Music Transcription Based on Bayesian Piece-Specific Score Models Capturing Repetitions

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Abstract—Most work on models for music transcription has focused on describing local sequential dependence of notes in musical scores and failed to capture their global repetitive structure, which can be a useful guide for transcribing music. Focusing on the rhythm, we formulate several classes of Bayesian Markov models of musical scores that describe repetitions indirectly by sparse transition probabilities of notes or note patterns. This enables us to construct piece-specific models for unseen scores with unfixed repetitive structure and to derive tractable inference algorithms. Moreover, to describe approximate repetitions, we explicitly incorporate a process of modifying the repeated notes/note patterns. We apply these models as a prior music language model for rhythm transcription, where piece-specific score models are inferred from performed MIDI data by unsupervised learning, in contrast to the conventional supervised construction of score models. Evaluations using vocal melodies of popular music showed that the Bayesian models improved the transcription accuracy for most of the tested model types, indicating the universal efficacy of the proposed approach.

Index Terms—Music transcription; music language model; Bayesian modelling; symbolic music processing; musical rhythm.

I. INTRODUCTION

Music transcription is an actively studied but yet unsolved problem in music information processing [1], [2]. One of the goals of music transcription is to convert a music performance signal into a human-readable symbolic musical score. While recent studies have achieved highly accurate pitch detection [3]–[7], it is also necessary to transcribe rhythms in order to obtain symbolic music representation [8]–[13]. Since there are many logically possible representations of rhythms (including meaningless ones for humans) for a given performance [11], using a score model that describes prior knowledge about musical scores is a key to solve this problem. A common approach for music transcription is to integrate a musical score (language) model and a performance/acoustic model to obtain a proper transcription that best fits an input performance signal, similarly to the method of statistical speech recognition. More recently, end-to-end approaches have also been attempted [19]–[21], which have been of limited success so far.

Various models have been studied as a score model for music transcription. They include Markov models (MMs) [12]–[14], [16], [17], [22], [23], hidden Markov models (HMMs) [24], recurrent neural networks (RNNs) [4], and long-short term memory (LSTM) networks [25]. Although all of these models are designed to capture local sequential dependence of musical notes, they typically fail to capture the repetitive structure of musical notes, which is a global structure commonly found in music of various styles [26], [27]. Repetitive structure can be a useful guide for transcription, which can complement the local information of musical scores. This is because by using repetitive structure one can in effect cancel out timing deviations and other "noises" in performances. Thus, the transcription problem will be easier if the repetitive structure is informed. In the practical situation of transcription, however, one needs to infer the repetitive structure as well as the score itself from input performance data.

Recently, a statistical model incorporating the repetitive structure has been proposed and shown to be effective for transcription [15]. This model generates musical scores in units of note patterns; that is, subsequences of notes corresponding to bars (Fig. 1). As a generative process, a piece-specific score model with sparse transition probabilities of note patterns is first generated from a generic score model by a Dirichlet process and a score is then individually generated from the piece-specific model. This model is similar to the topic model of natural language based on the latent Dirichlet allocation (LDA) [28], where a word distribution of individual text is generated from a specific word distribution of a collection of text. As a consequence of the sparseness of the piece-specific score model, repetitions of note patterns are naturally induced in the generated score. It is important that the piece-specific score model is stochastically generated and thus the
total model can describe unseen scores with unfixed repetitive structure. Moreover, by combining a process of modifying the generated patterns, the model can also describe approximate repetitions, which are commonly seen in music practice.

A model for music transcription was constructed by combining this score model with a performance model. The combined model was formulated as a hierarchical Bayesian model, with which the score, the underlying piece-specific score model, and pattern modification operations can be inferred jointly. The piece-specific model is constructed by unsupervised learning, in contrast to the conventional construction of “generic” score models by supervised learning. In other words, using the model we can induce the “grammar” specific to a target musical piece, whereas the conventional methods apply the same “grammar” for all target pieces. It was confirmed that both the unsupervised construction of score models and the modification process improved the transcription accuracy [15].

In this paper, we generalize this idea and study more classes of Bayesian score models capturing repetitions and their application to music transcription. While the repetitions were considered in units of note patterns in [15], we also consider repetitions in units of notes. In this way, we construct Bayesian score models based on the note value MM [12] and the metrical MM [13], [14], which are advantageous for computational efficiency compared to the note pattern MM considered in [15]. As in [15], we apply the constructed score models to rhythm transcription of monophonic music, which is the problem of recognizing score-notated musical rhythms from performance MIDI data with onset time deviations [9]–[14], [17]. All the score models are formulated so that they have the same search space (set of logically possible generated scores), unlike the uneven search space for the note pattern MM in [15], therefore removing the bias in the evaluation. We conduct extensive evaluations to examine the effect of capturing repetitions and to reveal the best model for the task.

After presenting statistical analyses on the repetitive structure in Sec. II, we formulate our models in Sec. III. Taking the note value MM, metrical MM, and note pattern MM as basic models, their Bayesian extensions and the integration of note modification processes (note divisions and onset shifts) are formulated there. A method for rhythm transcription based on the score models is presented in Sec. IV. Evaluations are carried out in Sec. V where models are compared in terms of the transcription error rate and computation time. The zeroth-order and second-order note value MMs and metrical MMs with and without the Bayesian extension are also compared. We also examine the influence of the parameterization of relevant hyperparameters. While the idea of statistical description of repetitions follows the work of [15], all the models except for the basic note value MM and the basic metrical MM in Sec. III-B are newly formulated and presented in this paper for the first time in the literature.

Our main results are as follows.

- The efficacy of the Bayesian piece-specific models for improving the transcription accuracy was confirmed consistently in many different model types.
- The second-order Bayesian metrical MM and the Bayesian note pattern MM were found to be the current state-of-the-art models. Incorporating the note modification process can slightly improve the accuracy.
- Use of note pattern MMs and incorporating the note modification process significantly increase the required computation time and are disadvantageous for computational efficiency and extendability.

II. STATISTICAL VIEW OF REPEITIVE STRUCTURE

Here we define the form of data we deal with and present statistical analyses that motivate our models.

A. Musical Score Data

The score data used in this study are extracted from a collection of vocal melodies of popular music. Specifically, we use 99 pieces in the RWC popular music dataset [29], 190 pieces by The Beatles, and 142 contemporary Japanese popular music (J-pop) pieces. To enable comparisons between different models, only pieces in 4/4 time are chosen, only rhythms (note onset positions) are used, the 16th-note length is used as the minimal resolution of beat, and each piece is segmented into a half-note length. In this step, we disregard note onsets in finer beat resolutions and segments without any note onsets. In addition, for simplicity, if a pair of consecutive note onsets in two segments are distant more than a half-note length, a new onset is added at the beginning of the latter segment so that the maximum note length will be a half-note length. Hereafter the obtained segments are called bars, that is, pieces are represented in 2/4 time. The relative positions of note onsets in each bar in units of 16th notes are called the metrical positions, and the number of metrical positions \( N_b = 8 \) is called the bar length. We should remark that the choices of time signature and bar length, and the manipulations made in preparing our data are not essential theoretically. We split the data into two sets, one for training the models and the other for evaluating them, whose contents are shown in Table I.

A note pattern (i.e., rhythmic pattern in a bar) can be represented as an \( N_b \)-bit binary vector \( \sigma_1 \sigma_2 \cdots \sigma_{N_b} \), where \( \sigma_b = 1 \) indicates an onset at metrical position \( b \) and otherwise \( \sigma_b = 0 \). The onset time of a note measured from the beginning of a piece in units of 16th notes is called an onset score time. A score-notated note length (difference in onset score time) is called a note value. As shown in Fig. 2, we can use one of three quantities (note value, metrical position, and note pattern) to represent musical rhythms. These three representations are equivalent, except that the metrical position of the first note onset is lost in the note value representation.

| Dataset       | Original data | Pieces | Bars | Notes |
|---------------|---------------|--------|------|-------|
| Train         | Beatles       | 180    | 16,746 | 40,913 |
|               | RWC           | 89     | 11,449 | 31,998 |
| Contemporary J-pop | 132 | 21,152 | 66,073 |
| Total         |               | 401    | 49,347 | 138,583 |
| Test          | Beatles       | 10     | 924   | 2,124 |
|               | RWC           | 10     | 1,452 | 3,950 |
| Contemporary J-pop | 10 | 1,518 | 4,672 |
| Total         |               | 30     | 3,894 | 10,716 |
Fig. 2. Representations of musical rhythms. The score example is taken from “Yasashii uta (tender song)” by a J-pop band Mr. Children. See text for definitions of the representations.

Fig. 3. A generic distribution of note patterns obtained from the training data and piece-specific distributions obtained from individual pieces in the same data. The note patterns are ordered according to the probability.

B. Repetitions and Sparseness

To quantitatively see how repetitive structure is reflected in the sparseness of piece-specific score models, a distribution (generic model) of note patterns obtained from all the pieces in our training dataset is shown with distributions (piece-specific models) obtained from individual pieces in Fig. 3. We use only the training dataset for the analysis in this subsection. The sparseness of the piece-specific distributions, which can be measured by the (Shannon) entropy, is evident. From the entropies of the piece-specific distributions of all the pieces in Fig. 4(a), we see that most pieces have a much lower entropy compared to the generic distribution with an entropy of 5.3.

The sparseness of the piece-specific distributions cannot be explained merely by statistical fluctuation of finite data. To confirm this, we drew 401 sets of samples (note patterns) from the generic distribution, each of which corresponds to a piece in the data and has the same number of bars (the average number of bars was 123). The entropies calculated from the distributions obtained from the sampled data are also plotted in Fig. 4(b). The result in Fig. 4(b) shows that these distributions still have much higher entropies than the real data, indicating that the sparseness of the real piece-specific distributions originates from the repetitive structure.

Our idea in this study is to use the Dirichlet process for describing the sparse piece-specific distributions. As explained in Sec. III-D, a Dirichlet process is a distribution of distributions whereby each piece-specific distribution is generated from the generic distribution. The sparseness of the generated distributions can be controlled by the concentration parameter $\alpha$. Entropies of distributions generated by a Dirichlet process are shown in Fig. 4 where $\alpha$ is adjusted to match the average entropy with the real data. Although the obtained distribution of entropies does not very well match the actual distribution, these distributions overlap much more than the actual distribution does with the entropy distribution of the sampled data from the generic model.

As mentioned above, the rhythmic patterns can also be described as sequences of metrical positions or note values (Fig. 2) and repetitions at the level of note patterns induce repetitions at the note level and vice versa. To capture the sequential nature of rhythmic patterns, we here consider transition probabilities of metrical positions and those of note values, which are the parameters of the note value MM and the metrical MM explained in Secs. III-B1 and III-B2. Similarly as for discrete distributions, we can define the entropy (rate) for transition probabilities $\mathcal{S}$, which can be used as a measure of sparseness for these models. In Figs. 5(a) and 5(b), we plot the distributions of entropies for these models, one for the real data, one for the sampled data from the generic model, and one for the piece-specific transition probabilities obtained from the Dirichlet processes. The statistical tendencies are the same as before and in particular we see that the Dirichlet process can generate transition probabilities with a similar entropy as the
actual piece-specific transition probabilities, which are much lower than the entropy of the generic model.

These results support our assertion that repetitive structure in music can be useful for transcription, from the viewpoint of generative modelling. Lower entropy means higher predictive ability in generative modelling. Thus, if we can infer the piece-specific score model appropriately, the transcription will be easier with the aid of its high predictive ability.

C. Note Modifications for Approximate Repetitions

In music, repetitions may appear with modifications, leading to approximate repetitions. The example in Fig. 2 illustrates the two most common types of modifications, note division/combination and onset shift [15, 31]. By a note division/combination (or simply, division/combination), a note onset is inserted/deleted while the other note onsets are unchanged. These modifications often appear in sung melodies where the number of syllables varies in repeated phrases or sections. By an onset shift (or simply, shift), a note onset is shifted forward or backward in time. This is another typical type of rhythmic variation that includes syncopations.

Modelling these modifications for describing musical scores with approximate repetitions can be useful for transcription because by identifying modifications we can induce more repetitions in data, which can lead to higher predictive ability. The concept of approximate repetitions is also important for humans to understand or transcribe music [29]. The example in Fig. 2 cannot be recognized as repeated phrases if modified note patterns are considered as completely different ones.

III. SCORE MODELS

Here we explain the proposed score models. We use the following notations (see Fig. 2). We represent a musical score as a sequence of onset score times \((r_{n})_{n=0}^{N}\), where \(n\) indexes note onsets and \(N\) is the number of notes \((N + 1\) note onsets are necessary to define the lengths of \(N\) notes). The onset score times are described in units of 16th-note lengths. In the example of Fig. 2, \(\tau_0 = 4\), \(\tau_1 = 6\), \(\tau_2 = 8\), \(\tau_3 = 12\), etc. Their absolute values are unimportant but we assume that \(\tau_n\) \((\text{mod} \ N_b)\) represents the metrical position \(b_n \in \{0, \ldots, N_b - 1\}\) of the \(n\)th note onset. The note value \(r_n\) of the \(n\)th note (\(n = 1, \ldots, N\)) is defined as \(r_n = \tau_n - \tau_{n-1}\). In the example of Fig. 2, \(b_0 = 4\), \(b_1 = 6\), \(b_2 = 0\), \(b_3 = 4\), etc. and \(r_1 = 2\), \(r_2 = 2\), \(r_3 = 4\), etc. Since the maximum note value and \(N_b\) are 8, we can also write \(r_n = b_n - b_{n-1}\) if \(b_n > b_{n-1}\) and \(r_n = b_n - b_{n-1} + N_b\) otherwise. Hereafter we use a notation \(\tau_{n1:n2} = (\tau_{n})_{n=n1}^{n2}\) etc. to indicate a sequence of variables.

A. Overview of Studied Models

A score model is a probabilistic generative model for sequences of onset score times that describes the probability \(P(\tau_{0:N})\), or equivalently, \(P(b_{0:N})\) or \(P(r_{1:N})\). We construct score models based on three basic models, note value MM, metrical MM, and note pattern MM, which are explained in Sec. III-B. Each basic model is extended in a Bayesian manner to describe the repetitive structure and combined with note modification models to describe approximate repetitions. The incorporation of note modifications is described in Sec. III-C and the Bayesian extensions are formulated in Sec. III-D.

The list of constructed models based on the note value MM and their acronyms are summarized in Table II. Similarly we construct 9 models (MetMM0, MetMM0B, . . . , MetMM2B) based on the metrical MM and 7 models (PatMM0, PatMM0B, . . . , PatMM1SDB) based on the note pattern MM. We do not consider the second-order note pattern MM and its extensions due to their impractical computational cost. Methods for learning model parameters are explained in Sec. IV-B.

B. Basic Score Models

1) Note Value Markov Models (NoteMM): The basic first-order note value MM (NoteMM1) [12] is defined with the initial and transition probabilities of note values:

\[
P(r_1 = r) = \pi_{iri} \quad P(r_n = r \mid r_{n-1} = r') = \pi_{rr'}.
\]

The zeroth-order note value MM (NoteMM0) is defined by using the unigram probabilities \(P(r_n)\) instead of the transition probabilities \(P(r_n \mid r_{n-1})\). The second-order note value MM (NoteMM2) and higher-order models can be constructed by considering transition probabilities of the form \(P(r_n \mid r_{n-1}, \ldots, r_{n-k})\). Since it is straightforward to formulate lower-order and higher-order models, we describe only the first-order models in the following.

2) Metrical Markov Models (MetMM): The basic first-order metrical MM (MetMM1) [13, 14] generates a sequence of metrical positions as

\[
P(b_0 = b) = \chi_{imb} \quad P(b_n = b \mid b_{n-1} = b') = \chi_{bb'}.
\]

The onset score times \(\tau_{n} = (\tau_{n})_{n=0}^{N}\) and the note values \(r_{n} = (r_{n})_{n=1}^{N}\) are then given as

\[
\tau_0 = b_0, \quad r_n = \tau_n - \tau_{n-1} = [b_n - b_{n-1}],
\]

\[
[b_{n-1}, b_n] := \begin{cases}
    b_n - b_{n-1}, & b_{n-1} < b_n; \\
    b_n - b_{n-1} + N_b, & b_{n-1} \geq b_n.
\end{cases}
\]

3) Note Pattern Markov Models (PatMM): The note pattern MMs can be described as a generalization of the metrical MMs. We denote a note pattern of metrical positions as

\[
B_k = (B_{k1}, \ldots, B_{klk}),
\]

TABLE II

| Acronym       | MM order | Bayesian | Modification |
|---------------|----------|----------|--------------|
| NoteMM0       | 0th      | ✓        | —            |
| NoteMM0B      | 0th      | ✓        | —            |
| NoteMM1       | 1st      | ✓        | —            |
| NoteMM1B      | 1st      | ✓        | —            |
| NoteMM1SB     | 1st      | ✓        | Shift only   |
| NoteMM1DB     | 1st      | ✓        | Division only|
| NoteMM1SDB    | 1st      | ✓        | Shift & division |
| NoteMM2       | 2nd      | ✓        | —            |
| NoteMM2B      | 2nd      | ✓        | —            |
where $k$ is an index in the set of note patterns, $I_k$ denotes the number of note onsets in note pattern $B_k$, and each $B_{k,i}$ ($i \in \{1, \ldots, I_k\}$) indicates a metrical position ($B_{k,i} < B_{k(i+1)}$). For example, the first two note patterns in Fig. 2 are represented as $(4, 6)$ and $(0, 4)$. Note that $B_{k,i}$ need not be 0; if $B_{k,i} \neq 0$ it indicates that the first note of pattern $B_k$ is a tied note. This is an extension of the note pattern model used in [15], which could not be described tied notes.

The basic first-order note pattern MM (PatMM)1 is described as a two-level hierarchical MM with a state space indexed by a pair $(k, i)$ of note-pattern index $k$ and an internal index $i \in \{1, \ldots, I_k\}$ of notes in each pattern $k$. The upper-level model generates a sequence of note patterns as

$$
\Gamma_{ini,k} = P(k_1 = k), \quad \Gamma_{k,k'} = P(k_m = k \mid k_{m-1} = k').
$$

The lower-level model generates internal positions as

$$
\gamma_{ini}^{K} = P(i_1 = i \mid k) = \delta_{i_1^1}, \quad \gamma_{k,i}^{K} = P(i_{k+1} = i \mid i_k = i', k) = \delta_{(i_{k+1})}, \quad \gamma_{I_k}^{K} = P(i_{k+1} = i \mid k) = \delta_{I_k},
$$

where $\delta$ denotes Kronecker’s delta. The initial and transition probabilities of the total model are given as

$$
\psi_{ini(k_i)} = P(k_1 = k, i_1 = i) = \Gamma_{ini,k}^{K}, \quad \psi_{(k\,')(k)(i)} = P(k_n = k, i_n = i \mid k_{n-1} = k', i_{n-1} = i') = \delta_{kk'}\gamma_{k',i}^{K} \Gamma_{k,k'}^{K} \gamma_{ini}^{K} = \delta_{kk'} \delta_{i(i') + 1} + \delta_{i'i_k} \Gamma_{k',k}^{K} \delta_{i,i_k},
$$

in which case we have $b_n = B_{k_{ini}}$. The onset score times and note values are given as in Eqs. (1) and (4).

\section*{C. Incorporation of Note Modifications}
\subsection*{1) Note Modification Operations:} We consider the most common types of note modifications, onset shifts, note divisions, and note combinations (Sec. III-C). As note divisions and combinations are inverse to each other, we only consider note divisions in our models. In [15], only onset shifts for notes on bar onsets (i.e., syncopations) were considered. Here we generalize the idea and consider onset shifts for any notes.

We denote the shift of onset score time of the $n$th note as $s_n$ and the note value and score time of the $n$th note before the application of onset shifts are notated as $\tilde{r}_n$ and $\tilde{s}_n$ (Fig. 6 (right)). An onset shift is then described as

$$
\tilde{r}_n \rightarrow r_n = \tilde{r}_n + s_n \quad \text{or} \quad \tilde{r}_n \rightarrow r_n = \tilde{r}_n + s_n - s_{n-1}.
$$

The shift variable $s_n$ describes the amount of shift and takes values in the range $[-N_b + 1, N_b - 1]$ with probability

$$
\xi_s = P(s_n = s).
$$

We assume a constraint $-\tilde{r}_n < s_n \leq \tilde{r}_n$ to make the onset shift interpretable as a modification. Musically, we should also have $r_n = \tilde{r}_n + s_n - s_{n-1} > 0$ for all $n$.

In the most general case, a note division is described as an operation $\tilde{r} \rightarrow q_h$ that maps a note value $\tilde{r}$ to a sequence of note values $q_h = q_{h1}, \ldots, q_{hb_h}$ (Fig. 6 (left)). Here, $h$ indexes patterns of note divisions and $G_h$ is the number of notes after a division. The division probability can be written as

$$
\zeta_{rh} = P(\tilde{r} \rightarrow q_h).
$$

We must have $\zeta_{rh} = 0$ unless $\tilde{r} = q_{h1} + \ldots + q_{hb_h}$. Using an index $g \in \{1, \ldots, G_h\}$, the pair of indices $(h, g)$ can specify the note value after applying the note division as $r_n = q_{h,g}$. When we combine onset shifts and note divisions, we first apply note divisions and then apply an onset shift to each of the divided notes. The resulting notes are indexed by $(\tilde{r}, h, g, s)$ and their note values are given as

$$
r_n = q_{h,g} + s_n - s_{n-1}.
$$

In this study, we only consider note divisions into two notes, that is, $G_h \leq 2$, to avoid impractical computational cost.

\subsection*{2) Score Models with Note Modifications:} Note value MMs can be extended to incorporate note modifications as follows. The model incorporating onset shifts (NoteMM1S) is described by an HMM with a state space indexed by $z_0 = s_0$ and $z_n = (\tilde{r}_n, s_n)$ ($n = 1, \ldots, N$), where $\tilde{r}_n$ indicates the note value before modification and $s_n$ indicates the amount of shift. The initial and transition probabilities are given as

$$
P(z_0 = s) = \xi_s, \quad P(z_1 = (\tilde{r}, s)) = \pi_{ini, \tilde{r}} \xi_s,
$$

and the final output is obtained from the output probability

$$
P(r_n | z_{n-1}, z_n) = \Pi(r_n = \tilde{r}_n + s_n - s_{n-1}),
$$

where $\Pi(C)$ is 1 when expression $C$ is true and is 0 otherwise. The note value MM incorporating note divisions (NoteMM1D) is described by an HMM with a state space indexed by $z = (\tilde{r}, h, g)$, where $\tilde{r}$ indicates the note value before note division and $h$ and $g$ indicate a note-division pattern and its internal note position (see Sec. III-C1). The initial and transition probabilities are given as

$$
P(z_1 = (\tilde{r}, h, g)) = \pi_{ini, r} \zeta_{rh} \delta_{g1},
$$

$$
P(z_n = (\tilde{r}, h, g) | z_{n-1} = (\tilde{r}', h', g')) = \delta_{\tilde{r}\tilde{r}'} \delta_{hh'} \delta_{g(g'+1)} + \delta_{gG_h} \pi_{\tilde{r}\tilde{r}'} \zeta_{rh} \delta_{g1},
$$

and the final output is obtained from the output probability

$$
P(r_n | z_n) = \Pi(r_n = q_{h,g}).
$$

The note value MM incorporating both onset shifts and note divisions (NoteMM1SD) is obtained by combining the above two models. It is described by an HMM with a state space indexed by $z_0 = s_0$ and $z_n = (\tilde{r}_n, h_n, g_n, s_n)$ ($n = 1, \ldots, N$) and the initial and transition probabilities are given as

$$
P(z_0 = s) = \xi_s, \quad P(z_1 = (\tilde{r}, h, g, s)) = \pi_{ini, r} \zeta_{rh} \delta_{g1} \xi_s, \quad P(z_n = (\tilde{r}, h, g, s) | z_{n-1} = (\tilde{r}', h', g', s')) = \delta_{\tilde{r}\tilde{r}'} \delta_{hh'} \delta_{g(g'+1)} + \delta_{gG_h} \pi_{\tilde{r}\tilde{r}'} \zeta_{rh} \delta_{g1} \xi_s.
$$
The final output is obtained from the output probability
\[ P(r_n | z_{n-1}, z_n) = I(r_n = q_{h_n g_n} + s_n - s_{n-1}). \] (23)

The model parameters of the (non-Bayesian) first-order note value models are summarized as follows. Hereafter we use \( r \) instead of \( \tilde{r} \) to unify the notation. Let us write \( \pi_{ini} = (\pi_{ini,r}), \pi_{r} = (\pi_{r'})_{r'}, \zeta_r = (\zeta_{rk})_r, \) and \( \xi = (\xi_s)_s. \)

- NoteMM1: \( \pi_{ini}, (\pi_{r}), \zeta_r \)
- NoteMM1S: \( \pi_{ini}, (\pi_{r}), \zeta_r, \xi \)
- NoteMM1D: \( \pi_{ini}, (\pi_{r}), (\zeta_{rk})_r, \zeta_r, \xi \)
- NoteMM1SD: \( \pi_{ini}, (\pi_{r}), (\zeta_{rk})_r, (\zeta_r), \zeta_r, \xi \)

We can similarly formulate four models (MetMM1, MetMM1S, MetMM1D, and MetMM1SD) based on the metrical MM with or without the note modification process and four models (PatMM1, PatMM1S, PatMM1D, and PatMM1SD) based on the note pattern MM. See Supplemental Material for explicit formulation.

D. Bayesian Extensions Based on Dirichlet Processes

We extend the score models in a Bayesian manner to formulate the generative process of piece-specific models from a generic model. We assume that piece-specific models and generic models have the same architecture but different parameterizations. For NoteMM1SD, the generative process can be formulated by putting prior distributions on the model parameters:

\[
\begin{align*}
\pi_{ini} & \sim \text{DP}(\alpha_{ini}, \bar{\pi}_{ini}), \\
\pi_{r} & \sim \text{DP}(\alpha_s, \bar{\pi}_{r}), \\
\zeta_{r} & \sim \text{DP}(\alpha_c, \bar{\zeta}_{r}), \\
\xi & \sim \text{DP}(\alpha_{c}, \bar{\xi}),
\end{align*}
\] (24)

where \( \text{DP} \) denotes a Dirichlet process \([33], \bar{\pi}_{ini}, \bar{\pi}_{r}, \bar{\zeta}_{r}, \bar{\xi} \) denote base distributions, and \( \alpha_{ini}, \alpha_s, \alpha_c, \alpha_{c} \) denote concentration parameters. Since the distributions are finite discrete distributions, the Dirichlet process can be described as Dirichlet distributions, for example,

\[ \pi_{r} \sim \text{DP}(\alpha_s, \bar{\pi}_{r}) = \text{Dir}(\alpha_s, \bar{\pi}_{r}). \] (25)

The expectation value of the distributions generated by a Dirichlet process is equal to the base distribution \([33]. \) Based on this fact, we can interpret the distributions \( (\pi_{r}, \zeta_{r}, \xi, \text{etc.}) \) generated by the Dirichlet process as the piece-specific models and the base distributions \( (\bar{\pi}_{r}, \bar{\zeta}_{r}, \bar{\xi}, \text{etc.}) \) as the generic model representing the average of all the piece-specific models. The distributions generated from a Dirichlet process become sparser as we use a smaller concentration parameter. As in the analysis in Sec. \( \text{II-B} \) we use small concentration parameters to account for the sparse piece-specific transition probabilities in the real data. The parameters of the note modification models \( \zeta_{r}, \xi \) are also considered for individual pieces to describe the situation that note modifications used in each piece have different statistical tendencies. How we can train the parameters of the base distributions and how we can determine the concentration parameters are explained in Sec. \( \text{IV-B} \).

We can similarly construct Bayesian extensions of metrical MMs and note pattern MMs. For metrical MMs we have

\[
\begin{align*}
\pi_{ini} & \sim \text{DP}(\alpha_{ini}, \bar{\pi}_{ini}), \\
\pi_{r} & \sim \text{DP}(\alpha_s, \bar{\pi}_{r}), \\
\zeta_{r} & \sim \text{DP}(\alpha_c, \bar{\zeta}_{r}), \\
\xi & \sim \text{DP}(\alpha_c, \bar{\xi}),
\end{align*}
\] (26)

and for note pattern MMs we have

\[
\begin{align*}
\pi_{ini} & \sim \text{DP}(\alpha_{ini}, \bar{\pi}_{ini}), \\
\pi_{r} & \sim \text{DP}(\alpha_s, \bar{\pi}_{r}), \\
\zeta_{r} & \sim \text{DP}(\alpha_c, \bar{\zeta}_{r}), \\
\xi & \sim \text{DP}(\alpha_c, \bar{\xi}),
\end{align*}
\] (27)

where \( \chi_{ini}, \chi_r, \bar{\chi}_{ini}, \bar{\chi}_{r} \) denote base distributions corresponding to the generic models and \( \alpha_{ini}, \alpha_s, \alpha_c, \alpha_{c} \) denote concentration parameters.

IV. RHYTHM TRANSCRIPTION METHOD

The aim of a rhythm transcription method is to estimate the score onset times \( t_{0:N} \) (or note values \( r_{1:N} \)) from input performance data with note onsets times \( t_{0:N} \) (or durations \( d_{1:N} \), where \( d_n = t_n - t_{n-1} \)) that are represented in the unit of second. We first construct a generative model of music performance that describes the probability \( P(t_{0:N}, t_{0:N}) \) or \( P(r_{1:N}, d_{1:N}) \) by combining a score model (one of the aforementioned models) and a performance model explained in Sec. \text{IV-A} \). We then derive a rhythm transcription algorithm that can estimate the score by maximizing the probability \( P(t_{0:N}, t_{0:N}) \) or \( P(r_{1:N}, d_{1:N}) \), which is explained in Sec. \text{IV-C} \. For the Bayesian score models, the model parameters for the piece-specific model are learned in the transcription step. This is described in Sec. \text{IV-B} \.

A. Performance Model

A performance (timing) model describes the generative process of durations \( d_{1:N} \) from note values \( r_{1:N} \), which gives the probability \( P(d_{1:N} | r_{1:N}) \). We consider a simplified model with a constant (inverse) tempo \( v_r \). Given a note value \( r_n \) for the \( n \)th note, the corresponding duration \( d_n \) is generated as

\[ d_n \sim \text{Gauss}(\nu r_n, \sigma_r^2), \] (30)

where \( \text{Gauss}(\mu, \Sigma) \) denotes a Gaussian distribution with mean \( \mu \) and variance \( \Sigma \), and \( \sigma_r \) describes the amount of onset time deviations. The onset times \( t_{0:N} \) can be determined by the durations \( d_{1:N} \) up to an initial time \( t_0 \), which is insignificant.

In the real situation of music transcription, the global tempo is unknown and the tempo changes in time, especially in solo performances and performances of classical music. The performance model can be generalized to describe these situations by introducing an additional process to generate a sequence of local tempos \( v_r \). Since we only consider a constant and known tempo in the experiments in Sec. \text{V} we refer to \text{[17]} for the details of this generalization.

B. Parameter Learning

For non-Bayesian score models, the model parameters are pretrained or preset and are fixed during the transcription step. The initial and transition probabilities can be directly learned from musical score data. The probabilities \( \zeta_{r} \) and \( \xi \) of the modification models cannot be directly learned from musical score data, and thus, they are manually preset to reflect the belief that modifications are rare. Specifically, we assign a probability \( \zeta_0 \) and \( \xi_0 \), which are slightly less than unity, for cases without modifications and other entries in \( \zeta_{r} \) and \( \xi \) are assumed to have uniform probabilities.
For Bayesian models, the hyperparameters of the prior distributions except for the concentration parameters are pretrained or preset to the parameterization of the corresponding non-Bayesian models. The concentration parameters can in principle be optimized according to the transcription accuracy. In our evaluation in Sec. [V-B] they are preset to a fixed value, and how the values of the concentration parameters for the unigram or transition probabilities influence the transcription accuracy is studied in Sec. [V-D].

The parameters of the Bayesian models other than the hyperparameters are treated as variables and estimated in the transcription step according to the input performance data. We use the Gibbs sampling method for estimating these parameters. If \( X = d_{1:N} \) (or \( t_{0:N} \)) denotes the input performance data, \( Z \) the set of internal variables of a score model including note values, \( \Theta \) the set of model parameters, and \( \Xi \) the set of hyperparameters, the generative process can be summarized as

\[
P(X, Z, \Theta | \Xi) = P(X|Z)P(Z|\Theta)P(\Theta|\Xi),
\]

where the first factor in the right-hand side represents the performance model, the second factor represents the (non-Bayesian part of the) score model, and the last factor represents the prior distributions. By the Gibbs sampling method, we can draw samples from the posterior probability \( P(Z, \Theta | X, \Xi) \). After some iterations, we obtain optimal parameters \( \Theta \) that maximizes the likelihood \( P(X|\Theta) = \sum_Z P(X|Z)P(Z|\Theta) \) among the sampled parameters. For details of the Gibbs sampling method, see Supplemental Material.

C. Algorithms for Rhythm Transcription

Our generative models for rhythm transcription constructed as combinations of a score model and a performance model are HMMs where latent states are the variables of the score model and observed variables are onset times or durations of an input performance signal (see explicit formulation in Supplemental Material). Thus, the standard Viterbi algorithm \([34]\) can be used to estimate the variables of the score model including note values or metrical positions, from the input performance signal. For Bayesian models, the model parameters are first estimated from the input signal as explained in Sec. [IV-B] and the latent variables are then estimated by the Viterbi algorithm.

For some of the present models, especially, PatMM1DB and PatMM1SDB, the latent state space is huge and the Viterbi algorithm requires an impractical amount of computation time. To solve this, we apply a beam search and only retain the top-\( W \) most probable states at each Viterbi update (\( W \) is a preset number called the beam width). For Bayesian extensions of these models, we also apply a similar method in the forward algorithm used for estimating the posterior probability.

V. EVALUATION

A. Setup

To evaluate the performance of the studied models, we conducted two evaluation experiments. In the first experiment (Sec. [V-B]), the predictive ability of the non-Bayesian score models is evaluated to compare the effects of different model architectures. In the second experiment (Sec. [V-C]), transcription accuracies of the models are measured to examine the effects of the Bayesian extensions and modification models. We also examine the influence of the hyperparameters of the studied models in Sec. [V-D].

The initial and transition probabilities of all the models were trained with the same training dataset (Sec. [II-A]). The probabilities were estimated by the maximum likelihood method with an additive smoothing constant of 0.1. We confirmed that the results were not sensitive to the smoothing constant, except for the transition probabilities of PatMM1 for which there were more parameters than the training samples. For this model, we applied a linear interpolation with the unigram probabilities (0.8 unigram probability + 0.2 transition probability) that was roughly optimized w.r.t. the transcription accuracy.

We used the evaluations of the test dataset consisting of melodies taken from 30 pieces of popular music (Sec. [II-A]). For transcription experiments, we collected performance MIDI data played by amateur musicians and recorded with a digital piano. Four musicians participated and were assigned some pieces in the test data exclusively. The first 40 bars of each piece were used and the musicians were asked to play the scores in a tempo of 105 BPM (beats per minute). For the reason explained later, we also used synthetic performance data generated by the performance timing model in Sec. [IV-A] with \( \sigma_t = 0.04 \) sec and a tempo of 144 BPM. The entire pieces in the test dataset were used for the synthetic data.

B. Evaluation of Score Models

We evaluated the non-Bayesian score models listed in Table [III] in terms of cross entropy, which is a standard measure for quantifying the quality of language models. Lower entropy means higher predictive ability. For all classes of models (note value MM, metrical MM, and note pattern MM) the cross entropy decreased as we increased the order. Comparing the note value MMs and metrical MMs, the former outperformed when the order is zero but the latter outperformed for the higher-order cases. The zeroth-order note pattern MM has lower cross entropy than the first-order note value MM and metrical MM. This demonstrates the strength of the note pattern models, which can capture long-range sequential dependence at the note level. The reason the first-order note pattern MM was worse than the second-order metrical MM is probably that the data sparseness was more severe for the former model.

C. Evaluation of Transcription Accuracy

We used the synthetic data in addition to the real data of human performances because several methods seemed to
reach a limiting transcription accuracy for the human data and the use of synthetic data made it easier to clearly examine the effects of these models. Another purpose was to double check the results. To run the rhythm transcription algorithms based on the studied models, we used the following setups. For evaluations on the synthetic data, we fixed the parameter $\sigma_t$ to its actual value (0.04 sec) used for the synthesis, and for the real data we set $\sigma_t = 0.035$ sec, which was roughly optimized in preliminary experiments. All the concentration parameters were set to 10, and $\xi_0 = \xi_0 = 0.9$. For estimating model parameters of the Bayesian models, we iterated the Gibbs sampling 100 times, except for models with too large computational cost. For these models (MetMM1SDB, PatMM1DB, and PatMM1SDB), we iterated 20 times. For PatMM1DB and PatMM1SDB, we set the beam width as $W = 200$. We use the error rate (i.e. the ratio of the number of notes with incorrectly estimated note values and the total number of notes) as an evaluation measure. Since the transcription results depend on random numbers used for Gibbs sampling for the Bayesian models, we run the methods 10 times with different random number seeds and obtained the average error rates.

The results are shown in Fig. 7. We first discuss the results for the synthetic data. For non-Bayesian models, higher-order models outperformed the corresponding lower-order models. The rank of transcription accuracy approximately matches with the rank of cross entropy in Table III. The Bayesian models without modification models had significantly lower error rates than the corresponding non-Bayesian models. The effect of the Bayesian extension was often larger than that of increasing the order of the models. For example, MetMM0B outperformed MetMM1 and MetMM1B outperformed MetMM2. As for the effects of the modification models, incorporating note divisions decreased the error rate for all model types, incorporating onset shifts did so only for the metrical MM, and incorporating both operations was no more effective than incorporating only note divisions for all model types. These results show that incorporation of modification models can often improve the transcription results but not significantly.

For the comparison among different model types, the metrical MMs consistently outperformed the corresponding note value MMs in most cases. The accuracies of PatMM0 and PatMM1 were close to that of MetMM2, and the effect of the Bayesian extension was larger for the metrical MMs. The best model in terms of accuracy was MetMM2B.

For the real data, most Bayesian models again outperformed the corresponding non-Bayesian models significantly. Incorporating the modification models was effective for some cases, but there were also cases where the error rates increased. We should notice that the error rates seem to saturate around 2.0% and many models remain within the range of statistical fluctuation. Particularly, the differences in the error rates between MetMM1 and MetMM2 and between MetMM1B and MetMM2B are much smaller than the case with the synthetic data. This fact also makes it difficult to clearly identify the best models; MetMM2B again had the lowest error rate but many other models had similar error rates. The note value MMs were consistently worse than the corresponding metrical MMs.

We manually analyzed the estimation errors made by MetMM2B, which had the lowest error rates, for the real data. There were around 70 errors (corresponding to an error rate of 2.08%) in the transcription results and 43 of them were clear performance errors. Note that a performance error of one note onset usually induces two estimation errors of note values. The remaining estimation errors were caused by less clear but significant timing deviations. There was a performance where complex rhythms with frequent tied notes were not accurately played, for which the model made 18 estimation errors. From these error analyses, we found that the limiting transcription accuracy of around 2% is reasonable for this test dataset.

The transcription examples in Fig. 8 demonstrate the effect of the Bayesian learning of piece-specific score models. This piece has repetitions of a tied dotted rhythm (see the first bars of the segments in Fig. 8), which are played with inaccurate timings. Since this rhythm is not common, the MetMM2 method using a generic score model made errors when the timing deviations were too large. In contrast, the MetMM2B method was able to recognize the correct rhythm in most cases by inducing the piece-specific score model capturing these repetitions and in effect cancelling out the timing deviations.
D. Influence of the Hyperparameters

We studied the influence of the values of hyperparameters on the transcription accuracy. We here focus on the Bayesian metrical MMs without incorporating the modification process to investigate the generic tendencies because the non-Bayesian models have poorer performance than the Bayesian models, and the Bayesian note pattern MMs and other Bayesian models with modification models have practically prohibitive computational costs for precise measurements.

The effects of varying the values of the three most relevant parameters, the concentration parameter for the unigram/transition probabilities, the number of iterations for Gibbs sampling, and the parameter $\sigma_t$ of the performance model, were investigated by measuring the transcription error rates as in Sec. V.C. When varying one of these parameter values, the other parameters were fixed to the values used in Sec. V.C. For the plots in Fig. 9, we run each algorithm with 10 different random number seeds and obtained the average error rate. For the concentration parameter and the number of iterations we used the synthetic performance data to obtain results with small statistical fluctuation, and for performance model parameter $\sigma_t$ we used the real performance data.

As for the concentration parameter of the unigram/transition probabilities (Fig. 9(a)), the optimal values for all the models were in the range [1, 100] but the values differ among the models. The theoretically optimal values at which the expectation value of entropies of the unigram/transition probabilities generated by the Dirichlet processes match the corresponding mean entropy of piece-specific unigram/transition probabilities of the training data are also shown there. We see that the theoretically optimal values do not necessarily match the empirically optimal values that maximizes the transcription accuracy. We can also confirm that the differences of error rates for these values and the value 10 used in Sec. V.C are within the range of one standard deviation of statistical fluctuation.

As for the number of iterations of the Gibbs sampling (Fig. 9(b)), the error rate monotonically decreased as the number of iterations increased until a plateau was reached for each model. For MetMM0B and MetMM1B the plateau was already reached with around 10 iterations, and for MetMM2B the error rate seemed to continue decreasing still at the 500th iteration. Since the computation time for parameter estimation is approximately proportional to the number of iterations, the trade off between computation time and precision of estimation is relevant especially for higher-order models.

As for the performance model parameter $\sigma_t$ (Fig. 9(c)), we see that different models had different optimal values in the range [0.03, 0.05] sec, but with a non-monotonic behaviour and large statistical fluctuation. From these results, we can understand that it is difficult to reliably find the precise optimal value of $\sigma_t$ for the real data and that the tentative value 0.035 sec used in Sec. V.C is at least not a bad choice.

E. Discussion on Computation Time and Extendability

Let us now discuss the computation time, which is another important aspect of transcription methods. The computation times for the studied models are listed in Table IV. These values were measured on a computer with a 3.6 GHz Intel Core i9 CPU and 64 GB of RAM. Roughly speaking, the computation time increases linearly with the number of notes in the input data and also linearly with the number of iterations for Gibbs sampling for the Bayesian models.

From the results we see that incorporating modification models significantly increases the computation time and note pattern MMs and metrical MMs require much more time than note value MMs and metrical MMs. Considering both the accuracy and computation time, the first-order and second-order metrical MMs
with Bayesian extensions are the most useful one in practical applications. Incorporating modification models to these models would increase the accuracy but also significantly increases the computation time. The order of a model, use of Bayesian extension and the number of iterations for Gibbs sampling, and the use of modification models should be determined according to the given resource of computation time.

In practical applications, we need to deal with longer note values and finer beat resolutions than those considered in this study. For example, if we consider the full bar length in 4/4 time and a beat resolution corresponding to one third of a 16th note (to accommodate triplets), \( N_b = 48 \). The computation times required for the first-order note value MM and metrical MM are roughly proportional to \( N_b \), and those for the second-order models are roughly proportional to \( N_b^2 \). On the other hand, the number of possible note patterns increases as \( 2^{N_b} \), which makes the computation times of the note pattern MMMs intractable, at least without refined searching techniques. This means that the metrical MMMs also have better extendability.

VI. CONCLUSION

We have studied the statistical description of repetitive structure of musical notes using Bayesian score models and its application to rhythm transcription. We have confirmed that the Bayesian score models capturing repetitions were indeed effective for improving the transcription accuracy. Considering the transcription accuracy and the computational efficiency, the second-order Bayesian metrical MM was found to be the best among the tested models. We have also shown that incorporating the note modification process can help capture approximate repetitions and therefore improve the accuracy but the effect was small and the computational cost significantly increased.

For future work, it is important to extend the model and incorporate pitches and multiple voices for applications to more general types of music transcription. The present approach of inferring piece-specific models can be even more effective in such cases that the amount of noise is larger than the case of rhythm transcription studied here. Another interesting possibility is to combine the present Bayesian approach with deep generative models that can learn more complex structure than what Markov models can learn.

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Supplemental Material for “Music Transcription Based on Bayesian Piece-Specific Score Models Capturing Repetitions”

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I. INTRODUCTION

In this Supplemental Material, we explicitly formulate three types of Markov models, their extensions incorporating note modifications, Bayesian extensions, and their integrations with the performance model. We also explicitly describe the Gibbs sampling methods for estimating model parameters using performance data.

Based on the convention in the main text, the labels NoteMM1, NoteMM1S, NoteMM1D, and NoteMM1SD are used for the score models based on the metrical MM, and PatMM1, PatMM1S, PatMM1D, and PatMM1SD are used for the score models based on the note value Markov model (MM). MetMM1, MetMM1S, MetMM1D, and MetMM1SD are used for the score models based on the metrical MM, and PatMM1, PatMM1S, PatMM1D, and PatMM1SD are used for the score models based on the note pattern MM. When these score models are integrated with the performance model, the integrated models are labelled as NoteHMM1, NoteHMM1S, etc.

II. NOTE VALUE MARKOV MODEL

A. Non-Bayesian Models

1) Basic Model (NoteMM1): The basic note value Markov model is defined with the initial and transition probabilities:

\[ P(r_1 = r) = \pi_{ini,r}, \quad P(r_n = r | r_{n-1} = r') = \pi_{r,r}. \] (32)

The complete-data probability is

\[ P(r_{1:N}) = \pi_{ini,r_1} \prod_{n=2}^{N} \pi_{r_{n-1},r_n}. \] (33)

2) Model with Only Onset Shifts (NoteMM1S): We introduce internal variables \( z_0 = s_0 \) and \( z_n = (\tilde{r}_n, s_n) \) \((n = 1, \ldots, N)\), where \( \tilde{r} \) indicates the note value before onset shift and \( s \) indicates the amount of onset shift. The model is defined as

\[ P(z_0 = s) = \xi_s, \quad P(z_1 = (\tilde{r}, s)) = \pi_{ini,\tilde{r}} \xi_s, \quad P(z_n = (\tilde{r}, s) | z_{n-1} = (\tilde{r}', s')) = \pi_{\tilde{r},\tilde{r}'} \xi_s, \] (34)

\[ P(r_n | z_{n-1}, z_n) = \| (r_n = \tilde{r}_n + s_n - s_{n-1}). \] (35)

3) Model with Only Note Divisions (NoteMM1D): We introduce an internal variable \( z = (\tilde{r}, h, g) \), where \( \tilde{r} \) indicates the note value before note division and \( h \) and \( g \) indicate division pattern and its internal note position. The model is defined as

\[ P(z_1 = (\tilde{r}, h, g)) = \pi_{ini} \Delta_{\tilde{r},h} \delta_{g1}, \] (36)

\[ P(z_n = (\tilde{r}, h, g) | z_{n-1} = (\tilde{r}', h', g')) = \delta_{\tilde{r},\tilde{r}'} \delta_{hh'} \delta_{g(g'+1)} + \delta_{g',g} \pi_{\tilde{r},\tilde{r}'} \xi_s, \] (37)

\[ P(r_n | z_n = (\tilde{r}, h, g)) = \| (r_n = q_{h,g}). \] (38)

and the complete-data probability is

\[ P(r_{1:N} | z_{1:N}) = \pi_{ini} \xi_{r_1} \delta_{g_1} \prod_{n=2}^{N} \left( \delta_{\tilde{r}_n,\tilde{r}_{n-1}} \delta_{h_n,h_{n-1}} \delta_{g_n(g_n+1)} + \delta_{g_{n-1},g_n} \pi_{\tilde{r}_{n-1},\tilde{r}_n} \xi_{r_n} \delta_{g_n} \right) \prod_{n=1}^{N} \| (r_n = q_{h,n,g}). \]

4) Model with Onset Shifts and Note Divisions (NoteMM1SD): We introduce internal variables \( z_0 = s_0 \) and \( z_n = (\tilde{r}_n, h_n, g_n) \) \((n = 1, \ldots, N)\). The model is defined as

\[ P(z_0 = s) = \xi_s, \quad P(z_1 = (\tilde{r}, h, g)) = \pi_{ini} \Delta_{\tilde{r},h} \delta_{g1} \xi_s, \] (39)

\[ P(z_n = (\tilde{r}, h, g) | z_{n-1} = (\tilde{r}', h', g')) = \delta_{\tilde{r},\tilde{r}'} \delta_{hh'} \delta_{g(g'+1)} + \delta_{g',g} \pi_{\tilde{r},\tilde{r}'} \xi_s, \] (40)

\[ P(r_n | z_{n-1}, z_n) = \| (r_n = q_{h,n,g} + s_n - s_{n-1}). \] (41)
B. Integration with the Performance Model

1) **NoteHMM1**: Latent variables: \(z_n = r_n\).

\[
P(z_1 = r) = \pi_{\text{ini} \, r}, \quad P(z_n = r \mid z_{n-1} = r') = \pi_{rr'},
\]
\[
P(d_n \mid z_n = r) = \phi_{rd_n} = \text{Gauss}(d_n; rv, \sigma_r^2).
\]

The complete-data probability is

\[
P(d_{1:N}, z_{1:N}) = \pi_{\text{ini} \, r_1} N \prod_{n=2}^{N} \pi_{r_{n-1} \, r_n} \prod_{n=1}^{N} \phi_{r_n d_n}.
\]

2) **NoteHMM1S**: Latent variables: \(z_0 = s_0, \ z_n = (\tilde{r}_n, s_n) \ (n = 1, \ldots, N).

\[
P(z_0 = s) = \xi_{s}, \quad P(z_1 = (\tilde{r}, s)) = \pi_{\text{ini} \, \tilde{r}} \xi_{s}, \quad P(z_n = (\tilde{r}, s) \mid z_{n-1} = (\tilde{r}' , s')) = \pi_{\tilde{r} \tilde{r}'} \xi_{s},
\]
\[
P(d_n \mid z_{n-1}, z_n) = \phi_{\tilde{r}_n s_{n-1} s_n d_n} = \text{Gauss}(d_n; (\tilde{r}_n + s_n - s_{n-1})v, \sigma_t^2)
\]

and the complete-data probability is

\[
P(d_{1:N}, z_{0:N}) = \pi_{\text{ini} \, \tilde{r}_1} N \prod_{n=2}^{N} \pi_{\tilde{r}_{n-1} \, \tilde{r}_n} \prod_{n=0}^{N} \xi_{s_n} \prod_{n=1}^{N} \phi_{\tilde{r}_n s_{n-1} s_n d_n}.
\]

3) **NoteHMM1D**: Latent variables: \(z_n = (\tilde{r}_n, h, g_n).

\[
P(z_1 = (\tilde{r}, h, g)) = \pi_{\text{ini} \, \tilde{r}} \xi_{h} \delta_{g_1},
\]
\[
P(z_n = (\tilde{r}, h, g) \mid z_{n-1} = (\tilde{r}' , h' , g')) = \delta_{\tilde{r} \tilde{r}'} \delta_{hh'} \delta_{g'(g'+1)} + \delta_{g'g} \pi_{\tilde{r} \tilde{r}'} \xi_{h} \delta_{g_1},
\]
\[
P(d_n \mid z_{n-1}, z_n) = \phi_{h g d_n} = \text{Gauss}(d_n; (q_{h_n g_n} + s_n - s_{n-1})v, \sigma_t^2)
\]

and the complete-data probability is

\[
P(d_{1:N}, z_{1:N}) = \pi_{\text{ini} \, \tilde{r}_1} \xi_{h_1} \delta_{g_1} N \prod_{n=2}^{N} \left( \delta_{\tilde{r}_n \tilde{r}_{n-1}} \delta_{h_n h_{n-1}} \delta_{g_n(g_n+1)} + \delta_{g_n g_{n-1}} \pi_{\tilde{r}_n \tilde{r}_{n-1}} \xi_{h_n h_n} \delta_{g_n} \right) \prod_{n=1}^{N} \phi_{h_n g_n d_n}.
\]

4) **NoteHMM1DS**: Latent variables: \(z_0 = s_0, \ z_n = (\tilde{r}_n, h, g_n, s_n) \ (n = 1, \ldots, N).

\[
P(z_0 = s) = \xi_{s}, \quad P(z_1 = (\tilde{r}, h, g, s)) = \pi_{\text{ini} \, \tilde{r}} \xi_{h} \delta_{g_1} \xi_{s},
\]
\[
P(z_n = (\tilde{r}, h, g, s) \mid z_{n-1} = (\tilde{r}' , h' , g', s')) = \delta_{\tilde{r} \tilde{r}'} \delta_{hh'} \delta_{g'(g'+1)} + \delta_{g'g} \pi_{\tilde{r} \tilde{r}'} \xi_{h} \delta_{g_1} \xi_{s},
\]
\[
P(d_n \mid z_{n-1}, z_n) = \phi_{h_g d_n} = \text{Gauss}(d_n; (q_{h_n g_n} + s_n - s_{n-1})v, \sigma_t^2),
\]

and the complete-data probability is

\[
P(d_{1:N}, z_{0:N}) = \pi_{\text{ini} \, \tilde{r}_1} \xi_{h_1} \delta_{g_1} N \prod_{n=2}^{N} \left( \delta_{\tilde{r}_n \tilde{r}_{n-1}} \delta_{h_n h_{n-1}} \delta_{g_n(g_n+1)} + \delta_{g_n g_{n-1}} \pi_{\tilde{r}_n \tilde{r}_{n-1}} \xi_{h_n h_n} \delta_{g_n} \right) \prod_{n=0}^{N} \xi_{s_n} \prod_{n=1}^{N} \phi_{h_n g_n s_{n-1} s_n d_n}.
\]

C. Bayesian Extension

We put prior models on the parameters \(\pi_{\text{ini}} = (\pi_{\text{ini} \, \tilde{r}}), \ \pi_{\tilde{r}} = (\pi_{\tilde{r} \tilde{r}'})', \ \xi_{s} = (\xi_{s})_s\), and \(\xi = (\xi_{s})_s\) as

\[
\pi_{\text{ini}} = \text{DP}(\alpha_{\text{ini}}, \pi_{\text{ini}}), \quad \pi_{\tilde{r}} = \text{DP}(\alpha_{\pi}, \pi_{\tilde{r}}'), \quad \xi_{s} = \text{DP}(\alpha_{\xi}, \xi_{s}), \quad \xi = \text{DP}(\alpha_{\xi}, \xi).
\]

D. Gibbs Sampling for Bayesian Learning

Bayesian learning of the model parameters using performance data can be done with the Gibbs sampling. Let \(\theta\) be the parameters, \(z\) be the set of latent variables, and \(\lambda\) be the collection of hyperparameters. We sample the distribution \(P(\theta, z, d, \lambda)\) by alternatingly sampling \(P(\theta \mid z, d, \lambda)\) (parameter sampling) and \(P(z \mid \theta, d, \lambda) = P(z \mid \theta, d)\) (latent variables sampling).
1. **Parameter Sampling for NoteHMM1 and NoteHMM1S**: The sampling of the parameters $\theta$ from $P(\theta|z, \lambda)$ can be done using the following formulas.

$$\pi_{ini} \sim \text{Dir}(\alpha_{ini} \pi_{ini} + c_{ini}), \quad c_{ini} \hat{\pi} = \delta_{\pi, \hat{\pi}},$$

$$\pi_{r'} \sim \text{Dir}(\alpha_{r'} \pi_{r'} + c_{r'}), \quad c_{r'} = \sum_{n=2}^{N} \delta_{r_{n-1}, r'} \delta_{r_{n}, \hat{\pi}},$$

$$\xi \sim \text{Dir}(\alpha_{\xi} \xi + c_{\xi}), \quad c_{\xi} = \sum_{n=0}^{N} \delta_{s_{n}, s}.$$  

Here, $c_{ini}, c_{r'},$ and $c_{\xi}$ count the numbers of times the relevant variables appear in the sequence $z$. Similar notation will be used in the following without mentioning.

2. **Parameter Sampling for NoteHMM1D and NoteHMM1SD**: The sampling of the parameters $\theta$ from $P(\theta|z, \lambda)$ can be done using the following formulas.

$$\pi_{ini} \sim \text{Dir}(\alpha_{ini} \pi_{ini} + c_{ini}), \quad c_{ini} \hat{\pi} = \delta_{\pi, \hat{\pi}},$$

$$\pi_{r'} \sim \text{Dir}(\alpha_{r'} \pi_{r'} + c_{r'}), \quad c_{r'} = \sum_{n=2}^{N} \delta_{r_{n-1}, r'} \delta_{r_{n}, \hat{\pi}},$$

$$\zeta_{r} \sim \text{Dir}(\alpha_{\zeta} \zeta + c_{\zeta}), \quad c_{\zeta} = \sum_{n=1}^{N} \delta_{r_{n}, h} \delta_{h_{n}, h},$$

$$\xi \sim \text{Dir}(\alpha_{\xi} \xi + c_{\xi}), \quad c_{\xi} = \sum_{n=0}^{N} \delta_{s_{n}, s}.$$  

3. **Latent Variables Sampling**: The latent variables can be sampled using the forward filtering-backward sampling method. The forward variable is defined as

$$\alpha_{n}(z_{n}) = P(d_{1:n}, z_{n}).$$

For NoteHMM1 and NoteHMM1D, the forward variable can be computed as

$$\alpha_{1}(z_{1}) = P(z_{1})P(d_{1}|z_{1}),$$

$$\alpha_{n}(z_{n}) = \sum_{z_{n-1}} P(d_{n}|z_{n})P(z_{n-1}|z_{n-1})\alpha_{n-1}(z_{n-1}),$$

$$P(d = d_{1:N}) = \sum_{z_{N}} \alpha_{N}(z_{N}).$$

The backward sampling step goes as

$$P(z_{N}|d) \propto P(d, z_{N}) = \alpha_{N}(z_{N}),$$

$$P(z_{N} | z_{n+1:N}, d) = P(z_{n} | z_{n+1}, d_{1:n}) \propto P(z_{n}, z_{n+1}, d_{1:n}) = P(z_{n+1}|z_{n})\alpha_{n}(z_{n}).$$

For NoteHMM1S and NoteHMM1SD, the forward variables can be computed as

$$\alpha_{0}(z_{0}) = P(z_{0}),$$

$$\alpha_{n}(z_{n}) = \sum_{z_{n-1}} P(d_{n-1} | z_{n-1}, z_{n})P(z_{n}|z_{n-1})\alpha_{n-1}(z_{n-1}),$$

$$P(d = d_{1:N}) = \sum_{z_{N}} \alpha_{N}(z_{N}).$$

The backward sampling step goes as

$$P(z_{N}|d) \propto P(d, z_{N}) = \alpha_{N}(z_{N}),$$

$$P(z_{n} | z_{n+1:N}, d) = P(z_{n} | z_{n+1}, d_{1:n+1}) \propto P(z_{n}, z_{n+1}, d_{1:n+1}) = P(z_{n+1}|z_{n})P(d_{n+1}|z_{n}, z_{n+1})\alpha_{n}(z_{n}).$$

### III. METRICAL MARKOV MODEL

#### A. Non-Bayesian Models

1. **Basic Model (MetMM1)**: The metrical positions $b_{0:N}$ are generated as

$$P(b_{0}) = \chi_{ini}, \quad P(b_{n}|b_{n-1}) = \chi_{b_{n-1}b_{n}}.$$
The note values and the onset score times are then given as

\[
\tau_0 = b_0, \quad r_n = \tau_n - \tau_{n-1} = [b_{n-1}, b_n]_{\bar{N}_b} = \begin{cases} 0 & b_{n-1} < b_n; \\ b_n - b_{n-1} + \bar{N}_b, & b_{n-1} \geq b_n. \end{cases}
\]

2) Model with Only Onset Shifts (MetMM1S): Introduce internal variables \( z_n = (\tilde{b}_n, s_n) \) \((n = 0, \ldots, N)\).

\[
P(z_0 = (\tilde{b}, s)) = \chi_{\text{ini}} b \xi_s, \quad P(z_n = (\tilde{b}, s) | z_{n-1} = (\tilde{b}', s')) = \chi_{\text{ini}} b \xi_{s}, \quad (73)
\]

\[
P(r_n | z_{n-1}, z_n) = \mathbb{I}(r_n = [\tilde{b}_{n-1}, \tilde{b}_n] + s_n - s_{n-1}). \quad (74)
\]

3) Model with Only Note Divisions (MetMM1D): Introduce internal variables \( z_0 = \tilde{b}_0, \ z_n = (\tilde{b}_n, h_n, g_n) \) \((n = 1, \ldots, N)\).

\[
P(z_0 = \tilde{b}_0) = \chi_{\text{ini}} b \xi_s, \quad P(z_1 = (\tilde{b}, h, g) | z_0 = (\tilde{b}', h') = \chi_{\text{ini}} b \xi_{s}, \quad (75)
\]

\[
P(z_n = (\tilde{b}, h, g) | z_{n-1} = (\tilde{b}', h', g') = \delta_{\text{ini}} \delta_{hh} \delta_{g(g'+1)} + \delta_{\text{ini}} G_h \chi_{\text{ini}} b \xi_{s}, \quad (76)
\]

\[
P(r_n | z_{n-1}, z_n) = \mathbb{I}(r_n = q_{h_n} g_n). \quad (77)
\]

4) Model with Onset Shifts and Note Divisions (MetMM1SD): Introduce internal variables \( z_0 = (\tilde{b}_0, s_0), \ z_n = (\tilde{b}_n, h_n, g_n, s_n) \) \((n = 1, \ldots, N)\).

\[
P(z_0 = (\tilde{b}, s)) = \chi_{\text{ini}} b \xi_s, \quad P(z_1 = (\tilde{b}, h, g, s) | z_0 = (\tilde{b}', s')) = \xi_s \chi_{\text{ini}} b \xi_{s}, \quad (78)
\]

\[
P(z_n = (\tilde{b}, h, g, s) | z_{n-1} = (\tilde{b}', h', g', s')) = \xi_s \delta_{\text{ini}} \delta_{hh} \delta_{g(g'+1)} + \delta_{\text{ini}} G_h \chi_{\text{ini}} b \xi_{s}, \quad (79)
\]

\[
P(r_n | z_{n-1}, z_n) = \mathbb{I}(r_n = q_{h_n} g_n + s_n - s_{n-1}). \quad (80)
\]

B. Integration with the Performance Model

1) MetHMM1: Latent variables: \( z_n = b_n \) \((n = 0, \ldots, N)\).

\[
P(z_0 = b) = \chi_{\text{ini}} b \xi_s, \quad P(z_n = b | z_{n-1} = b') = \chi_{b'} \xi_s, \quad (81)
\]

\[
P(d_n | z_{n-1} = b', z_n = b) = \phi_{b' \text{ini} b} = \text{Gauss}(d_n; [b', b], \sigma_f^2), \quad (82)
\]

and the complete-data probability is

\[
P(d_1:N, z_0:N) = \chi_{\text{ini}} b_0 \prod_{n=1}^{N} (\chi_{b_n - 1 \cdot b_n} \phi_{b_n - 1 \cdot b_n, d_n}). \quad (83)
\]

2) MetHMM1S: Latent variables: \( z_n = (\tilde{b}_n, s_n) \) \((n = 0, \ldots, N)\).

\[
P(z_0 = (\tilde{b}, s)) = \chi_{\text{ini}} b \xi_s, \quad P(z_1 = (\tilde{b}, h, g, s) | z_0 = (\tilde{b}', s')) = \chi_{\text{ini}} b \xi_{s}, \quad (83)
\]

\[
P(d_n | z_{n-1} = b', z_n = b) = \phi_{b' \text{ini} b} = \text{Gauss}(d_n; [b', b], \sigma_f^2), \quad (84)
\]

and the complete-data probability is

\[
P(d_1:N, z_0:N) = \chi_{\text{ini}} b_0 \prod_{n=1}^{N} (\chi_{b_n - 1 \cdot b_n} \xi_{s_n} \phi_{b_n - 1 \cdot b_n, s_n, d_n}). \quad (85)
\]

3) MetHMM1D: Latent variables: \( z_0 = \tilde{b}_0, \ z_n = (\tilde{b}_n, h_n, g_n) \) \((n = 1, \ldots, N)\).

\[
P(z_0 = \tilde{b}_0) = \chi_{\text{ini}} b \xi_s, \quad P(z_1 = (\tilde{b}, h, g) | z_0 = (\tilde{b}', h') = \chi_{\text{ini}} b \xi_{s}, \quad (86)
\]

\[
P(z_n = (\tilde{b}, h, g) | z_{n-1} = (\tilde{b}', h', g') = \chi_{\text{ini}} b \xi_{s}, \quad (87)
\]

\[
P(d_n | z_n) = \phi_{h_n, g_n} = \text{Gauss}(d_n; [b_n, g_n], \sigma_f^2), \quad (88)
\]

and the complete-data probability is

\[
P(d_1:N, z_0:N) = \chi_{\text{ini}} b_0 \chi_{b_0 \text{ini} b_1} \xi_{[b_0, b_1]} \delta_{g_1 1} \prod_{n=1}^{N} \phi_{h_n, g_n, d_n}
\]

\[
\cdot \prod_{n=2}^{N} (\delta_{b_n b_{n-1}} \delta_{h_n h_{n-1}} \delta_{g_n (g_{n-1} + 1)} + \delta_{g_n - 1 G_{h_n - 1}} \chi_{\text{ini}} b_{n-1} \xi_{[b_{n-1}, b_n]} h_n \delta_{g_n 1}). \quad (89)
\]
4) MetHMM1SD: Latent variables: \( z_0 = (\tilde{b}_0, s_0), z_n = (\tilde{b}_n, h_n, g_n, s_n) \) \( (n = 1, \ldots, N) \).

\[
P(z_0 = (\tilde{b}, s)) = \chi_{\text{ini}} b, \quad P(z_1 = (\tilde{b}, h, g, s) \mid z_0 = (\tilde{b}', s')) = \xi_s \chi_{\tilde{b}} \delta_{\tilde{b}'\tilde{b}} \delta_{g1},
\]

\[
P(z_n = (\tilde{b}, h, g, s) \mid z_{n-1} = (\tilde{b}', h', g', s')) = \xi_n (\delta_{\tilde{b}\tilde{b}'} \delta_{h\tilde{h}} \delta_{g(g'+1)} + \delta_{g'\tilde{g}'} \chi_{\tilde{b}} \delta_{g1}),
\]

\[
P(d_n \mid z_{n-1}, z_n) = \phi_{h_n, g_n, s_n-1, s_n, d_n} = \text{Gauss}(d_n; (\hat{q}_{h_n, g_n} + s_n - s_{n-1})v, \sigma_n^2),
\]

and the complete-data probability is

\[
P(d_{1:N} \mid z_{0:N}) = \chi_{\text{ini}} b, P(\alpha_{\text{ini}}, \chi_{\text{ini}}), \quad \chi_{\tilde{b}} = \text{DP}(\alpha_{\chi}, \chi_{\tilde{b}}), \quad \xi = \text{DP}(\alpha_{\xi}, \xi).
\]

C. Bayesian Extension

We put prior models on the parameters as

\[
\begin{align*}
\chi_{\text{ini}} &= \text{DP}(\alpha_{\text{ini}}, \chi_{\text{ini}}), \\
\chi_{\tilde{b}} &= \text{DP}(\alpha_{\chi}, \chi_{\tilde{b}}), \\
\xi &= \text{DP}(\alpha_{\xi}, \xi).
\end{align*}
\]

D. Gibbs Sampling for Bayesian Learning

The general procedure for Bayesian learning is same as in Sec. [II-D]

1) Parameter Sampling for MetHMM1 and MetHMM1S:

\[
\chi_{\text{ini}} \sim \text{Dir}(\alpha_{\text{ini}}, \chi_{\text{ini}} + e_{\text{ini}}), \quad e_{\text{ini}} = \delta_{\tilde{b}b},
\]

\[
\chi_{\tilde{b}} \sim \text{Dir}(\alpha_{\chi}, \chi_{\tilde{b}} + e_{\tilde{b}}), \quad e_{\tilde{b}} = \sum_{n=1}^{N} \delta_{\tilde{b}_{n-1}b} \delta_{b_n, b},
\]

\[
\xi \sim \text{Dir}(\alpha_{\xi}, \xi + e_{\xi}), \quad e_{\xi} = \sum_{n=0}^{N} \delta_{s_n s}.
\]

2) Parameter Sampling for MetHMM1D and MetHMM1SD:

\[
\chi_{\text{ini}} \sim \text{Dir}(\alpha_{\text{ini}}, \chi_{\text{ini}} + e_{\text{ini}}), \quad e_{\text{ini}} = \delta_{\tilde{b}b},
\]

\[
\chi_{\tilde{b}} \sim \text{Dir}(\alpha_{\chi}, \chi_{\tilde{b}} + e_{\tilde{b}}), \quad e_{\tilde{b}} = \sum_{n=1}^{N} \delta_{g_{n-1}b} \delta_{\tilde{b}_{n-1}b},
\]

\[
\xi \sim \text{Dir}(\alpha_{\xi}, \xi + e_{\xi}), \quad e_{\xi} = \sum_{n=0}^{N} \delta_{s_n s}.
\]

3) Latent Variables Sampling: The forward variable is defined as

\[
\alpha_n(z_n) = P(d_{1:n} \mid z_n),
\]

which can be computed as

\[
\begin{align*}
\alpha_0(z_0) &= P(z_0), \\
\alpha_n(z_n) &= \sum_{z_{n-1}} P(d_n \mid z_{n-1}, z_n) P(z_n \mid z_{n-1}) \alpha_{n-1}(z_{n-1}),
\end{align*}
\]

\[
P(d = d_{1:N}) = \sum_{z_N} \alpha_N(z_N).
\]

The backward sampling step goes as follows:

\[
P(z_N \mid d) \propto P(d, z_N) = \alpha_N(z_N),
\]

\[
P(z_n \mid z_{n+1:N}, d) = P(z_n \mid z_{n+1}, d_{1:n+1}) \propto P(z_n, z_{n+1}, d_{1:n+1}) \propto P(d_{n+1} \mid z_n, z_{n+1}) P(z_{n+1} \mid z_n) \alpha_n(z_n).
\]
IV. NOTE PATTERN MARKOV MODEL

A. Non-Bayesian Models

1) Basic Model (PatMMI): The basic note pattern Markov model is described with internal variables \( z_n = (k_n, i_n) \) (\( n = 1, \ldots, N \)). The initial and transition probabilities are given as

\[
P(z_1 = (k, i)) = \psi_{\text{init}}(k, i) = \Gamma_{\text{init}} k \gamma_{\text{init}}^k \Gamma_{\text{init}} \delta_{i1},
\]

\[
P(z_n = (k, i) | z_{n-1} = (k', i')) = \psi(k' | (k, i)) = \delta_{k'k} \gamma_{i'}^k + \gamma_{i' \text{end}} \Gamma_{\text{init}} k \gamma_{\text{init}}^k \Gamma_{\text{init}} \delta_{i1},
\]

\[
P(r_n | z_n, z_{n-1}) = \mathbb{I}(r_n = [B_{k_{n-1}i_{n-1}}, B_{k_ni_n}]).
\]

2) Model with Only Onset Shifts (PatMMIS): Introduce internal variables \( z_n = (k_n, i_n, s_n) \) (\( n = 0, \ldots, N \)),

\[
P(z_0 = (k, i, s)) = \psi_{\text{init}}(k, i) \xi_s,
\]

\[
P(z_n = (k, i, s) | z_{n-1} = (k', i', s')) = \psi(k' | (k, i)) \xi_s,
\]

\[
P(r_n | z_n, z_{n-1}) = \mathbb{I}(r_n = [B_{k_{n-1}i_{n-1}}, B_{k_ni_n} + s_n - s_{n-1}]).
\]

3) Model with Only Note Divisions (PatMMID): Introduce internal variables \( z_n = (k_0, i_0, s_0), z_n = (k_n, i_n, h_n, g_n) \) (\( n = 1, \ldots, N \)),

\[
P(z_0 = (k, i, s)) = \psi_{\text{init}}(k, i),
\]

\[
P(z_n = (k, i, h, g) | z_0 = (k', i')) = \psi(k' | (k, i)) \xi_s, \quad \delta_{kk'} \xi_s = \delta_{kk'} \delta_{i,i'} \delta_{h1} \delta_{g1} \psi_{\text{init}}(k, i) \xi_s,
\]

\[
P(r_n | z_n, z_{n-1}) = \mathbb{I}(r_n = \{gh_{h_n}g_n \}).
\]

4) Model with Onset Shifts and Note Divisions (PatMMID): Introduce internal variables \( z_n = (k_0, i_0, s_0), z_n = (k_n, i_n, h_n, g_n) \) (\( n = 1, \ldots, N \)),

\[
P(z_0 = (k, i, s)) = \psi_{\text{init}}(k, i),
\]

\[
P(z_n = (k, i, h, g) | z_0 = (k', i', s')) = \psi(k' | (k, i)) \xi_s, \quad \delta_{kk'} \xi_s = \delta_{kk'} \delta_{i,i'} \delta_{h1} \delta_{g1} \psi_{\text{init}}(k, i) \xi_s,
\]

\[
P(r_n | z_n, z_{n-1}) = \mathbb{I}(r_n = \{gh_{h_n}g_n + s_n - s_{n-1} \}).
\]

B. Integration with the Performance Model

1) PatHMMI: Latent variables: \( z_n = b_n \) (\( n = 0, \ldots, N \)),

\[
P(z_0 = (k, i)) = \psi_{\text{init}}(k, i), \quad P(z_n = (k, i) | z_{n-1} = (k', i')) = \psi(k' | (k, i)),
\]

\[
P(d_n | z_n, z_{n-1}) = \phi_i(k', (k, i)) \xi_s = \text{Gauss}(d_n; [B_{k_{i'}}B_{k_{i}}]v, \sigma_v^2),
\]

and the complete-data probability is

\[
P(d_{1:N}, z_{0:N}) = \psi_{\text{init}}(k_0i_0) \prod_{n=1}^{N} (\psi_{\text{init}}(k_{n-1}i_{n-1}) (k_ni_n) \phi_{\text{init}}(k_{n-1}i_{n-1})(k_ni_n)d_n).
\]

2) PatHMMIS: Latent variables: \( z_n = (k_n, i_n, s_n) \) (\( n = 0, \ldots, N \)),

\[
P(z_0 = (k, i, s)) = \psi_{\text{init}}(k, i) \xi_s, \quad \psi_{\text{init}}(k, i) \xi_s = \text{Gauss}(d_n; [B_{k_{i'}}B_{k_{i}}]v, \sigma_v^2),
\]

and the complete-data probability is

\[
P(d_{1:N}, z_{0:N}) = \psi_{\text{init}}(k_0i_0) \xi_{s_0} \prod_{n=1}^{N} (\psi_{\text{init}}(k_{n-1}i_{n-1}) (k_ni_n) \xi_{s_n} \phi_{\text{init}}(k_{n-1}i_{n-1} s_{n-1} k_ni_n s_n d_n)).
\]

3) PatHMMID: Latent variables: \( z_0 = (k_0, i_0), z_n = (k_n, i_n, h_n, g_n) \) (\( n = 1, \ldots, N \)),

\[
P(z_0 = (k, i, s)) = \psi_{\text{init}}(k, i), \quad \psi_{\text{init}}(k, i) \xi_s = \text{Gauss}(d_n; [B_{k_{i'}}B_{k_{i}}]v, \sigma_v^2),
\]

and the complete-data probability is

\[
P(d_{1:N}, z_{0:N}) = \psi_{\text{init}}(k_0i_0) \xi_{s_0} \prod_{n=1}^{N} (\psi_{\text{init}}(k_{n-1}i_{n-1}) (k_ni_n) \xi_{s_n} \phi_{\text{init}}(k_{n-1}i_{n-1} s_{n-1} k_ni_n s_n d_n)).
\]
4) PathHMM1SD: Latent variables: \( z_0 = (k_0, i_0, s_0), \ z_n = (k_n, i_n, h_n, g_n, s_n) \) \( (n = 1, \ldots, N) \).

\[
P(z_0 = (k, i, s)) = \psi_{ini}(k) \xi_s, \quad P(z_1 = (k, i, h, g, s) \mid z_0 = (k', i', s')) = \xi_s \psi(k' \mid (k \mid i) \zeta_{B_{k' i'}} B_{k i}), h \delta g_1,
\]

\[
P(z_n = (k, i, h, g, s) \mid z_{n-1} = (k', i', h', g', s')) = \xi_s (\delta_{k k'} \delta_{i i'} \delta_{h h'} \delta_{g g'} \delta_{s s'}) + \delta_{g g'} \psi_{ini}(k) \zeta_{B_{k' i'}} B_{k i}) h \delta g_1,
\]

\[
P(d_n \mid z_{n-1}, z_n) = \phi_{h_n g_n s_n-1 s_n d_n} = \text{Gauss}(d_n; (q_{h_n g_n} + s_n - s_n-1) \psi, \sigma_n^2),
\]

and the complete-data probability is

\[
P(d_{1:N}, z_0:N) = \psi_{ini}(k_0 i_0) \psi_{ini}(k_1 i_1) \zeta_{B_{k_0 i_0 B_{k_1 i_1}}} h_1 \delta_{g_1}. \prod_{n=0}^{N} \xi_s \prod_{n=1}^{N} \phi_{h_n g_n s_n-1 s_n d_n}
\]

\[
+ \prod_{n=2}^{N} (\delta_{k_n k_{n-1}} \delta_{i_n i_{n-1}} \delta_{h_n h_{n-1}} \delta_{g_n(g_n+1)} + \delta_{g_n g_{n-1}} \psi_{ini}(k_{n-1} i_{n-1}) (k_n i_n) \zeta_{B_{k_{n-1} i_{n-1}} B_{k_{n} i_{n}}}, h_n \delta_{g_n 1}).
\]

C. Bayesian Extension

We put prior models on the parameters as

\[
\Gamma_{ini} = \text{DP}(\alpha_{ini}, \bar{\Gamma}_{ini}), \quad \Gamma_k = \text{DP}(\alpha_r, \bar{\Gamma}_k), \quad \zeta_r = \text{DP}(\alpha_\zeta, \bar{\zeta}_r), \quad \xi = \text{DP}(\alpha_\xi, \bar{\xi}). \quad (120)
\]

D. Gibbs Sampling for Bayesian Learning

The general procedure for Bayesian learning is same as in Sec. II-D.

1) Parameter Sampling for PathHMM1 and PathHMM1S:

\[
\Gamma_{ini} \sim \text{Dir}(\alpha_{ini} \bar{\Gamma}_{ini} + c_{ini}), \quad c_{ini k} = \delta_{k o_k},
\]

\[
\Gamma_{k'} \sim \text{Dir}(\alpha_T \bar{\Gamma}_{k'} + c_{k'}), \quad c_{k' k} = \sum_{n=1}^{N} \delta_{h_n} \delta_{k_{n-1} k_{n} k_{n-1}} \delta_{g_n},
\]

\[
\xi \sim \text{Dir}(\alpha_\xi \bar{\xi} + c_{\xi}), \quad c_{\xi n} = \sum_{n=0}^{N} \delta_{s_n},
\]

2) Parameter Sampling for PathHMM1D and PathHMM1SD:

\[
\Gamma_{ini} \sim \text{Dir}(\alpha_{ini} \bar{\Gamma}_{ini} + c_{ini}), \quad c_{ini k} = \delta_{k o_k},
\]

\[
\Gamma_{k'} \sim \text{Dir}(\alpha_T \bar{\Gamma}_{k'} + c_{k'}), \quad c_{k' k} = \sum_{n=1}^{N} \delta_{h_n} \delta_{k_{n-1} k_{n} k_{n-1}} \delta_{g_n},
\]

\[
\zeta_r \sim \text{Dir}(\alpha_\zeta \bar{\zeta} + c_{\zeta}), \quad c_{\zeta n} = \sum_{n=1}^{N} \delta_{g_n} \delta_{[B_{k_{n-1} i_{n-1}}, B_{k_{n} i_{n}}]},
\]

\[
\xi \sim \text{Dir}(\alpha_\xi \bar{\xi} + c_{\xi}), \quad c_{\xi n} = \sum_{n=0}^{N} \delta_{s_n},
\]

3) Latent Variables Sampling: The forward variable is defined as

\[
\alpha_n(z_n) = P(d_{1:n}, z_n),
\]

which can be computed as

\[
\alpha_0(z_0) = P(z_0),
\]

\[
\alpha_n(z_n) = \sum_{z_{n-1}} P(d_n \mid z_{n-1}, z_n) P(z_n \mid z_{n-1}) \alpha_{n-1}(z_{n-1}),
\]

\[
P(d = d_{1:N}) = \sum_{z_{1:N}} \alpha_N(z_N). \quad (130)
\]

The backward sampling step goes as follows:

\[
P(z_N \mid d) \propto P(d, z_N) = \alpha_N(z_N),
\]

\[
P(z_n \mid z_{n+1:N}, d) = P(z_n \mid z_{n+1}, d_{1:n+1}) \propto P(z_n, z_{n+1}, d_{1:n+1}) \propto P(d_{n+1} \mid z_n, z_{n+1}) P(z_{n+1} \mid z_n) \alpha_n(z_n).
\]