Filtering and Smoothing Equations in Bayesian Inference of a First-Order Polynomial Normal Dynamic Linear Model [1]

The equations described below are formulated for the forward genomic index order of the NDLM. The reverse-order NDLM equations are identical, except that the input data sequence is processed in reverse from the start.

S_i is signal-probability-sum. $(i = 1 \ldots N)$ NDLM is given by:

$$S_i = \theta_i + h_i, \quad h_i \sim N(0, H) \tag{1}$$

$$\theta_i = \theta_{i-1} + q_i, \quad q_i \sim N(0, Q) \tag{2}$$

$$\theta_0 \sim N(m_0, C_0) \tag{3}$$

The filtering distribution of $\theta_i \sim N(m_i, C_i)$ is computed as follows:

$$filterting\ distribution\ \ \theta_{i-1} \sim N(m_{i-1}, C_{i-1}) \tag{4}$$

$$prior\ distribuion\ \theta_i \sim N(m_{i-1}, K_i) \tag{5}$$

$$K_i = C_{i-1} + Q \tag{5-1}$$

$$One\ step\ forecast\ distribution\ S_i \sim N(m_{i-1}, K_i + H) \tag{6}$$

$$filtering\ distribution\ \theta_i \sim N(m_i, C_i) \tag{7}$$

$$e_i = S_i - m_{i-1} \tag{8}$$

$$A_i = K_i * (K_i + H)^{-1} \tag{9}$$

$$m_i = m_{i-1} + A_i * e_i \tag{10}$$

$$C_i = K_i - A_i * (K_i + H) * A_i \tag{11}$$

The smoothing distribution of $\theta_i \sim N(a_i, R_i)$ is computed from the filtering distribution as follows:

$$smoothing\ distribution\ \theta_i \sim N(a_i, R_i) \tag{12}$$

$$a_i = a_N(i - N) \tag{13}$$

$$R_i = R_N(i - N) \tag{14}$$

$$a_N(i - N) = m_i - B_i[m_i - a_N(i - N + 1)] \tag{15}$$

$$R_N(i - N) = C_i - B_i[K_{i+1} - R_N(i - N + 1)] * B_i \tag{16}$$

$$i = (N - 1), (N - 2), \ldots, 0 \tag{17}$$

$$B_i = C_i * K_{i+1}^{-1} \tag{18}$$

$$a_N(0) = m_N, \quad R_N(0) = C_N \tag{19}$$

Reference

1. Prado R, Ferreira MAR, West M. Time Series: Modeling, Computation, and Inference. 2nd edition. Boca Raton: Chapman and Hall/CRC; 2021. https://doi.org/10.1201/9781351259422.