text{B.1.6})$$

in which

$$M_t^{-1}C_t = \begin{bmatrix} A_{t-1}^{-1} & 0 \\ 0 & \sigma^2 \end{bmatrix} C_t = \sigma^2 C_t,$$

$$u_t^\top C_t = \begin{bmatrix} 0 & \cdots & 0 & \frac{-\phi}{\tau} & \frac{1}{\tau} \end{bmatrix} \begin{bmatrix} 0 \\ \vdots \\ 0 \\ 1 \end{bmatrix} = \frac{1}{\tau}.$$

Then the above equation becomes

$$A_t^{-1}C_t = \sigma^2 C_t - \frac{M_t^{-1}u_t \frac{\sigma^2}{\tau}}{1 + u_t^\top M_t^{-1}u_t}. \quad (\text{B.1.7})$$

Moreover,

$$M_t^{-1}u_t = \begin{bmatrix} A_{t-1}^{-1} & 0 \\ 0 & \sigma^2 \end{bmatrix} \begin{bmatrix} 0 \\ \vdots \\ 0 \\ -\frac{\phi}{\tau} \\ \frac{1}{\tau} \end{bmatrix} = \begin{bmatrix} A_{t-1}^{-1} & 0 \\ 0 & \sigma^2 \end{bmatrix} \begin{bmatrix} -\frac{\phi}{\tau} C_{t-1} \\ \frac{1}{\tau} \end{bmatrix} = \begin{bmatrix} -\frac{\phi}{\tau} A_{t-1}^{-1} C_{t-1} \\ \frac{\sigma^2}{\tau} \end{bmatrix},$$

$$u_t^\top M_t^{-1}u = \begin{bmatrix} 0 & \cdots & 0 & -\frac{\phi}{\tau} & \frac{1}{\tau} \end{bmatrix} \begin{bmatrix} -\frac{\phi}{\tau} A_{t-1}^{-1} C_{t-1} \\ \frac{\sigma^2}{\tau} \end{bmatrix} = \begin{bmatrix} -\frac{\phi}{\tau} C_{t-1}^\top & \frac{1}{\tau} \end{bmatrix} \begin{bmatrix} -\frac{\phi}{\tau} A_{t-1}^{-1} C_{t-1} \\ \frac{\sigma^2}{\tau} \end{bmatrix}$$

$$= \frac{\phi^2}{\tau^2} C_{t-1}^\top A_{t-1}^{-1} C_{t-1} + \frac{\sigma^2}{\tau^2}.$$

Thus

$$\begin{aligned}
A_t^{-1}C_t &= \begin{bmatrix} -b_t \\ \sigma^2 - K_t \end{bmatrix} = \sigma^2 C_t - \frac{1}{1 + \frac{\phi^2}{\tau^2} C_{t-1}^\top A_{t-1}^{-1} C_{t-1} + \frac{\sigma^2}{\tau^2}} \begin{bmatrix} -\frac{\phi\sigma^2}{\tau^2} A_{t-1}^{-1} C_{t-1} \\ \frac{\sigma^4}{\tau^2} \end{bmatrix} \\
&= \sigma^2 C_t - \frac{1}{\tau^2 + \phi^2 C_{t-1}^\top A_{t-1}^{-1} C_{t-1} + \sigma^2} \begin{bmatrix} -\phi\sigma^2 A_{t-1}^{-1} C_{t-1} \\ \sigma^4 \end{bmatrix}
\end{aligned} \tag{B.1.8}$$

and

$$\begin{aligned}
\sigma^2 - K_t &= \sigma^2 - \frac{\sigma^4}{\tau^2 + \phi^2 C_{t-1}^\top A_{t-1}^{-1} C_{t-1} + \sigma^2} \\
&= \sigma^2 - \frac{\sigma^4}{\tau^2 + \sigma^2 + \phi^2 (\sigma^2 - K_{t-1})}.
\end{aligned}$$

Hence,

$$K_t = \frac{\sigma^4}{\tau^2 + \sigma^2 + \phi^2 (\sigma^2 - K_{t-1})}, \tag{B.1.9}$$

and

$$b_t = \begin{bmatrix} \frac{b_{t-1}\phi K_t}{\sigma^2} \\ \frac{K_t(\sigma^2 + \tau^2) - \sigma^4}{\phi\sigma^2} \end{bmatrix},$$

$$\begin{aligned}
\bar{\mu}_t &= 0 - \sigma^4 K_t^{-1} b_t^\top (Z - b_t K_t^{-1} b_t^\top)^{-1} \sigma^{-4} (Z - b_t K_t^{-1} b_t^\top) y_{1:t-1} \\
&= -K_t^{-1} b_t^\top y_{1:t-1} \\
&= \frac{\phi}{\sigma^2} K_{t-1} \bar{\mu}_{t-1} + \phi \left( 1 - \frac{K_{t-1}}{\sigma^2} \right) y_{t-1}, \\
\bar{\Sigma}_t &= \sigma^4 (K_t - b_t^\top Z^{-1} b_t)^{-1} \\
&\quad - \sigma^4 K_t^{-1} b_t^\top (Z_t - b_t K_t^{-1} b_t^\top)^{-1} (Z_t - b_t K_t^{-1} b_t^\top) Z_t^{-1} b_t (K_t - b_t^\top Z_t^{-1} b_t)^{-1} \\
&= \sigma^4 (I - K_t^{-1} b_t^\top Z_t^{-1} b_t) (K_t - b_t^\top Z_t^{-1} b_t)^{-1} \\
&= \sigma^4 K_t^{-1},
\end{aligned}$$

where  $K_1 = \frac{\sigma^4}{\sigma^2 + \tau^2 + L^2 \phi^2}$ .

## The Estimation Distribution

As introduced before,  $p(x_t | y_{1:t})$  is a mixture Gaussian distribution with given  $\theta$  and its mean and variance can be found by

$$\mu_x^{(t)} = \frac{1}{N} \sum_i \mu_i \quad (\text{B.1.10})$$

$$\begin{aligned} \text{Var}[x^{(t)}] &= \text{E}[\text{Var}(x | y, \theta)] + \text{Var}[\text{E}(x | y, \theta)] \\ &= \frac{1}{N} \sum_i (\mu_i \mu_i^\top + \Sigma_i) - \frac{1}{N^2} \left( \sum_i \mu_i \right) \left( \sum_i \mu_i \right)^\top. \end{aligned} \quad (\text{B.1.11})$$

To find  $\mu_i$  and  $\Sigma_i$ , we will use the joint distribution of  $x_t$  and  $y_{1:t}$ , which is  $p(x_t, y_{1:t} | \theta) \sim N(0, \Gamma)$  and

$$\Gamma = \begin{bmatrix} C_t^\top (A - B)^{-1} C_t & C_t^\top (A - B)^{-1} \\ (A - B)^{-1} C_t & (I - A^{-1} B)^{-1} B^{-1} \end{bmatrix}.$$

Because of

$$C_t^\top A_t^{-1} = \begin{bmatrix} -b_t^\top & \sigma^2 - K_t \end{bmatrix},$$

thus, for any given  $\theta_i$ ,  $x_t | y_{1:t}, \theta_i \sim N\left(\mu_t^{(x)}, \sigma_t^{(x)2}\right)$ , where

$$\begin{aligned} \mu_i &= \phi \hat{x}_{t-1} + C_t^\top (A - B)^{-1} B (I - A^{-1} B) y_{1:t} \\ &= \phi \hat{x}_{t-1} + C_t^\top A^{-1} B y_{1:t} \\ &= \phi \hat{x}_{t-1} + \frac{1}{\sigma^2} C_t^\top A^{-1} y_{1:t} \\ &= 0 + \frac{1}{\sigma^2} \begin{bmatrix} -b_t^\top & \sigma^2 - K_t \end{bmatrix} \begin{bmatrix} y_{1:t-1} \\ y_t \end{bmatrix} \\ &= -\frac{1}{\sigma^2} b_{t-1}^\top y_{1:t-1} + \left(1 - \frac{K_t}{\sigma^2}\right) y_t \\ &= \frac{K_t \bar{\mu}_t}{\sigma^2} + \left(1 - \frac{K_t}{\sigma^2}\right) y_t \\ \Sigma_i &= C_t^\top (A - B)^{-1} C_t - C_t^\top (A - B)^{-1} B (I - A^{-1} B) (A - B)^{-1} C_t \\ &= C_t^\top (A - B)^{-1} C_t - C_t^\top A^{-1} B (A - B)^{-1} C_t \\ &= C_t^\top A^{-1} C_t \\ &= \sigma^2 - K_t. \end{aligned}$$

By substituting them into the equation (5.37) and (5.38), the estimated  $\hat{x}_t$  is easily got.

## B.2 OU-Process Calculation

### The Forecast Distribution

We are now using the capital letter  $Y$  to represent the joint  $\{y, v\}$  and  $Y_{1:t} = \{y_1, v_1, y_2, v_2, \dots, y_t, v_t\}$ ,  $Y_{t+1} = \{y_{t+1}, v_{t+1}\}$ . It is known that

$$\begin{aligned} p(Y_{1:t}, \theta) &\sim N\left(0, \Sigma_{YY}^{(t)}\right) \\ p(Y_{t+1}, Y_{1:t}, \theta) &\sim N\left(0, \Sigma_{YY}^{(t+1)}\right) \\ p(Y_{t+1} | Y_{1:t}, \theta) &\sim N\left(\bar{\mu}_{t+1}, \bar{\Sigma}_{t+1}\right) \end{aligned}$$

where the covariance matrix of the joint distribution is  $\Sigma_{YY}^{(t+1)} = (I_{t+1} - A_{t+1}^{-1}B_{t+1})^{-1}B_{t+1}^{-1}$ . Then, by taking its inverse, we will get

$$\Sigma_{YY}^{(t+1)(-1)} = B_{t+1}(I_{t+1} - A_{t+1}^{-1}B_{t+1})^{-1}.$$

To be clear, the matrix  $B_t$  is short for the matrix  $B_t(\sigma^2, \tau^2)$ , which is  $2t \times 2t$  diagonal matrix with elements  $\frac{1}{\sigma^2}, \frac{1}{\tau^2}$  repeating for  $t$  times on its diagonal. For instance, the very simple  $B_1(\sigma^2, \tau^2) = \begin{bmatrix} \frac{1}{\sigma^2} & 0 \\ 0 & \frac{1}{\tau^2} \end{bmatrix}_{2 \times 2}$  is a  $2 \times 2$  matrix.

Because of  $A$  is symmetric and invertible,  $B$  is the diagonal matrix defined as above, then they have the following property

$$\begin{aligned} AB &= A^\top B^\top = (BA)^\top, \\ A^{-1}B &= A^{-\top}B^\top = (BA^{-1})^\top. \end{aligned}$$

Followed up the form of  $\Sigma_{YY}^{(t+1)(-1)}$ , we can find out that

$$\begin{aligned} \Sigma_{YY}^{(t+1)(-1)} &= B_{t+1}(I_{t+1} - A_{t+1}^{-1}B_{t+1})^{-1} \\ &= B_{t+1}(B_{t+1}^{-1} - A_{t+1}^{-1})B_{t+1}^{-1} \\ &\triangleq \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} \begin{bmatrix} Z_{t+1} & b_{t+1} \\ b_{t+1}^\top & K_{t+1} \end{bmatrix} \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix}^{-1} \end{aligned}$$

where  $Z_{t+1}$  is a  $2t \times 2t$  matrix,  $b_{t+1}$  is a  $2t \times 2$  matrix and  $K_{t+1}$  is a  $2 \times 2$  matrix. Thus by taking its inverse again, we will get

$$\Sigma_{YY}^{(t+1)} = \begin{bmatrix} B_t^{-1}(Z_{t+1} - b_{t+1}K_{t+1}^{-1}b_{t+1}^\top)^{-1}B_t^{-1} & -B_t^{-1}Z_{t+1}^{-1}b_{t+1}(K_{t+1} - b_{t+1}^\top Z_{t+1}^{-1}b_{t+1})^{-1}B_1^{-1} \\ -B_1^{-1}K_{t+1}^{-1}b_{t+1}^\top(Z_{t+1} - b_{t+1}K_{t+1}^{-1}b_{t+1}^\top)^{-1}B_t^{-1} & B_1^{-1}(K_{t+1} - b_{t+1}^\top Z_{t+1}^{-1}b_{t+1})^{-1}B_1^{-1} \end{bmatrix}.$$

It is easy to find the relationship between  $A_{t+1}$  and  $A_t$  in the Sherman-Morrison-Woodbury form, which is

$$A_{t+1} = \begin{bmatrix} A_t & \cdot & \cdot \\ \cdot & \frac{1}{\sigma^2} & \cdot \\ \cdot & \cdot & \frac{1}{\tau^2} \end{bmatrix} + U_{t+1}U_{t+1}^\top \triangleq M_{t+1} + U_{t+1}U_{t+1}^\top,$$

$$\text{where } M_{t+1} = \begin{bmatrix} A_t & \cdot & \cdot \\ \cdot & \frac{1}{\sigma^2} & \cdot \\ \cdot & \cdot & \frac{1}{\tau^2} \end{bmatrix} = \begin{bmatrix} A_t & 0 \\ 0 & B_1 \end{bmatrix} \text{ and its inverse is } M_{t+1}^{-1} = \begin{bmatrix} A_t^{-1} & 0 \\ 0 & B_1^{-1} \end{bmatrix}.$$

Additionally,  $U$  is a  $2t+2 \times 2$  matrix in the following form

$$U_{t+1} = \frac{1}{\sqrt{1-\rho_{t+1}^2}} \begin{bmatrix} \mathbf{0}_{2t-2} & \mathbf{0}_{2t-2} \\ \frac{1}{\sigma_{t+1}^{(x)}} & 0 \\ \frac{1-e^{-\gamma\Delta_{t+1}}}{\gamma\sigma_{t+1}^{(x)}} - \frac{\rho_{t+1}e^{-\gamma\Delta_{t+1}}}{\sigma_{t+1}^{(u)}} & \frac{\sqrt{1-\rho_{t+1}^2}e^{-\gamma\Delta_{t+1}}}{\sigma_{t+1}^{(u)}} \\ -\frac{1}{\sigma_{t+1}^{(x)}} & 0 \\ \frac{\rho_{t+1}}{\sigma_{t+1}^{(u)}} & -\frac{\sqrt{1-\rho_{t+1}^2}}{\sigma_{t+1}^{(u)}} \end{bmatrix} \triangleq \begin{bmatrix} C_{t+1} \\ D_{t+1} \end{bmatrix},$$

$$\text{where } S_{t+1} = \frac{1}{\sqrt{1-\rho_{t+1}^2}} \begin{bmatrix} \frac{1}{\sigma_{t+1}^{(x)}} & 0 \\ \frac{1-e^{-\gamma\Delta_{t+1}}}{\gamma\sigma_{t+1}^{(x)}} - \frac{\rho_{t+1}e^{-\gamma\Delta_{t+1}}}{\sigma_{t+1}^{(u)}} & \frac{\sqrt{1-\rho_{t+1}^2}e^{-\gamma\Delta_{t+1}}}{\sigma_{t+1}^{(u)}} \end{bmatrix},$$

$$D_{t+1} = \frac{1}{\sqrt{1-\rho_{t+1}^2}} \begin{bmatrix} -\frac{1}{\sigma_{t+1}^{(x)}} & 0 \\ \frac{\rho_{t+1}}{\sigma_{t+1}^{(u)}} & -\frac{\sqrt{1-\rho_{t+1}^2}}{\sigma_{t+1}^{(u)}} \end{bmatrix} \text{ and } C_{t+1} = \begin{bmatrix} 0 & 0 \\ \vdots & \vdots \\ 0 & 0 \\ 1 & 0 \\ 0 & 1 \end{bmatrix} = \begin{bmatrix} \mathbf{0}_t \\ I_2 \end{bmatrix}.$$

By post-multiplying  $\Sigma_{YY}^{(t+1)(-1)}$  with  $C_{t+1}$ , it gives us

$$\begin{aligned} \Sigma_{YY}^{(t+1)(-1)} C_{t+1} &= B_{t+1} (I_{t+1} - A_{t+1}^{-1} B_{t+1}) C_{t+1} \\ &= \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} \left( \begin{bmatrix} B_t^{-1} & 0 \\ 0 & B_1^{-1} \end{bmatrix} - A_{t+1}^{-1} \right) \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} C_{t+1} \\ &= \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} \begin{bmatrix} Z_{t+1} & b_{t+1} \\ b_{t+1}^\top & K_{t+1} \end{bmatrix} \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} C_{t+1} \\ &= \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} \begin{bmatrix} b_{t+1} B_1 \\ K_{t+1} B_1 \end{bmatrix}. \end{aligned}$$

and the property of  $A_{t+1}^{-1}$  is

$$A_{t+1}^{-1}C_{t+1} = \begin{bmatrix} -b_{t+1} \\ B_1^{-1} - K_{t+1} \end{bmatrix}.$$

Moreover, by pre-multiplying  $C_{t+1}^\top$  on the left side of the above equation, we will have

$$C_{t+1}^\top A_{t+1}^{-1} C_{t+1} = B_1^{-1} - K_{t+1}, \quad (\text{B.2.1})$$

$$K_{t+1} = B_1^{-1} - C_{t+1}^\top A_{t+1}^{-1} C_{t+1}. \quad (\text{B.2.2})$$

We may use Sherman-Morrison-Woodbury formula to find the inverse of  $A_{t+1}$  in a recursive way, which is

$$A_{t+1}^{-1} = (M_{t+1} + U_{t+1}U_{t+1}^\top)^{-1} = M_{t+1}^{-1} - M_{t+1}^{-1}U_{t+1}(I + U_{t+1}^\top M_{t+1}^{-1}U_{t+1})^{-1}U_{t+1}^\top M_{t+1}^{-1}. \quad (\text{B.2.3})$$

Consequently, it is easy to find that  $M_{t+1}^{-1}C_{t+1} = \begin{bmatrix} 0 \\ B_1^{-1} \end{bmatrix}$  and

$$\begin{aligned} A_{t+1}^{-1}C_{t+1} &= \begin{bmatrix} 0 \\ B_1^{-1} \end{bmatrix} - \begin{bmatrix} A_t^{-1} & 0 \\ 0 & B_1^{-1} \end{bmatrix} \begin{bmatrix} C_t S_{t+1} \\ D \end{bmatrix} (I + U_{t+1}^\top M_{t+1}^{-1}U_{t+1})^{-1} \begin{bmatrix} S_{t+1}^\top C_t^\top & D_{t+1}^\top \end{bmatrix} \begin{bmatrix} 0 \\ B_1^{-1} \end{bmatrix} \\ &= \begin{bmatrix} 0 \\ B_1^{-1} \end{bmatrix} - \begin{bmatrix} A_t^{-1} C_t S_{t+1} \\ B_1^{-1} D_{t+1} \end{bmatrix} (I + U_{t+1}^\top M_{t+1}^{-1}U_{t+1})^{-1} D_{t+1}^\top B_1^{-1} \\ &= \begin{bmatrix} 0 \\ B_1^{-1} \end{bmatrix} - \begin{bmatrix} A_t^{-1} C_t S_{t+1} \\ B_1^{-1} D_{t+1} \end{bmatrix} (I + S_{t+1}^\top C_t^\top A_t^{-1} C_t S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-1} D_{t+1}^\top B_1^{-1} \\ &= \begin{bmatrix} 0 \\ B_1^{-1} \end{bmatrix} - \begin{bmatrix} A_t^{-1} C_t S_{t+1} \\ B_1^{-1} D_{t+1} \end{bmatrix} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-1} D_{t+1}^\top B_1^{-1}. \end{aligned}$$

Thus, by using the equation (B.2.2), we will get

$$K_{t+1} = B_1^{-1} D_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-1} D_{t+1}^\top B_1^{-1}, \quad (\text{B.2.4})$$

and

$$\begin{aligned} b_{t+1} &= A_t^{-1} C_t S_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-1} D_{t+1}^\top B_1^{-1} \\ &= \begin{bmatrix} -b_t \\ B_1^{-1} - K_t \end{bmatrix} S_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-1} D_{t+1}^\top B_1^{-1}. \end{aligned}$$

To achieve the recursive updating formula, firstly we need to find the form of  $b_{t+1}^\top B_t^2 Y_{1:t}$ .

In fact, it is

$$\begin{aligned}
b_{t+1}^\top B_t Y_{1:t} &= B_1^{-\top} D_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-\top} S_{t+1}^\top \begin{bmatrix} -b_t^\top & B_1^{-1} - K_t \end{bmatrix} B_t \begin{bmatrix} Y_{1:t-1} \\ Y_t \end{bmatrix} \\
&= B_1^{-\top} D_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-\top} S_{t+1}^\top \\
&\quad (-b_t^\top B_{t-1} Y_{1:t-1} + (B_1^{-1} - K_t) B_1 Y_t) \\
&= B_1^{-\top} D_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-\top} S_{t+1}^\top (K_t B_1 \bar{\mu}_t + (I - K_t B_1) Y_t),
\end{aligned}$$

By using equation (B.2.4) and simplifying the above equation, one can achieve a recursive updating form of the mean, which is

$$\begin{aligned}
\bar{\mu}_{t+1} &= -B_1 K_{t+1}^{-1} b_{t+1}^\top B_t Y_{1:t} \\
&= -D_{t+1}^{-\top} S_{t+1}^\top (K_t B_1 \bar{\mu}_t + (I - K_t B_1) Y_t) \\
&= -D_{t+1}^{-\top} S_{t+1}^\top (Y_t + K_t B_1 (\bar{\mu}_t - Y_t)),
\end{aligned}$$

where by simplifying  $D^{-\top} S^\top$ , one may find

$$D_{t+1}^{-\top} S_{t+1}^\top = \begin{bmatrix} -1 & -\frac{1-e^{-\gamma\Delta_{t+1}}}{\gamma} \\ 0 & -e^{-\gamma\Delta_{t+1}} \end{bmatrix} = -\Phi_{t+1},$$

which is the negative of forward process. Then the final form of recursive updating formula are

$$\begin{cases} \bar{\mu}_{t+1} = \Phi_{t+1} K_t B_1 \bar{\mu}_t + \Phi_{t+1} (I - K_t B_1) Y_t \\ \bar{\Sigma}_{t+1} = (B_1 K_{t+1} B_1)^{-1} \end{cases}. \quad (\text{B.2.5})$$

The matrix  $K_{t+1}$  is updated via

$$K_{t+1} = B_1^{-1} D_{t+1} (I + S_{t+1}^\top (B_1^{-1} - K_t) S_{t+1} + D_{t+1}^\top B_1^{-1} D_{t+1})^{-1} D_{t+1}^\top B_1^{-1}, \quad (\text{B.2.6})$$

or updating its inverse in the following form makes the computation faster, that is

$$\begin{cases} K_{t+1}^{-1} = B_1 D_{t+1}^{-\top} D_{t+1}^{-1} B_1 + B_1 \Phi_{t+1} (B_1^{-1} - K_t) \Phi_{t+1}^\top B_1 + B_1, \\ \bar{\Sigma}_{t+1} = D_{t+1}^{-\top} D_{t+1}^{-1} + \Phi_{t+1} (B_1^{-1} - K_t) \Phi_{t+1}^\top + B_1^{-1} \end{cases}$$

$$\text{and } K_1 = B_1^{-1} - A_1^{-1} = \begin{bmatrix} \frac{\sigma^4}{\sigma^2 + L_x^2} & 0 \\ 0 & \frac{\tau^4}{\tau^2 + L_u^2} \end{bmatrix}.$$

## The Estimation Distribution

Because of the joint distribution (5.58), one can find the best estimation with a given  $\theta$  by

$$\begin{aligned} X | Y, \theta &\sim N(A^{-1}BY, A^{-1}) \\ &\sim N(L^{-\top}L^{-1}BY, L^{-\top}L^{-1}) \\ &\sim N(L^{-\top}W, L^{-\top}L^{-1}), \end{aligned}$$

thus

$$\hat{X} = L^{-\top}(W + Z),$$

where  $Z \sim N(0, I(\sigma, \tau))$ .

For  $X_{t+1}$ , the joint distribution with  $Y$  updated to stage  $t+1$  is

$$X_{t+1}, Y | \theta \sim N\left(0, \begin{bmatrix} C_{t+1}^\top (A - B)^{-1} C_{t+1} & C_{t+1}^\top (A - B)^{-1} \\ (A - B)^{-1} C_{t+1} & (I - A^{-1}B)^{-1} B^{-1} \end{bmatrix}\right),$$

where  $C_{t+1}^\top = \begin{bmatrix} 0 & \cdots & 0 & 1 & 0 \\ 0 & \cdots & 0 & 0 & 1 \end{bmatrix}$  is a  $2 \times 2(t+1)$  matrix. Thus

$$X_{t+1} | Y, \theta \sim N\left(\bar{\mu}_{t+1}^{(X)}, \bar{\Sigma}_{t+1}^{(X)}\right),$$

where

$$\begin{aligned} \bar{\mu}_{t+1}^{(X)} &= C_{t+1}^\top A^{-1}BY = C_{t+1}^\top L^{-\top}W, \\ \bar{\Sigma}_{t+1}^{(X)} &= C_{t+1}^\top A^{-1}C_{t+1} = U_{t+1}^\top U_{t+1}, \end{aligned}$$

and  $U_{t+1} = L^{-1}C_{t+1}$ .

The filtering distribution of the state with given parameters is  $p(X_t | Y_{1:t}, \theta)$ . To find its form, one can use the joint distribution of  $X_{t+1}$  and  $Y_{1:t+1}$ , which is  $p(X_{t+1}, Y_{1:t+1} | \theta) \sim N(0, \Gamma)$ , where

$$\Gamma = \begin{bmatrix} C_{t+1}^\top (A - B)^{-1} C_{t+1} & C_{t+1}^\top (A - B)^{-1} \\ (A - B)^{-1} C_{t+1} & (I - A^{-1}B)^{-1} B^{-1} \end{bmatrix}.$$

Because of

$$C_{t+1}^\top A_{t+1}^{-1} = \begin{bmatrix} -b_{t+1}^\top & B_1^{-1} - K_{t+1} \end{bmatrix},$$

then  $X_{t+1} | Y_{1:t+1}, \theta \sim N\left(\bar{\mu}_{t+1}^{(X)}, \bar{\sigma}_{t+1}^{(X)2}\right)$ , where

$$\begin{aligned}
\bar{\mu}_{t+1}^{(X)} &= \Phi \hat{x}_t + C_{t+1}^\top (A - B)^{-1} B (I - A^{-1} B) Y_{1:t+1} \\
&= \Phi \hat{x}_t + C_{t+1}^\top A^{-1} B Y_{1:t+1} \\
&= 0 + \begin{bmatrix} -b_{t+1}^\top & B_1^{-1} - K_{t+1} \end{bmatrix} \begin{bmatrix} B_t & 0 \\ 0 & B_1 \end{bmatrix} \begin{bmatrix} Y_{1:t} \\ Y_{y+1} \end{bmatrix} \\
&= -b^\top B_t Y_{1:t} + (I - B_1 K_{t+1}) Y_{t+1} \\
&= K_{t+1} B_1 \bar{\mu}_{t+1} + (I - B_1 K_{t+1}) Y_{t+1} \\
\bar{\sigma}_{t+1}^{(X)2} &= C_{t+1}^\top (A - B)^{-1} C_{t+1} - C_{t+1}^\top (A - B)^{-1} B (I - A^{-1} B) (A - B)^{-1} C_{t+1} \\
&= C_{t+1}^\top (A - B)^{-1} C_{t+1} - C_{t+1}^\top A^{-1} B (A - B)^{-1} C_{t+1} \\
&= C_{t+1}^\top A^{-1} C_{t+1} \\
&= B_1^{-1} - K_{t+1}.
\end{aligned}$$

### B.3 Covariance Matrix in Details

$$\begin{aligned}
\Sigma_t &= \begin{bmatrix} \sigma_t^{(x)2} & \rho_t \sigma_t^{(x)} \sigma_t^{(u)} \\ \rho_t \sigma_t^{(x)} \sigma_t^{(u)} & \sigma_t^{(u)2} \end{bmatrix} \\
\Sigma_t^{-1} &= \frac{1}{1 - \rho_t^2} \begin{bmatrix} \frac{1}{\sigma_t^{(x)2}} & -\frac{\rho_t}{\sigma_t^{(x)} \sigma_t^{(u)}} \\ -\frac{\rho_t}{\sigma_t^{(x)} \sigma_t^{(u)}} & \frac{1}{\sigma_t^{(u)2}} \end{bmatrix} \\
M_t^\top &= \begin{bmatrix} 1 & 0 \\ \frac{1-e^{-\gamma\Delta_t}}{\gamma} & e^{-\gamma\Delta_t} \end{bmatrix} \\
z_t &= \begin{bmatrix} x_t \\ u_t \end{bmatrix} \\
M_t^\top \Sigma_t^{-1} &= \frac{1}{1 - \rho_t^2} \begin{bmatrix} \frac{1}{\sigma_t^{(x)2}} & -\frac{\rho_t}{\sigma_t^{(x)} \sigma_t^{(u)}} \\ \frac{1-e^{-\gamma\Delta_t}}{\gamma \sigma_t^{(x)2}} - \frac{\rho_t e^{-\gamma\Delta_t}}{\sigma_t^{(x)} \sigma_t^{(u)}} & -\frac{\rho_t (1-e^{-\gamma\Delta_t})}{\gamma \sigma_t^{(x)} \sigma_t^{(u)}} + \frac{e^{-\gamma\Delta_t}}{\sigma_t^{(u)2}} \end{bmatrix} \\
M_t^\top \Sigma_t^{-1} M_t &= \frac{1}{1 - \rho_t^2} \begin{bmatrix} \frac{1}{\sigma_t^{(x)2}} & \frac{1-e^{-\gamma\Delta_t}}{\gamma \sigma_t^{(x)2}} - \frac{\rho_t e^{-\gamma\Delta_t}}{\sigma_t^{(x)} \sigma_t^{(u)}} \\ \frac{1-e^{-\gamma\Delta_t}}{\gamma \sigma_t^{(x)2}} - \frac{\rho_t e^{-\gamma\Delta_t}}{\sigma_t^{(x)} \sigma_t^{(u)}} & \frac{(1-e^{-\gamma\Delta_t})^2}{\gamma^2 \sigma_t^{(x)2}} - \frac{2\rho_t e^{-\gamma\Delta_t} (1-e^{-\gamma\Delta_t})}{\gamma \sigma_t^{(x)} \sigma_t^{(u)}} + \frac{e^{-2\gamma\Delta_t}}{\sigma_t^{(u)2}} \end{bmatrix}
\end{aligned}$$

$$\Sigma_4^{(X)-1} = \frac{1}{1 - \rho_t^2} \begin{bmatrix} \frac{1 - \rho_t^2}{\sigma_1^{(x)2}} + \frac{1}{\sigma_2^{(x)2}} & -\frac{1}{\sigma_2^{(x)2}} & 0 & 0 & 0 & 0 \\ -\frac{1}{\sigma_2^{(x)2}} + \frac{1}{\sigma_3^{(x)2}} & \frac{1}{\sigma_2^{(x)2}} + \frac{1}{\sigma_3^{(x)2}} & -\frac{1}{\sigma_3^{(x)2}} & 0 & 0 & 0 \\ 0 & -\frac{1}{\sigma_3^{(x)2}} & \frac{1}{\sigma_3^{(x)2}} + \frac{1}{\sigma_4^{(x)2}} & -\frac{1}{\sigma_4^{(x)2}} & 0 & 0 \\ 0 & 0 & -\frac{1}{\sigma_4^{(x)2}} & \frac{1}{\sigma_4^{(x)2}} & 0 & 0 \\ 0 & \top & \top & \top & \top & \top \\ \top & \top & \top & 0 & 0 & 0 \end{bmatrix} + \frac{1 - e^{-\gamma\Delta_t}}{\gamma\sigma_t^{(x)2}} \frac{(1 - e^{-\gamma\Delta_t})^2}{\sigma_t^{(u)2}} + \frac{e^{-2\gamma\Delta_t}}{\gamma\sigma_t^{(x)}\sigma_t^{(u)}} - \frac{2\rho_t e^{-\gamma\Delta_t}(1 - e^{-\gamma\Delta_t})}{\gamma\sigma_t^{(x)}\sigma_t^{(u)}}, \quad \Delta_t = T_t - T_{t-1}. \text{ Symbol } \top \text{ indicates the transpose term in the matrix.}$$

## B.4 Real Data Implementation

### Efficiency Plots

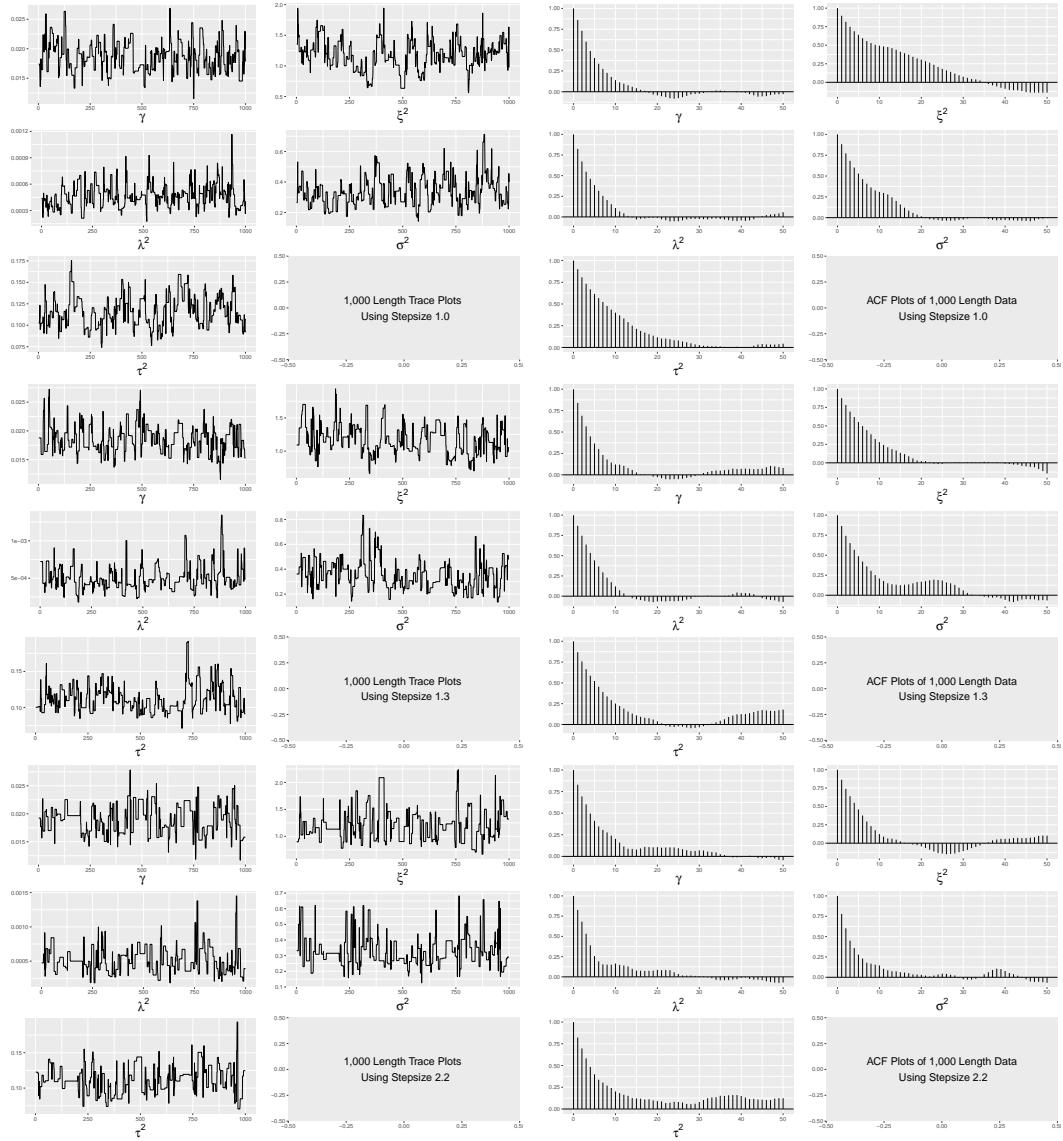




Figure B.1: Running the same amount of time and taking the same length of data, the step size  $\epsilon = 2.5$  returns the highest ESSUT value and generates more effective samples in a lower correlated relationship.

## Comparing Estimation with Different Length of Data

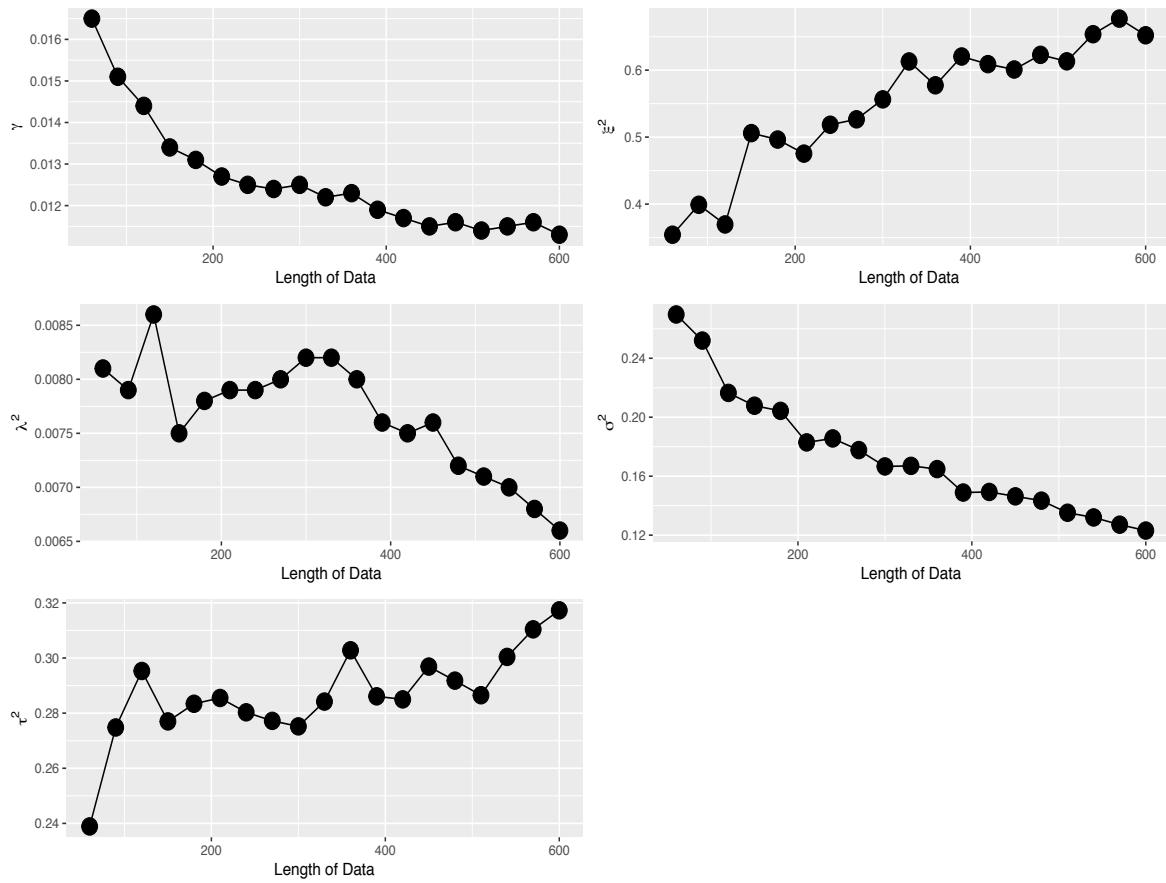


Figure B.2: Impacts of data length on optimal parameter. There is an obvious trend on the estimation against length of data in the estimation process.

Table B.1: Parameter estimation by running the whole surface learning and DA MH processes with different length of data

Length	Time	$\gamma$	$\xi^2$	$\lambda^2$	$\sigma^2$	$\tau^2$	$\alpha_1$	$\alpha_2$	$x$	$u$	$y$	$v$
<b>Obs</b>	-	-	-	-	-	-	-	-	-339.0569	0.0413	-100.2065	1.1825
<b>600</b>	85.96	0.0113	0.6521	0.0066	0.1231	0.3173	0.0536	0.7873	-339.0868	0.4331	-100.1498	-0.7498
<b>570</b>	85.72	0.0116	0.6770	0.0068	0.1271	0.3104	0.0542	0.7638	-339.0872	0.4292	-100.1476	-0.7356
<b>540</b>	84.25	0.0115	0.6537	0.0070	0.1320	0.3004	0.0662	0.7553	-339.0889	0.4326	-100.1435	-0.7375
<b>510</b>	85.13	0.0114	0.6132	0.0071	0.1352	0.2865	0.0684	0.7310	-339.0907	0.4376	-100.1387	-0.7425
<b>480</b>	81.23	0.0116	0.6229	0.0072	0.1434	0.2918	0.0534	0.8127	-339.0921	0.4368	-100.1359	-0.7408
<b>450</b>	81.57	0.0115	0.6010	0.0076	0.1463	0.2969	0.0580	0.7931	-339.0924	0.4432	-100.1348	-0.7521
<b>420</b>	80.31	0.0117	0.6090	0.0075	0.1493	0.2850	0.0626	0.7636	-339.0938	0.4392	-100.1310	-0.7397
<b>390</b>	78.84	0.0119	0.6204	0.0076	0.1489	0.2861	0.0620	0.7581	-339.0931	0.4373	-100.1320	-0.7354
<b>360</b>	76.66	0.0123	0.5774	0.0080	0.1648	0.3028	0.0554	0.7762	-339.0971	0.4457	-100.1248	-0.7563
<b>330</b>	76.38	0.0122	0.6130	0.0082	0.1670	0.2842	0.0636	0.7830	-339.0969	0.4403	-100.1220	-0.7336
<b>300</b>	73.27	0.0125	0.5564	0.0082	0.1666	0.2752	0.0548	0.8212	-339.0989	0.4457	-100.1174	-0.7443
<b>270</b>	73.68	0.0124	0.5266	0.0080	0.1777	0.2772	0.0636	0.6698	-339.1027	0.4489	-100.1104	-0.7546
<b>240</b>	71.85	0.0125	0.5185	0.0079	0.1856	0.2803	0.0548	0.7336	-339.1050	0.4495	-100.1067	-0.7590
<b>210</b>	71.26	0.0127	0.4754	0.0079	0.1829	0.2855	0.0656	0.7561	-339.1057	0.4559	-100.1065	-0.7754
<b>180</b>	70.25	0.0131	0.4964	0.0078	0.2043	0.2834	0.0566	0.7880	-339.1107	0.4498	-100.0955	-0.7620
<b>150</b>	70.87	0.0134	0.5060	0.0075	0.2078	0.2770	0.0582	0.7801	-339.1129	0.4436	-100.0916	-0.7507
<b>120</b>	68.38	0.0144	0.3696	0.0086	0.2165	0.2953	0.0570	0.7754	-339.1168	0.4705	-100.0825	-0.8057
<b>90</b>	65.73	0.0151	0.3990	0.0079	0.2520	0.2748	0.0552	0.8188	-339.1296	0.4550	-100.0556	-0.7740
<b>60</b>	68.81	0.0165	0.3543	0.0081	0.2697	0.2389	0.0694	0.7176	-339.1412	0.4527	-100.0204	-0.7573

## B.5 Comparison Between Batch and Sliding Window Methods

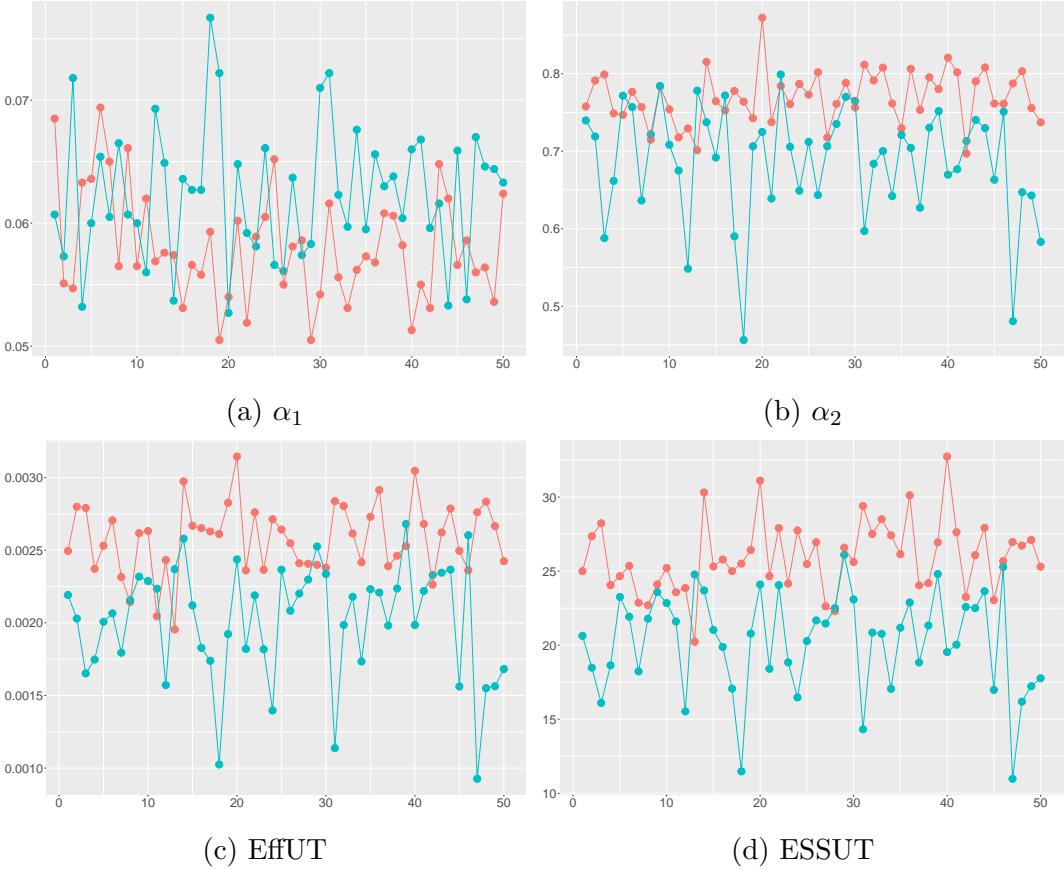


Figure B.3: Comparison of  $\alpha_1$ ,  $\alpha_2$ , EffUT and ESSUT between batch MCMC (orange) and sliding window MCMC (green).

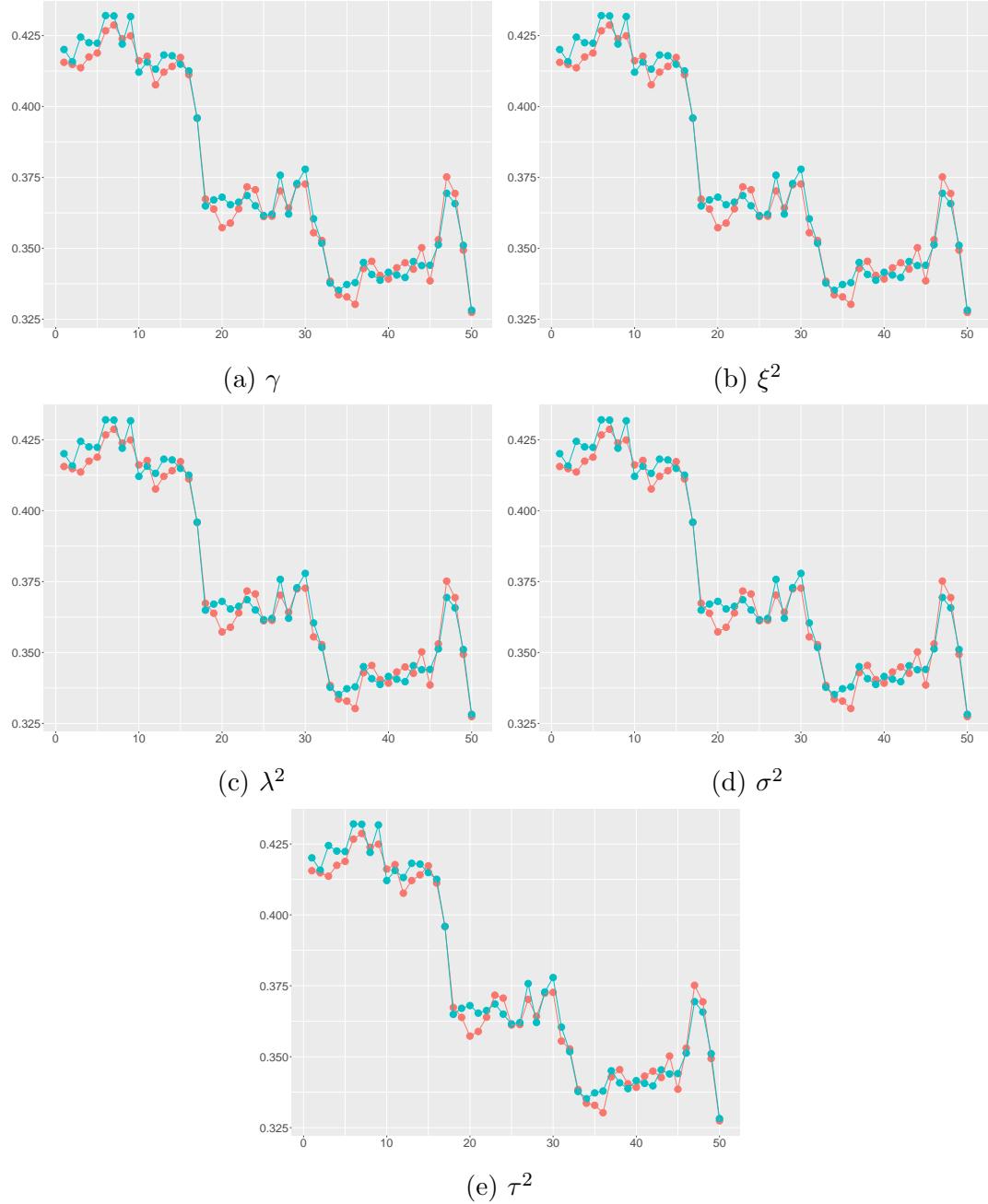


Figure B.4: Comparison of parameters estimation between batch MCMC (orange) and sliding window MCMC (green).

## B.6 Parameter Evolution Visualization









Figure B.4: Parameter Evolution Visualization. The correlation among parameters does not change two much. The parameters are considered static.

# Appendix C

## A Spin-off Outcome: Data Simplification Method

### C.1 Introduction

GPS devices are widely used in orchard planting and maintenance. This location-based system allows orchardist to check trajectory of tractors. The trajectory is a connection by a time series successive positions recorded by GPS devices. A classical GPS device records skeleton information, including time mark, latitude, longitude, number of available satellites, etc. Recently, researchers try to enrich trajectory (called Semantic Trajectory) by adding background geographic information to discover meaningful pattern (Ying *et al.*, 2011).

Normally GPS units record more data than necessary and cause more errors due to weak signals or shelter from branches. To obtain a higher accurate observation dataset and to save local storage space, several data simplification methods were proposed and are focusing on simplifying data set by making either a local or global decision.

A local simplification algorithm focuses on a couple of particular consecutive points. By analyzing the relationship between these points, a decision is made that which point can be deleted or retained. Distance threshold algorithm is one of these algorithms. All points, whose distance to the preceding track point is less than a predetermined threshold, are deleted. Direction changing algorithm is another one. The point is retained if the change in direction is greater than a predetermined threshold (Ivanov, 2012).

Alternatively, global simplification algorithms have an overview of all tracked points. After analyzing the relationships among these points, a decision will be made about

which one or more points to delete or to retain. The Douglas-Peucker algorithm is the most popular one (Douglas and Peucker, 1973). A proposed simplification method, represented by Chen *et al.* (2009), consider both the skeleton information and semantic meanings of a trajectory when performing simplification.

Intuitively, the global simplification algorithms can be applied on off-line data analyses and local simplification algorithms will perform better on on-line or real-time track simplification. However, a pertinent algorithm is required in our case.

In our case, a GPS log is a sequence time series points  $p_i \in P$ ,  $P = \{p_1, p_2, \dots, p_n\}$ . Each GPS point  $p_i$  contains information of time mark, latitude, longitude and semantic information of velocity, heading direction and boom status, which can be written in form of

$$T = \{p_t = [x_t, y_t, v_t, \theta_t, b_t] \mid t \in \mathbb{R}\}. \quad (\text{C.1.1})$$

Sequentially connect these points will give us a trajectory of a moving vehicle. Particularly, a tractor working on an orchard generates two kinds of boom status information: operating and not-operating. This information is recorded by GPS units and is indicated by  $b = 1$  for operating and  $b = 0$  for not-operating.

To move further, here are two concepts that will be useful to understand the simplification scheme.

- **Segment** A segment is a part of the consecutive trajectory. Regarding the status of the boom, the trajectory can be simply divided into two kinds of the segment in our dataset, one is boom-operating, the other is boom-not-operating.
- **Direction.** Direction  $\theta$  denotes the heading direction of a tractor at a specific point location. This parameter uses north direction as a basis, in which way  $0^\circ \leq \theta < 360^\circ$ .

## C.2 Simplification Algorithm

The first two steps are designed to reduce some errors caused by misoperation and GPS units bugs.

- Merging Phase. If the length of a segment composed of consecutive boom operating or not-operating points is less than a threshold, merge this one into its backward segment.
- Removing Phase. If two or more data points have duplicated time mark, remove the latter ones.

Now only two types of segment points are left in GPS log, boom operating, and not-operating and the length of each segment are greater than the predetermined threshold.

The following algorithm is based on the relationship between a candidate point  $p_i$  and its neighboring points  $p_{i-1}$  and  $p_{i+1}$ , and the importance of the  $p_i$  in the segment where it belongs to,  $i = 2, \dots, n - 1$ .

- Rule 1. The candidate point  $p_i$  is retained if it is not linear predictable or cannot be used for linear predicting. With the velocity information  $v_{i-1}, v_i$  at point  $p_{i-1}, p_i$  and time differences  $\Delta t_{i-1} = |t_i - t_{i-1}|, \Delta t_i = |t_{i+1} - t_i|$ , an estimated position can be calculated by  $\hat{p}_i = \Delta t_{i-1}p_{i-1}, \hat{p}_{i+1} = \Delta t_i p_i$ . If the distance  $|\hat{p}_i - p_i|$  or  $|\hat{p}_{i+1} - p_{i+1}|$  is less than a threshold, then the point  $p_i$  is not linear predictable or cannot be used for linear predicting.
- Rule 2. Select a candidate point  $p_i$ . Retain this point if the distance between  $p_i$  and  $p_{i-1}$  is greater than the threshold  $d$ , where  $d$  is the mean distances of these points  $p_{i-1}, p_i, \dots, p_{i+k}$  with same boom status  $b_{i-1} = b_i = \dots = b_{i+k}$ .
- Rule 3. Neighbor Heading Changing. The candidate point  $p_i$  belongs to the track if  $|\theta_i - \theta_{i-1}| + |\theta_i - \theta_{i+1}| > \theta$ , where  $|\theta_i - \theta_{i-1}|$  and  $|\theta_i - \theta_{i+1}|$  are the direction changes between points  $p_i$  and  $p_{i-1}$  and between points  $p_i$  and  $p_{i+1}$ ,  $\theta$  is predefined threshold.
- Rule 4. The candidate point  $p_i$  belongs to the track if the boom status  $b_i \neq b_{i-1}$ .

Finally, the point  $p_i$  belongs to the track if Rule 1 = TRUE or Rule 2 = TRUE or Rule 3 = TRUE or Rule 4 = TRUE.

### C.3 Evaluation

Errors are measured by Synchronized Euclidean Distance (Lawson *et al.*, 2011). SED measures the distances between the original and compressed trace at the same time. As shown in figure C.1, the green points  $P_{t1}, \dots, P_{t5}$  are original positions. After simplification, the points  $P_{t2}, P_{t3}$  and  $P_{t4}$  were removed. The black curve is the original trajectory, in contrast, the gray dash-dot line is the simplified trajectory. The blue points  $P'_{t2}, P'_{t3}$  and  $P'_{t4}$  on simplified trajectory have the same time difference as the point  $P_{t2}, P_{t3}$  and  $P_{t4}$  on original trajectory did. For instance, the time difference between  $P_{t2}$  and  $P_{t3}$  is the same as that between  $P'_{t2}$  and  $P'_{t3}$ . Further, the distances between  $P_{t2}$  and  $P'_{t2}$ ,  $P_{t3}$  and  $P'_{t3}$  and  $P_{t4}$ ,  $P'_{t4}$  can be calculated.

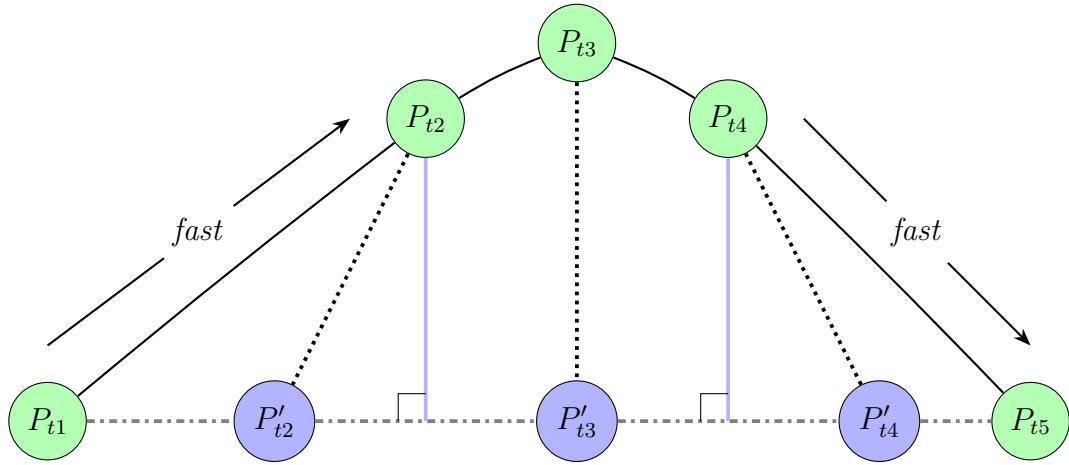


Figure C.1: Synchronized Euclidean Distance

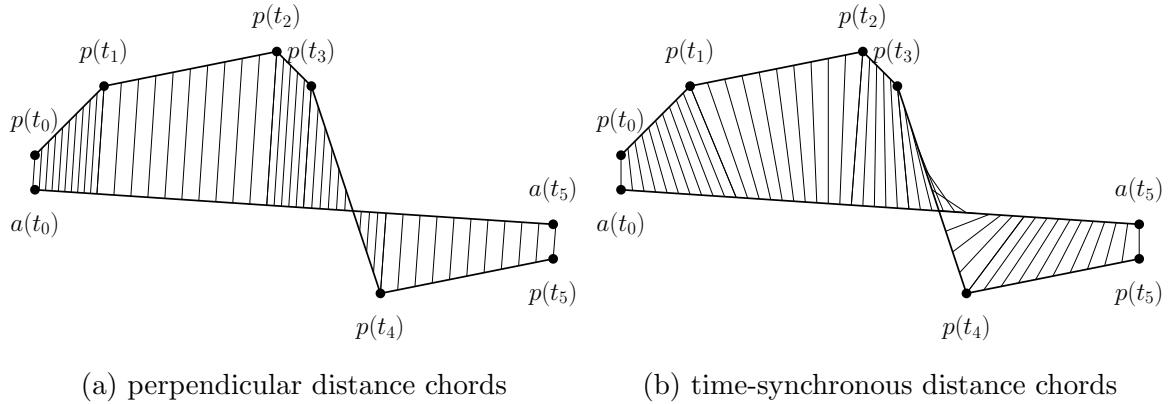


Figure C.2: C.2a indicates that the errors are measured at fixed sampling rate as sum of perpendicular distance chords. C.2b indicates that the errors are measured at fixed sampling rates as sum of time-synchronous distance chords.

Another way to calculate the difference between a GPS trace and its compressed version is to measure the perpendicular distance. This algorithm ignores the temporal component and uses simple perpendicular distance (Meratnia and Rolf, 2004). The figure C.2 expresses these differences clearly.

## C.4 Numerical Study

In the numerical simulation study, we are using *Kalman filter* (KF) to fit the trajectory after data simplification. The KF equations describe the prediction step in such

Table C.1: Comparison between raw data and simplified data

	<b>Original Data</b>	<b>DP Algorithm</b>	<b>Proposed Algorithm</b>
<b>Remaining Points</b>	1021	847	847
<b>Tracked Distances(m)</b>	74041.31	74038.33	74012.56
<b>SED (m)</b>	NA	1316.715	607.9587

a following way:

$$\begin{aligned}\hat{x}_k^- &= A\hat{x}_{k-1} + Bu_k \\ P_k^- &= AP_{k-1}A^\top + Q\end{aligned}$$

where  $\hat{x}_k^-$  is a priori state estimate,  $\hat{x}_k$  is a posteriori state estimate,  $A$  is status transition matrix,  $P_k^-$  is a priori estimate for error covariance,  $u_k$  is an input parameter and  $Q$  is process noise covariance. When a new observation comes into the data stream, KF update and corrects its estimation by:

$$\begin{aligned}K_k &= P_k^- H^\top (HP_k^- H^\top + R)^{-1} \\ \hat{x}_k &= \hat{x}_k^- + K_k (z_k - H\hat{x}_k^-) \\ P_k &= (I - K_k H)P_k^-\end{aligned}$$

where  $K_k$  is the Kalman gain matrix,  $z_k$  is the observed data.

The original data set contains 1021 rows, including latitude, longitude, velocity, bearing (heading direction) and boom status. Douglas-Peucker Algorithm, with distance threshold 0.205m, retained 847 points. The proposed algorithm, given a predictable distance 5m and heading direction changing threshold 30°, returns the same amount of simplified points. Under the same circumstance, we calculated SED and other information.

Table C.1 describes the results after being simplified by DP algorithm and the proposed algorithm. Figure C.3 demonstrates the simplified raw data and figure C.4 is the fitted trajectories by KF.

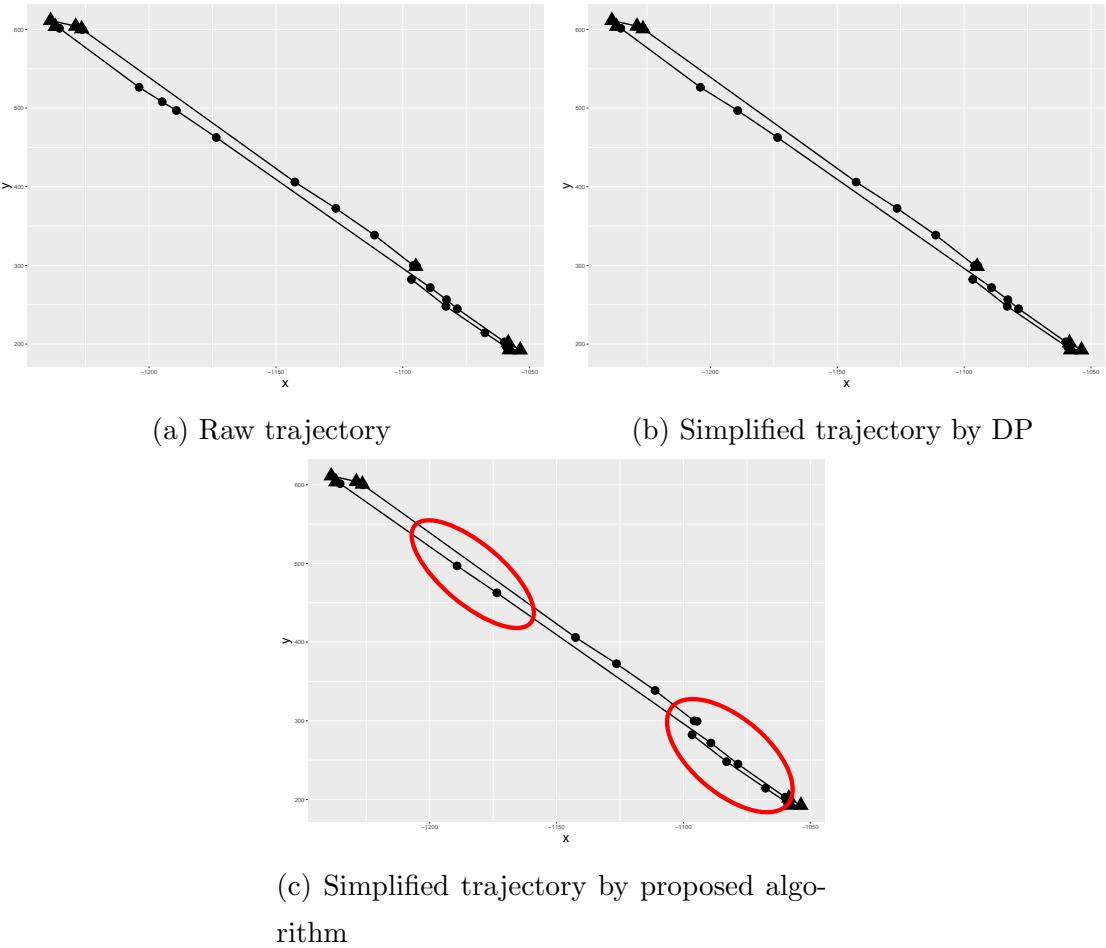
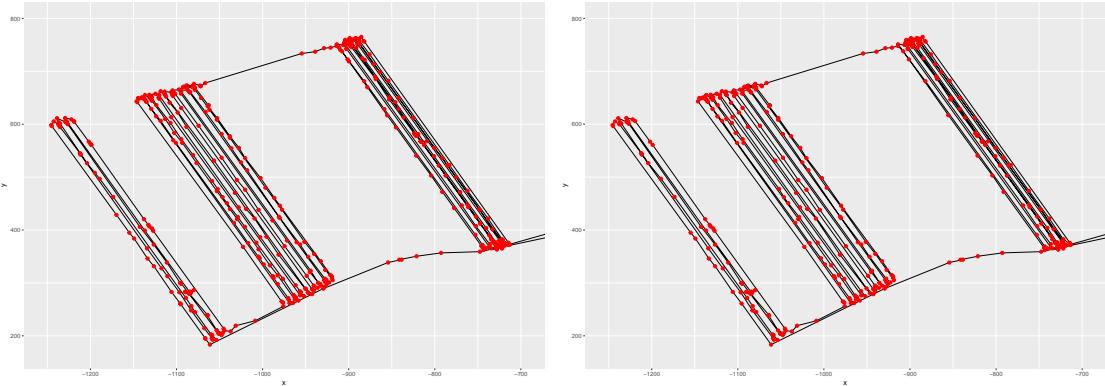
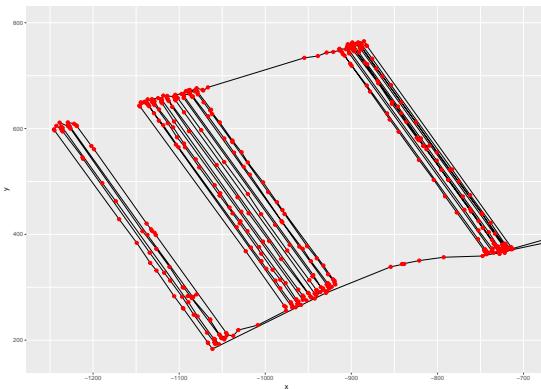


Figure C.3: A segment start from time  $t = 2000$  to  $3000$ , recorded by GPS units.  $\blacktriangle$  indicates that the boom is not operating.  $\bullet$  indicates that the boom is operating. Figure C.3a, the trajectory connected by raw data with 27 points. Figure C.3b, the trajectory connected by simplified data with Douglas-Peucker algorithm with 24 points. Figure C.3c, the trajectory connected by simplified data with proposed simplification algorithm with 23 points.



(a) Fitted Kalman filter with raw data

(b) Fitted Kalman filter with simplified data by DP



(c) Fitted Kalman filter with simplified data by proposed algorithm

Figure C.4: Trajectory fitted by Kalman filter. The mean squared errors of raw data, DP and proposed algorithm are 26.8922, 23.9788 and 23.9710 respectively.

## C.5 Conclusion

The data simplification algorithm was originally proposed to solve the fitting-drift problem. Duplicated and short-distance points cause reconstruction issues in spline fitting. The advantage of using data simplification algorithm is that less data points will potentially increase computation efficiency and save storage space without of losing information in reconstruction.

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