

M526: Final

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1. First, we implement the normalized forward filtering algorithm on our corrupted data using the following model:

$$\begin{aligned} s_1 &\sim \text{Categorical}_{\sigma_{1:M}}(\tilde{\rho}) \\ s_n | s_{n-1} &\sim \text{Categorical}_{\sigma_{1:M}}(\pi), & n = 2, \dots, N \\ w_n | s_n &\sim \text{Poisson}(\phi_{s_n}), & n = 1, \dots, N \end{aligned}$$

$$\text{Where } \tilde{\rho} = \begin{bmatrix} 1/5 \\ 1/5 \\ 1/5 \\ 1/5 \\ 1/5 \end{bmatrix}, \pi = \begin{bmatrix} 25/26 & 1/26 & 0 & 0 & 0 \\ 1/27 & 25/27 & 1/27 & 0 & 0 \\ 0 & 1/27 & 25/27 & 1/27 & 0 \\ 0 & 0 & 1/27 & 25/27 & 1/27 \\ 0 & 0 & 0 & 1/26 & 25/26 \end{bmatrix}, \text{ and } \tilde{\phi} = \begin{bmatrix} 8 \\ 15 \\ 24 \\ 31 \\ 42 \end{bmatrix}.$$

We find the (marginal) log-likelihood of our data to be -7.7447×10^3 .

2. Now we that we have computed our filters, we implement the Viterbi Algorithm on our data to classify the category each data point belongs in. See Figure 1

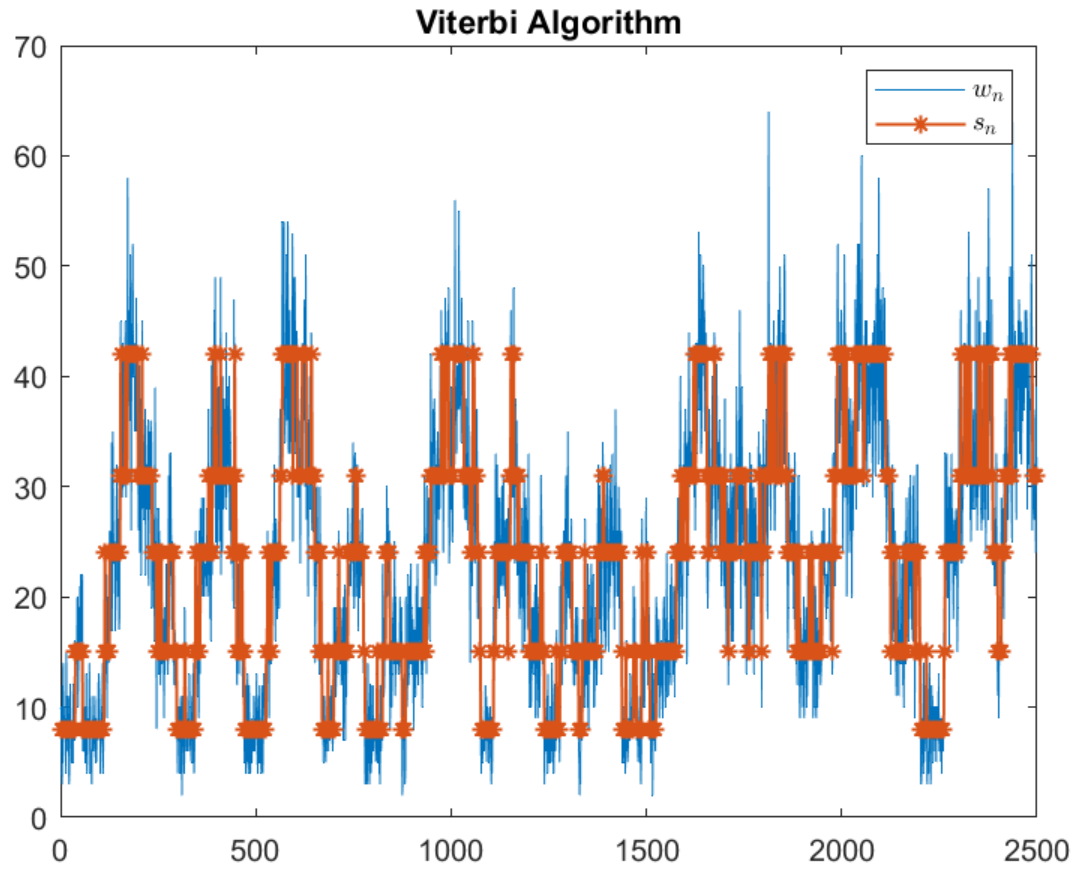


Figure 1: A visualization of the Viterbi Algorithm. We first classify each datum into a category, then plot it at the expected number of occurrences of its prescribed category. We see that the algorithm closely matches the data.

3. We now create a Bayesian Model to estimate all model parameters.

$$\begin{aligned}
\tilde{\rho} &\sim \text{Dirichlet}_{\sigma_{1:M}}(\alpha\tilde{\beta}) \\
\tilde{\pi}_{\sigma_1} &\sim \text{Dirichlet}_{\sigma_{1:M}}(\alpha\tilde{\beta}) \\
\tilde{\pi}_{\sigma_2} &\sim \text{Dirichlet}_{\sigma_{1:M}}(\alpha\tilde{\beta}) \\
\tilde{\pi}_{\sigma_3} &\sim \text{Dirichlet}_{\sigma_{1:M}}(\alpha\tilde{\beta}) \\
\tilde{\pi}_{\sigma_4} &\sim \text{Dirichlet}_{\sigma_{1:M}}(\alpha\tilde{\beta}) \\
\tilde{\pi}_{\sigma_5} &\sim \text{Dirichlet}_{\sigma_{1:M}}(\alpha\tilde{\beta}) \\
\phi_{\sigma_1} &\sim \text{Gamma}(A_1, B_1) \\
\phi_{\sigma_2} &\sim \text{Gamma}(A_2, B_2) \\
\phi_{\sigma_3} &\sim \text{Gamma}(A_3, B_3) \\
\phi_{\sigma_4} &\sim \text{Gamma}(A_4, B_4) \\
\phi_{\sigma_5} &\sim \text{Gamma}(A_5, B_5) \\
s_1|\tilde{\rho} &\sim \text{Categorical}_{\sigma_{1:M}}(\tilde{\rho}) \\
s_n|s_{n-1}, \tilde{\pi}_{\sigma_{1:M}} &\sim \text{Categorical}_{\sigma_{1:M}}(\pi), & n = 2, \dots, N \\
w_n|s_n &\sim \text{Poisson}(\phi_{s_n}) & n = 1, \dots, N
\end{aligned}$$

where α , $\tilde{\beta}$, $A_{1:M}$, and $B_{1:M}$ are known parameters. We choose this model since a Poisson likelihood with Gamma prior is conjugate so we do not need to include a Metropolis–Hasting sampler inside of our Gibb’s sampler.

4. Finally, we describe a MCMC method we could use to sample from this model’s posterior. We describe a Gibb’s Sampler and derive the conditionals which we could sample from. We begin by choosing an initial value for each of our model parameters; we use the notation ξ^0 . Now we need to pick $\tilde{\rho}^1$.

$$p(\tilde{\rho}^1|\tilde{\pi}_{\sigma_{1:M}}^0, \phi_{\sigma_{1:M}}^0, s_{1:N}^0, w_{1:N}) = p(\tilde{\rho}^1|s_1^0) = \text{Dirichlet}_{\sigma_{1:M}}(\tilde{\rho}; \alpha\tilde{\beta} + \tilde{c}(s_1^0)).$$

We then sample $\tilde{\rho}^1$ from this distribution. Next we need to choose each $\tilde{\pi}_{\sigma_m}^1$ for $m = 1, \dots, M$.

$$p(\tilde{\pi}_{\sigma_m}^1|\tilde{\rho}^1, \tilde{\pi}_{\sigma_{-m}}^0, \phi_{\sigma_{1:M}}^0, s_{1:N}^0, w_{1:N}) = p(\tilde{\pi}_{\sigma_m}^1|s_{1:N}^0) = \text{Dirichlet}_{\sigma_{1:M}}(\tilde{\pi}_{\sigma_m}^1; \alpha\tilde{\beta} + \tilde{c}(s^0)).$$

We then sample each $\tilde{\pi}_{\sigma_m}$ from this distribution. Next, we need to sample each $\phi_{\sigma_m}^1$.

$$\begin{aligned}
p(\tilde{\phi}_{\sigma_m}^1|\tilde{\rho}^1, \tilde{\pi}_{\sigma_{1:M}}^1, \phi_{\sigma_{-m}}^0, s_{1:N}^0, w_{1:N}) &= p(\tilde{\phi}_{\sigma_m}^1|\phi_{\sigma_{-m}}^0, s_{1:N}^0, w_{1:N}) \\
&= \text{Gamma}(\phi_{\sigma_m}^1; A_m + \sum_{s_n=\sigma_m} w_n, B_m + c(s^0)).
\end{aligned}$$

Where $c(s^0)$ is the count of the number of data points in the category of interest. Lastly, we need to sample $s_{1:N}^1$. We could continue using our Gibb’s Sampler to

sample each s_n individually, but this is inefficient, so we instead choose an entire sequence for $s_{1:N}$ using ancestral sampling. This is simple since each s_n relies only on s_{n-1} and $\tilde{\pi}_{\sigma_{1:M}}$. Once we have completed sampling all of ξ^1 , we repeat this process J times. J is chosen to be large enough to adequately sample our posterior.