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An Efficient Pattern Mining Approach for Event Detection in Multivariate Temporal Data

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Abstract This work proposes a pattern mining approach to learn event detection models from complex multivariate temporal data, such as electronic health records. We present Recent Temporal Pattern mining, a novel approach for efficiently finding predictive patterns for event detection problems. This approach first converts the time series data into time-interval sequences of temporal abstractions. It then constructs more complex time-interval patterns backward in time using temporal operators. We also present the Minimal Predictive Recent Temporal Patterns framework for selecting a small set of predictive and non-spurious patterns. We apply our methods for predicting adverse medical events in real-world clinical data. The results demonstrate the benefits of our methods in learning accurate event detection models, which is a key step for developing intelligent patient monitoring and decision support systems.

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1 Introduction

Advances in data collection and data storage technologies have led to the emergence of complex multivariate temporal datasets, where the data instances are traces of complex behaviors characterized by time series of multiple variables. Designing algorithms capable of analyzing and learning from such data is one of the most challenging topics of data mining research.

In this work, we study the supervised learning task of event detection in multivariate temporal data. In this task, the labels denote different events that are associated with specific time points during the temporal instances. The goal is to learn how to accurately detect (in time) the occurrence of these events for future instances (a monitoring task). This setting appears in a wide range of applications, such as the detection of adverse medical events (e.g., onsets of diseases or drug toxicity) in clinical data (Hauskrecht et al. 2010), the detection of equipment malfunctions (Guttormsson et al. 1999), fraud detection (Srivastava et al. 2008), environmental monitoring (Papadimitriou et al. 2005), intrusion detection (Chandola et al. 2006) and others.

Given that the events are associated with specific time points during the instances, the temporal observations that are close to the time of the event are typically the most important for prediction. Consequently, the context for prediction is often local and affected by the most recent behavior of the monitored instance. The focus of this paper is to develop a temporal pattern mining method that takes into account the local nature of decisions for monitoring and event detection problems.

We primarily focus on data in Electronic Health Record (EHR) systems. In this data, each record (instance) consists of multiple time series of clinical variables collected for a specific patient, such as laboratory test results and medication orders. The data also provide temporal information about the incidence of several adverse medical events, such as diseases or drug toxicities. The task is to learn how to predict these adverse medical events for future patients. This is practically very useful for intelligent patient monitoring, outcome prediction and clinical decision support.

Temporal modeling for EHR data is challenging because the data are *multivariate* and the time series for clinical variables are *irregularly sampled in time* (measured asynchronously at different time moments). Therefore, most existing times series classification methods (Blasiak & Rangwala 2011, Vail et al. 2007), time series similarity measures (Yang & Shahabi 2004, Ratanamahatana & Keogh 2005) and time series feature extraction methods (Li et al. 2010, Batal & Hauskrecht 2009, Weng & Shen 2008) cannot be directly applied to the raw EHR data.

In this paper, we present a pattern mining approach that can handle complex temporal data such as EHR. The first step is to define a pattern language that can adequately represent the temporal dimension of the data. To do this, we rely on temporal abstractions (Shahar 1997) to convert time series variables into *time-interval* sequences of abstract states and on Höppner's representation of time-interval patterns (Höppner 2001, 2003) to define complex temporal interactions among multiple states. For example, this allows us to express a concept like "the administration of heparin precedes a decreasing trend in platelet counts".

After defining the pattern language, we need to design an efficient algorithm for finding useful patterns in time-interval (temporally abstracted) data. Unlike the existing methods that mine all frequent time-interval patterns in an unsupervised setting (Wu & Chen 2007, Winarko & Roddick 2007, Papapetrou et al. 2005, Sacchi et al. 2007, Moerchen 2006*a*, Höppner 2001, Kam & Fu 2000), we are only interested in mining those patterns that are important for the event detection task (patterns that describe the temporal behavior that led to the development of the event).

To achieve this goal, we propose *Recent Temporal Pattern* (***RTP***) mining, a novel approach that mines frequent time-interval patterns backward in time starting from patterns related to the most recent observations, which we argue are typically the most important for prediction. Applying this technique, temporal patterns that extend far into the past are likely to have low support in the data and hence would not be considered for prediction. Incorporating the concept of recency in temporal pattern mining is a new research direction that, to the best of our knowledge, has not been previously explored in the pattern mining literature.

In addition, we present the concept of *Minimal Predictive Recent Temporal Patterns* (***MPRTP***), a pattern selection technique for choosing a small set of predictive and non-redundant RTPs. MPRTP applies Bayesian inference to evaluate the predictiveness of each RTP. Moreover, it considers the structure of patterns to ensure that every RTP in the result is significantly more predictive than all of its simplifications, which we demonstrate can eliminate a lot of spurious and redundant RTPs.

We test and demonstrate the usefulness of our methods on two real-world EHR datasets. The first dataset is a large-scale data that contains health records for 13,558 diabetic patients. The task is predict and diagnose various types of disorders that are frequently associated with diabetes, such as cardiological, renal or neurological disorders. The second dataset contains records of post cardiac surgical patients (Hauskrecht et al. 2010, 2012) and the task is to predict patients who are at risk of developing Heparin Induced Thrombocytopenia (HIT), a life threatening condition that may develop in patients treated with heparin.

Our main contributions are summarized as follows:

- We propose recent temporal pattern (RTP) mining to find predictive time-interval patterns for event detection problems.
- We present an algorithm that mines frequent RTPs backward in time and show that it is much more scalable than mining all frequent time-interval patterns.
- We propose the concept of minimal predictive recent temporal patterns (MPRTP) for selecting predictive and non-spurious patterns.
- We present a mining algorithm which integrates MPRTP evaluation with frequent RTP mining and applies efficient pruning techniques to speed up the mining.
- We apply our methods to two real-world clinical datasets and show that they are able to efficiently find useful patterns for detecting adverse medical events. Furthermore, we show that the mined patterns are easy to interpret by domain experts, which is beneficial for knowledge discovery purposes.

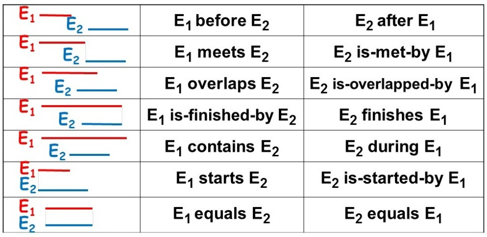
Roadmap: The rest of the paper is organized as follows. Section 2 outlines related research. Section 3 describes the background on temporal abstraction and temporal patterns for time-interval data. Section 4 describes the recent temporal patterns (RTPs) framework and explains our algorithm for mining frequent RTPs.

Section 5 describes the minimal predictive recent temporal patterns (MPRTPs) framework and explains our mining algorithm. Section 6 presents the experimental evaluation. Finally, Section 7 concludes the paper.

2 Related Research

This paper studies the problem of mining predictive time-interval patterns (defined over temporal abstractions) for event detection. The problem of mining time-interval patterns is a relatively young research field. Most of the techniques extend methods for mining sequential patterns (time-point patterns) (Agrawal & Srikant 1995, Zaki 2001, Pei et al. 2001, Yan et al. 2003) to deal with the more complex case of time-interval data[1].

In (Allen 1984), Allen formalized a logic on time intervals by specifying 13 possible temporal relations and showing their completeness. These relations are shown in Figure 1. Allen's temporal relations have been used by the majority of research on mining time-interval data (Kam & Fu 2000, Höppner 2001, Papapetrou et al. 2005, Winarko & Roddick 2007, Patel et al. 2008*a*, Moskovitch & Shahar 2009).



E_1 E_2	E_1 before E_2	E_2 after E_1
E_1 E_2	E_1 meets E_2	E_2 is-met-by E_1
E_1 E_2	E_1 overlaps E_2	E_2 is-overlapped-by E_1
E_1 E_2	E_1 is-finished-by E_2	E_2 finishes E_1
E_1 E_2	E_1 contains E_2	E_2 during E_1
E_1 E_2	E_1 starts E_2	E_2 is-started-by E_1
E_1 E_2	E_1 equals E_2	E_2 equals E_1

Fig. 1 Allen's temporal relations.

Kam and Fu (Kam & Fu 2000) were the first to propose using Allen's relations for defining time-interval patterns (patterns consisting of multiple states). However, their representation was shown to be ambiguous (the same situation in the data can be described using several different patterns). Höppner (Höppner 2001) was the first to propose a non-ambiguous representation of time-interval patterns. The idea is to represent the pattern in the normalized form and to explicitly specify the temporal relations between all pairs of states. Höppner's representation has been later used by several research papers (Papapetrou et al. 2005, Winarko & Roddick 2007, Moskovitch & Shahar 2009), and we adopt it as well in our work. Moerchen (Moerchen 2006*a*) proposed the time series knowledge representation (TSKR) as an alternative to using Allen's relations. TSKR is based on the concept of cords, which describe coincidence of several states. Another representation appeared in (Wu & Chen 2007), where a time-interval pattern is represented as a sequence of the boundaries of its states. Although this representation is con-

[1] Sequential pattern mining is a special case of time-interval pattern mining, in which all intervals are simply time points with zero durations.

ceptually different from Höppner's representation, it can be shown that there is a one-to-one correspondence between them.

The related work on mining time-interval patterns (Kam & Fu 2000, Höppner 2001, Papapetrou et al. 2005, Moerchen 2006*a*, Sacchi et al. 2007, Winarko & Roddick 2007, Wu & Chen 2007, Moskovitch & Shahar 2009) have been mostly applied in an unsupervised setting for mining all frequent patterns. On the other hand, our work studies the supervised event detection task for mining the most predictive patterns, which we achieve by incorporating the concept of recency in the mining process.

3 Preliminaries and Definitions

In this section, we describe temporal abstraction and define temporal patterns for time-interval data. For temporal abstraction, we use trend and value abstractions. For the pattern language, we use Höppner's representation of time-interval patterns (Höppner 2001, 2003) with a simplified set of Allen's temporal relations.

3.1 Temporal Abstraction

Temporal abstraction takes a numeric time series (e.g., series of creatinine values) and produces a sequence of abstractions $\langle v_1[s_1, e_1], ..., v_n[s_n, e_n]\rangle$, where $v_i \in \Sigma$ is an abstraction that holds from time s_i to time e_i and Σ is the abstraction alphabet (a finite set of permitted abstractions).

In our work, we use two types of temporal abstractions:

1. *Trend abstractions* segment the time series based on its local trends. We use the following abstractions: *Decreasing* (D), *Steady* (S) and *Increasing* (I), i.e., $\Sigma = \{D,\ S,\ I\}$. We obtain these abstractions by applying the sliding window segmentation method (Keogh et al. 1993) and labeling the states according to the slopes of the fitted segments. For more information about trend segmentation, see (Keogh et al. 1993).
2. *Value abstractions* segment the time series based on its values. We use the following abstractions: *Very Low* (VL), *low* (L), *Normal* (N), *High* (H) and *Very High* (VH), i.e., $\Sigma = \{VL,\ L,\ N,\ H,\ VH\}$. We obtain these abstractions using the 10th, 25th, 75th and 90th percentiles on the lab values. That is, a value below the 10th percentile is *very low* (VL), a value between the 10th and 25th percentiles is *low* (L), and so on.

Figure 2 shows the trend and value abstractions on a time series of creatinine values.

3.2 Multivariate State Sequences

Let a **state** be an *abstraction value for a specific variable.* We denote a state S by a pair (F, V), where F is a temporal variable (e.g., creatinine) and $V \in \Sigma$ is an abstraction value. Let a **state interval** be a *state that holds during an interval.* We denote a state interval E by a 4-tuple (F, V, s, e), where F is a temporal variable,

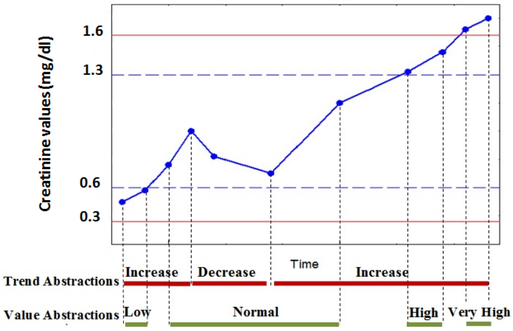


Fig. 2 An example illustrating trend abstractions and value abstractions. The blue dashed lines represent the 25th and 75th percentiles of the values and the red solid lines represent the 10th and 90th percentiles of the values.

$V \in \Sigma$ is an abstraction value, and s and e are the start time and end time (respectively) of the state interval $(E.s \leq E.e)^2$. For example, assuming the time granularity is days, state interval $(glucose, H, 5, 10)$ represents high glucose values from day 5 to day 10.

After abstracting all time series variables, each multivariate time series instance in the data becomes a multivariate state sequence.

Definition 1 A **Multivariate State Sequence (MSS)** is represented as a series of state intervals that are ordered according to their start times[3]:

$$Z = \langle\, E_1, E_2, ..., E_l \,\rangle : \;\; E_i.s \leq E_{i+1}.s \;\; \forall i \in \{1, ..., l-1\}$$

Note that we do not require $E_i.e$ to be less than $E_{i+1}.s$ because the state intervals are obtained from different temporal variables and their intervals may overlap. Let $\boldsymbol{Z.end}$ denote the end time of the MSS.

Example 1 Figure 3 shows an MSS (Z) with three temporal variables: creatinine (C), glucose (G) and BUN (Blood Urea Nitrogen) (B), where the variables are abstracted using value abstractions: $\Sigma = \{\,VL,\ L,\ N,\ H,\ VH\}$. Assuming the time granularity is days, this MSS represents 24 days of the patient's record $(Z.end = 24)$. For instance, we can see that creatinine values are normal from day 2 until day 14, then become high from day 15 until day 24. We represent this MSS as follows: $\langle\, E_1 = (G, H, 1, 5),\ E_2 = (C, N, 2, 14),\ E_3 = (B, N, 4, 20),\ E_4 = (G, N, 6, 9),\ E_5 = (G, H, 10, 13),\ E_6 = (C, H, 15, 24),\ E_7 = (G, VH, 16, 23)\,\rangle$.

[2] If $E.s = E.e$, state interval E corresponds to a time point.

[3] If two state intervals have the same start time, we sort them by their end time. If they also have the same end time, we sort them by lexical order of their variable names (as proposed by (Höppner 2003)).

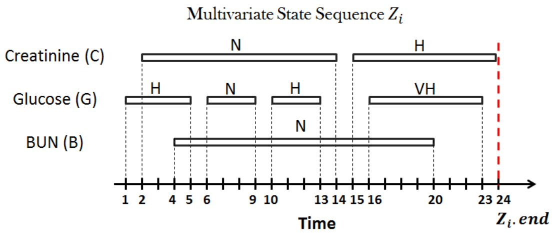


Fig. 3 An MSS representing 24 days of a patient record. In this example, there are three temporal variables (creatinine, glucose and BUN) that are abstracted using value abstractions.

3.3 Temporal Relations

Most of Allen's relations require equality of one or two of the intervals boundaries. That is, there is only a slight difference between *overlaps*, *is-finished-by*, *contains*, *starts* and *equals* relations (see Figure 1). Using all Allen's relations can be problematic when the time information in the data is *noisy* (not very precise), which is the case for EHR data. The reason is that this leads to the problem of *pattern fragmentation* (Moerchen 2006*b*), which means that we obtain many different temporal patterns that describe a very similar concept in the data. Furthermore, if we use all Allen's relations, the search space of temporal patterns becomes extremely large.

To alleviate the above mentioned problems, we opt to use only two temporal relations, namely ***before*** (**b**) and ***co-occurs*** (**c**), which we define as follows: Given two state intervals E_i and E_j:

- E_i is ***before*** E_j, denoted as $\mathbf{b(E_i, E_j)}$, if $E_i.e < E_j.s$ (E_i finishes before E_j starts), which is the same as Allen's *before*.
- E_i ***co-occurs*** with E_j, denoted as $\mathbf{c(E_i, E_j)}$, if $E_i.s \leq E_j.s \leq E_i.e$ (E_i starts before E_j and there is a nonempty time period where both E_i and E_j occur). Note that this relation covers the following Allen's relations: *meets*, *overlaps*, *is-finished-by*, *contains*, *starts* and *equals* (see Figure 1).

3.4 Temporal Patterns

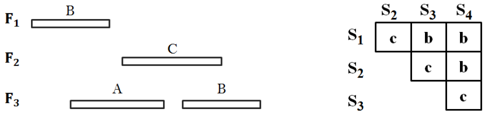
In order to define temporal patterns for abstracted time-interval data (time-interval patterns), we combine basic states (abstractions for specific variables) using temporal relations. We adopt Höppner's representation of time-interval patterns (Höppner 2001), where the permitted temporal relations are either *before* (**b**) or *co-occurs* (**c**) (defined above). From hereafter, we use the terms "temporal pattern" and "time-interval pattern" interchangeably.

Definition 2 A **temporal pattern** is defined as $P = (\langle S_1, ..., S_k \rangle, R)$ where S_i is the i^{th} state of the pattern and R is an upper triangular matrix that defines the temporal relations between each state and all of its following states:

$i \in \{1, ..., k-1\} \wedge j \in \{i+1, ..., k\} : R_{i,j} \in \{\mathbf{b}, \mathbf{c}\}$ specifies the relation between S_i and S_j.

The size of a temporal pattern P is the number of states it contains. If P contains k states, we say that P is a *k-pattern*. Hence, a single state is a *1-pattern* (a singleton). When a pattern contains only 2 states: $(\langle S_1, S_2 \rangle, R_{1,2})$, we sometimes write it simply as $S_1\ R_{1,2}\ S_2$ because it is easier to read.

Figure 4 shows a graphical representation of a *4-pattern* with states: $S_1 = (F_1, B)$, $S_2 = (F_3, A)$, $S_3 = (F_2, C)$, and $S_4 = (F_3, B)$. These states are abstractions of temporal variables F_1, F_2 and F_3 using abstraction alphabet $\Sigma = \{A, B, C\}$ (the abstractions in Σ can be trend abstractions, value abstractions or any other type). The half matrix on the right represents the temporal relations between every state and the states that follow it. For example, $R_{2,3} = \mathbf{c}$ means that the second state $S_2 = (F_3, A)$ *co-occurs* with the third state $S_3 = (F_2, C)$.



	S2	S3	S4
S1	c	b	b
S2		c	b
S3			c

Fig. 4 A temporal pattern with states $\langle\ (F_1, B),\ (F_3, A),\ (F_2, C),\ (F_3, B)\ \rangle$ and temporal relations $R_{1,2} = \mathbf{c}$, $R_{1,3} = \mathbf{b}$, $R_{1,4} = \mathbf{b}$, $R_{2,3} = \mathbf{c}$, $R_{2,4} = \mathbf{b}$ and $R_{3,4} = \mathbf{c}$.

Definition 3 Given an MSS $Z = \langle\ E_1, E_2, ..., E_l\ \rangle$ and a temporal pattern $P = (\langle S_1, ..., S_k \rangle, R)$, we say that Z **contains** P, denoted as $\boldsymbol{P \in Z}$, if there is an injective mapping π that matches every state S_i in P to a state interval $E_{\pi(i)}$ in Z such that:

$$\forall i \in \{1, ..., k\} :\ \ S_i.F = E_{\pi(i)}.F\ \wedge\ S_i.V = E_{\pi(i)}.V$$
$$\forall i \in \{1, ..., k-1\} \wedge j \in \{i+1, ..., k\} :\ \ R_{i,j}\left(E_{\pi(i)}\ ,\ E_{\pi(j)}\right)$$

The definition says that checking whether an MSS contains a *k-pattern* requires: 1) matching all k states of the pattern and 2) checking that all $k(k-1)/2$ temporal relations are satisfied.

Example 2 Let Z be the MSS (abstracted EHR) in Figure 3 and let P be temporal pattern $\langle\ (G, H), (C, N), (G, VH)\ \rangle$, $R_{1,2} = \mathbf{c}$, $R_{1,3} = \mathbf{b}, R_{2,3} = \mathbf{b}$) (i.e., Glucose=High co-occurs with Creatinine=Normal and both of them are before Glucose=Very High). P is contained in Z ($P \in Z$) because every state of P can be matched with a state interval in Z and these state intervals satisfy all the relations specified by P.

4 Mining Recent Temporal Patterns

In this section, we first introduce the concept of *recent temporal patterns* (RTPs) and illustrate their properties. After that, we describe an efficient algorithm for mining frequent RTPs.

4.1 Recent Temporal Patterns

In this work, we study the problem of mining predictive temporal patterns for event detection. In this setting, each training instance x_i is a multivariate temporal instance up to time t_i (e.g., the first 5 days of the health record for a specific patient) and it is associated with a label that indicates whether or not the event of interest (e.g., a specific disorder) occurred at time t_i. The objective to learn temporal patterns that capture the behavior that led to the development of the event and apply these patterns to detect the occurrence of events in future instances (e.g., monitor new patients).

For event detection problems, recent observations of the temporal variables of x_i (observations close to t_i) are typically the most important for predicting the label. For example, in the clinical domain, recent lab measurements are usually more indicative of the patient's current health status (hence more predictive) than old lab measurements. For instance, to diagnose a disease, the physician usually first looks at the most recent data and then looks back in time to understand how the data evolved over time. Our objective is to develop a temporal pattern mining method that takes into account this local nature of decisions for monitoring and event detection problems. We start by defining the concept of recent temporal patterns and then present an efficient algorithm to automatically mine these patterns from data[4].

Definition 4 Given an MSS $Z = \langle\ E_1, E_2, ..., E_l\ \rangle$ and a maximum gap parameter g, we say that $E_j \in Z$ is a **recent state interval** in Z, denoted as $\boldsymbol{r_g(E_j, Z)}$, if **any** of the following two conditions is satisfied:

1. $Z.end - E_j.e \leq g$.
2. $\nexists\ E_k \in Z : E_k.F = E_j.F \wedge k > j$.

The first condition is satisfied if E_j is less than g time units away from the end of the MSS ($Z.end$) and the second condition is satisfied if E_j is the most recent state interval for its variable (there is no state interval for the variable of E_j that appears after E_j). Note that if the maximum gap $g = \infty$, any state interval of Z ($E_j \in Z$) would be a recent state interval.

Definition 5 Given an MSS $Z = \langle E_1, E_2, ..., E_l \rangle$ and a maximum gap parameter g, we say that temporal pattern $P = (\langle S_1, ..., S_k \rangle, R)$ is a **Recent Temporal Pattern (RTP)** for Z, denoted as $\boldsymbol{R_g(P, Z)}$, if **all** of the following conditions are satisfied:

1. $P \in Z$ (Definition 3) with a mapping π from the states of P to the state intervals of Z.
2. S_k matches a recent state interval in Z: $r_g(E_{\pi(k)}, Z)$.
3. $\forall i \in \{1, ..., k-1\}$, S_i and S_{i+1} match state intervals that are no more than g time units away from each other: $E_{\pi(i+1)}.s - E_{\pi(i)}.e \leq g$.

[4] This section contains materials that have been published in (Batal, Fradkin, Harrison, Moerchen & Hauskrecht 2012).

The definition says that in order for temporal pattern P to be an RTP for MSS Z, 1) P should be contained in Z (Definition 3), 2) the last state of P should map to a recent state interval in Z (Definition 4), and 3) any pair of consecutive states in P should map to state intervals that are "close to each other" (within the maximum gap g). This definition forces P to be *close to the end of* Z and to have *limited temporal extension* in the past. Note that g is a parameter that specifies the restrictiveness of the RTP definition. If $g = \infty$, any pattern $P \in Z$ would be considered to be an RTP for Z. Let us denote an RTP that contains k states as a ***k*-RTP**.

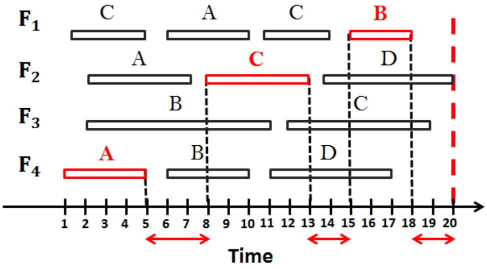


Fig. 5 An MSS with four temporal variables (F_1, F_2, F_3 and F_4) that are abstracted using abstraction alphabet $\Sigma = \{A, B, C, D\}$. Temporal pattern ($\langle$ (F_4, A), (F_2, C), (F_1, B) $\rangle$, $R_{1,2} =$ **b**, $R_{1,3} =$ **b**, $R_{2,3} =$ **b**) is an RTP for this MSS when the maximum gap parameter $g \geq 3$.

Example 3 Let Z be the MSS in Figure 5, which has 4 temporal variables (F_1 to F_4) that are abstracted using alphabet $\Sigma = \{A, B, C, D\}$. Let the maximum gap parameter be $g = 3$. Temporal pattern $P =$ ($\langle$ (F_4, A), (F_2, C), (F_1, B) $\rangle$, $R_{1,2} =$ **b**, $R_{1,3} =$ **b**, $R_{2,3} =$ **b**) is an RTP for Z because $P \in Z$ (shown in red in Figure 5), $(F_1, B, 15, 18)$ is a recent state interval in Z, $(F_2, C, 8, 13)$ is "close to" $(F_1, B, 15, 18)$ $(15 - 13 \leq g)$ and $(F_4, A, 1, 5)$ is "close to" $(F_2, C, 8, 13)$ $(8 - 5 \leq g)$.

Example 4 Let Z be the MSS (abstracted EHR) in Figure 3 and let $g = 3$ days. Temporal pattern $P_1 = (B, N)$ c (C, H) (i.e., BUN=Normal co-occurs with Creatinine=High) is an RTP in Z. On the other hand, $P_2 = (G, H)$ b (G, N) (i.e., Glucose=High before Glucose=Normal) is contained in Z: $P_2 \in Z$, but it is not an RTP because the second condition of Definition 5 is violated: $(G, N, 6, 9)$ is not a recent state interval.

Definition 6 Given temporal patterns $P = (\langle S_1, ..., S_{k_1}\rangle, R)$ and $P' = (\langle S'_1, ..., S'_{k_2}\rangle, R')$ with $k_1 < k_2$, we say that P is a **suffix subpattern** of P', denoted as **Suffix(P, P')**, if:

$$\forall i \in \{1, ..., k_1\} \ \wedge \ j \in \{i{+}1, ..., k_1\} : \ S_i = S'_{i+k2-k1} \ \wedge \ R_{i,j} = R'_{i+k2-k1,j+k2-k1}$$

This definition simply says that for a k_1*-pattern* P to be a suffix subpattern of a k_2*-pattern* P' ($k_1 < k_2$), P should match the last k_1 states of P' and should satisfy among them the same temporal relations that are satisfied in P'. For example, pattern ($\langle\ (F_3, A),\ (F_2, C),\ (F_3, B)\ \rangle,\ R_{1,2} = \mathbf{c},\ R_{1,3} = \mathbf{b},\ R_{2,3} = \mathbf{c}$) is a suffix subpattern of the pattern in Figure 4.

If P is a suffix subpattern of P', we say that P' is a **backward-extension superpattern** of P, which we abbreviate as ***b-extension***.

Proposition 1 *Given an MSS* Z *and temporal patterns* P *and* P'*, if* P' *is an RTP for* Z *and* P *is a suffix subpattern of* P'*, then* P *is an RTP for* Z*:*

$$R_g(P', Z)\ \wedge\ \mathit{Suffix}(P, P')\ \Longrightarrow\ R_g(P, Z)$$

The proof follows directly from the Definition of RTP.

Example 5 In Example 3, we showed that pattern ($\langle\ (F_4, A),\ (F_2, C),\ (F_1, B)\ \rangle,\ R_{1,2} = \mathbf{b},\ R_{1,3} = \mathbf{b},\ R_{2,3} = \mathbf{b}$) is an RTP for MSS Z in Figure 5 when the maximum gap is 3. Proposition 1 says that its suffix subpattern ($\langle\ (F_2, C),\ (F_1, B)\ \rangle,\ R_{1,2} = \mathbf{b}$) must also be an RTP for Z. However, this does not imply that subpattern ($\langle\ (F_4, A),\ (F_2, C)\ \rangle, R_{1,2} = \mathbf{b}$) must be an RTP (the second condition of Definition 5 is violated) nor that subpattern ($\langle\ (F_4, A),\ (F_1, B)\ \rangle, R_{1,2} = \mathbf{b}$) must be an RTP (the third condition of Definition 5 is violated).

One of the most used statistics in pattern mining is the support of the pattern (Agrawal & Srikant 1994) that counts the occurrences of the pattern in data. We define the support for RTPs as follows:

Definition 7 Given a dataset D of MSS and a maximum gap parameter g, the support of RTP P in D is defined as $\textbf{RTP-sup}_{\boldsymbol{g}}\boldsymbol{(P, D)}$= $|\ \{Z_i : Z_i \in D\ \wedge\ R_g(P, Z_i)\}\ |$.

Given a user defined minimum support threshold σ, temporal pattern P is a **frequent RTP** in D given σ if $\mathit{RTP}\text{-}\mathit{sup}_g(P, D) \geq \sigma$.

A key property that all frequent pattern mining algorithms rely on is the Apriori property (Agrawal & Srikant 1994), which states that the support of a pattern is no more than the support of any of its subpatterns. This property holds for RTPs on suffix subpatterns. In particular, Proposition 1 implies that the *RTP-sup* of an RTP cannot be larger than the *RTP-sup* of its suffix subpatterns:

Corollary 1 *If* P *and* P' *are two temporal patterns such that* $\mathit{Suffix}(P, P')$*, then* $\mathit{RTP}\text{-}\mathit{sup}_g(P, D) \geq \mathit{RTP}\text{-}\mathit{sup}_g(P', D)$.

This corollary will be used by our algorithm for mining frequent RTPs.

4.2 The Mining Algorithm

In this section, we present the algorithm for mining frequent RTPs. In order to improve the efficiency and effectiveness of the mining algorithm, we utilize the label information and mine frequent RTPs for each class label separately using a *local minimum support* that is related to the size of the population of that label. For example, suppose we have 10K instances, 1K of them has the event of interest (positives) and 9K do not have the event (negatives). If we set the local minimum support to be 10% the number of instances, we mine frequent RTPs from the positives and the negatives separately using $\sigma_{pos} = 100$ for the positives and $\sigma_{neg} = 900$ for the negatives. This approach is more appropriate when mining pattern in a supervised setting compared to mining frequent patterns from the entire data using a single global minimum support for the following reasons:

1. Mining patterns that are frequent for one of the classes (hence potentially predictive for that class) is more efficient than mining patterns that are globally frequent[5].
2. For unbalanced data, mining frequent patterns using a global minimum support may result in missing many important patterns for the rare class.

The algorithm for mining frequent RTPs for class y takes as input D_y: the MSS from y, g: the maximum gap parameter and σ_y: the local minimum support threshold for y. It outputs all temporal patterns that have an *RTP-sup* (Definition 7) in D_y that is larger or equal to σ_y:

$$\{P_1, ..., P_m : \textit{RTP-sup}_g(P_i, D_y) \geq \sigma_y\}$$

The algorithm explores the space of temporal patterns level by level. It first finds all frequent *1-RTPs* (RTPs that consist of a single state). Then it extends these patterns ***backward in time*** to find more complex patterns (frequent *2-RTPs*, then frequent *3-RTPs* and so on). For each level k, the algorithm performs the following two steps to obtain the frequent *(k+1)-RTPs*:

1. **Candidate generation:** Generate candidate *(k+1)-patterns* by extending frequent *k-RTPs* backward in time.
2. **Counting:** Obtain the frequent *(k+1)-RTPs* by removing the candidates with *RTP-sup* less than σ_y.

This process repeats until no more frequent RTPs can be found.

In the following, we describe in detail the candidate generation algorithm. Then we propose techniques to improve the efficiency of both candidate generation and counting.

4.2.1 Backward Candidate Generation

We generate a candidate *(k+1)-pattern* by appending a new state (an abstraction value for a specific variable) to the beginning of a frequent *k-RTP*. Let us assume that we are backward extending pattern $P = (\langle S_1, ..., S_k\rangle, R)$ with state S_{new} to generate candidates *(k+1)-patterns* of the form $(\langle S'_1, ..., S'_{k+1}\rangle\ , R')$. First of all, we set $S'_1 = S_{new}$, $S'_{i+1} = S_i$ for $i \in \{1, ..., k\}$ and $R'_{i+1,j+1} = R_{i,j}$ for $i \in \{1, ..., k-1\} \wedge j \in \{i+1, ..., k\}$. This way, we know that every candidate P' of this form is a *b-extension* of P.

[5] It is more efficient to mine patterns that cover more than n instances in one of the classes compared to mining patterns that cover more than n instances in the entire database (the former is always a subset of the latter).

In order to fully define a candidate, we still need to specify the temporal relations between the new state S'_1 and states $S'_2, ..., S'_{k+1}$, i.e., we should define $R'_{1,i}$ for $i \in \{2, ..., k+1\}$. Since we have two possible temporal relations (*before* and *co-occurs*), there are 2^k possible ways to specify the missing relations, which results in 2^k different candidates. If we denote the set of all possible states by L and the set of all frequent *k-RTPs* by $\mathbf{F_k}$, generating the *(k+1)-candidates* naïvely in this fashion results in $2^k \times |L| \times |\mathbf{F_k}|$ candidate *(k+1)-patterns.*

This large number of candidates makes the mining algorithm computationally very expensive and greatly limits its scalability. Below, we describe the concept of incoherent patterns and introduce a method that generates fewer candidates without missing any real pattern from the results.

4.2.2 Improving the Efficiency of Candidate Generation

Definition 8 A temporal pattern P is **incoherent** if there does not exist any valid MSS that contains P.

Clearly, we do not have to generate and count incoherent candidates because we know that they will have zero support in the data (they are invalid patterns). We introduce the following two lemmas to avoid generating incoherent candidates when specifying the relations $R'_{1,i} : i \in \{2, ..., k{+}1\}$ in candidates of the form $P' = (\langle S'_1, ..., S'_{k+1}\rangle, R')$. The first lemma restricts the patterns that include the same variable with two co-occurring states. The second lemma restricts the patterns that would violate the ordering of relations in time.

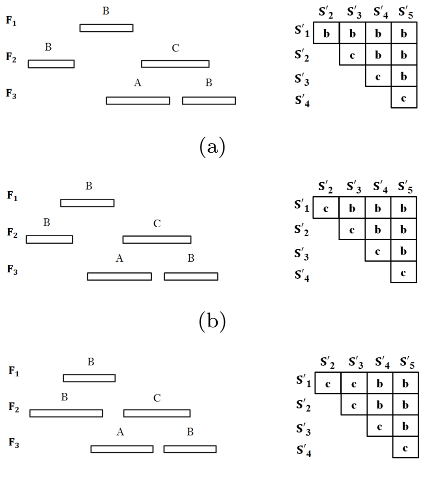
Lemma 1 *$P' = (\langle S'_1, ..., S'_{k+1}\rangle, R')$ is incoherent if $\exists i \in \{2, ..., k{+}1\} : R'_{1,i} = \mathbf{c}$ and $S'_1.F = S'_i.F$.*

Proof Two state intervals that belong to the same temporal variable cannot co-occur.

Lemma 2 *$P' = (\langle S'_1, ..., S'_{k+1}\rangle, R')$ is incoherent if $\exists i \in \{2, ..., k{+}1\} : R'_{1,i} = \mathbf{b} \wedge \exists j > i : R'_{1,j} = \mathbf{c}$.*

Proof Assume that there exists an MSS $Z = \langle E_1, ..., E_l\rangle$ where $P' \in Z$. Let π be the mapping from the states of P' to the state intervals of Z. The definition of temporal patterns (Definition 2) and the fact that state intervals in Z are ordered by their start values (Definition 1) implies that the matching state intervals $\langle E_{\pi(1)}, ..., E_{\pi(k+1)}\rangle$ are also ordered by their start times: $E_{\pi(1)}.s \leq ... \leq E_{\pi(k+1)}.s$. Hence, $E_{\pi(j)}.s \geq E_{\pi(i)}.s$ since $j > i$. We also know that $E_{\pi(1)}.e < E_{\pi(i)}.s$ because $R'_{1,i} = \mathbf{b}$. Therefore, $E_{\pi(1)}.e < E_{\pi(j)}.s$. However, since $R'_{1,j} = \mathbf{c}$, then $E_{\pi(1)}.e \geq E_{\pi(j)}.s$, which is a contradiction. Therefore, there is no MSS that contains P'. □

Example 6 Assume we want to extend $P = (\ \langle S_1 = (F_1, B),\ S_2 = (F_3, A),\ S_3 = (F_2, C),\ S_4 = (F_3, B)\rangle,\ R_{1,2} = \mathbf{c},\ R_{1,3} = \mathbf{b},\ R_{1,4} = \mathbf{b},\ R_{2,3} = \mathbf{c},\ R_{2,4} = \mathbf{b},\ R_{3,4} = \mathbf{c}\ )$ in Figure 4 with state $S_{new} = (F_2, B)$ to generate candidates of the form $(\langle S'_1 = (F_2, B),\ S'_2 = (F_1, B),\ S'_3 = (F_3, A),\ S'_4 = (F_2, C),\ S'_5 = (F_3, B)\rangle,\ R')$. First, we set the relations in R' for the last four states (S'_2, S'_3, S'_4 and S'_5) to be the same as defined by R. Now, we have to specify relations $R'_{1,i}$ for $i \in \{2, ..., k{+}1\}$. $R'_{1,2}$ is allowed to be either before ($R'_{1,2} = \mathbf{b}$) or co-occurs ($R'_{1,2} = \mathbf{c}$). If $R'_{1,2} = \mathbf{b}$, then all the following relations must be before according to Lemma 2, resulting in the candidate shown in Figure 6:a. If $R'_{1,2}=\mathbf{c}$, then $R'_{1,3}$ is allowed to be either before ($R'_{1,3}=\mathbf{b}$) or co-occurs ($R'_{1,3}=\mathbf{c}$), resulting in the candidates shown in Figure 6:b and Figure 6:c, respectively. Now, according to Lemma 1, $R'_{1,4}\neq\mathbf{c}$ because both S'_1 and S'_4 belong to the same temporal variable (variable F_2). As we see, we have reduced the number of candidates that result from adding state (F_2,B) to a *4-RTP P* from $2^4=16$ in the naïve way to only 3.



	S'₂	S'₃	S'₄	S'₅
S'₁	b	b	b	b
S'₂		c	b	b
S'₃			c	b
S'₄				c

(a)

	S'₂	S'₃	S'₄	S'₅
S'₁	c	b	b	b
S'₂		c	b	b
S'₃			c	b
S'₄				c

(b)

	S'₂	S'₃	S'₄	S'₅
S'₁	c	c	b	b
S'₂		c	b	b
S'₃			c	b
S'₄				c

(c)

Fig. 6 Coherent candidates that result from extending the temporal pattern in Figure 4 backward with state (F_2,B).

The following theorem gives the bound on the number of possible extensions of an RTP with a new state (an abstraction value for a specific variable).

Theorem 1 *There are at most $k+1$ coherent candidates that result from extending a single k-RTP backward with a new state.*

Proof We know that every candidate $P'=(\langle S'_1,...,S'_{k+1}\rangle,R')$ corresponds to a specific assignment of $R'_{1,i}\in\{\mathbf{b},\mathbf{c}\}$ for $i\in\{2,...,k+1\}$. When we assign the temporal relations, once a relation becomes *before*, all the following relations have to be *before* as well according to Lemma 2. We can see that the relations can be *co-occurs* in the beginning of the pattern, but once we have a *before* relation at some point $q\in\{2,...,k+1\}$ in the pattern, all subsequent relations ($i>q$) should be *before* as well:

$$R'_{1,i}=\mathbf{c}:i\in\{2,...,q-1\};\quad R'_{1,i}=\mathbf{b}:i\in\{q,...,k+1\}$$

Therefore, the total number of coherent candidates cannot be more than $k+1$, which is the total number of different combinations of consecutive *co-occurs* relations followed by consecutive *before* relations. □

In some cases, the number of coherent candidates is less than $k+1$. Assume that there are some states in P' that belong to the same variable as state S'_1. Let S'_j be the first such state ($j \leq k+1$). According to Lemma 1, $R'_{1,j} \neq \mathbf{c}$. In this case, the number of coherent candidates is $j-1 < k+1$.

Algorithm 1 illustrates how to extend a *k-RTP* P with a new state S_{new} to generate coherent candidates (without violating Lemmas 1 and 2).

Algorithm 1: Extend backward a *k-RTP* P with a state S_{new}.

```
Input: A k-RTP: $P = (\langle S_1, ..., S_k \rangle, R)$; a new state: $S_{new}$
Output: Coherent candidates: $C$
$S'_1 = S_{new}$; $S'_{i+1} = S_i : i \in \{1, ..., k\}$;
$R'_{i+1,j+1} = R_{i,j} : i \in \{1, ..., k-1\}, j \in \{i+1, ..., k\}$;
$R'_{1,i} = b : i \in \{2, ..., k+1\}$;    $P' = (\langle S'_1, ..., S'_{k+1} \rangle, R')$;
$C = \{P'\}$;
for $i$=2 to $k$+1 do
    if ($S'_1.F = S'_i.F$) then
        break;
    else
        $R'_{1,i} = c$;    $P' = (\langle S'_1, ..., S'_{k+1} \rangle, R')$;
        $C = C \cup \{P'\}$;
    end
end
return $C$
```

The bound on the number of possible extensions of a *k-RTP* with a new state can be used to calculate the bound on the total number of possible extensions of size k+1.

Corollary 2 *Let L denote the set of all possible states and let $\mathbf{F_k}$ denote the set of all frequent k-RTPs. The number of coherent (k+1)-candidates is no more than* $(k+1) \times |L| \times |\mathbf{F_k}|$.

4.2.3 Improving the Efficiency of Counting

Even after eliminating incoherent candidates, the mining algorithm is still computationally expensive because for every candidate, we need to scan the *entire database* in the counting phase to compute its *RTP-sup*. The question we try to answer in this section is whether we can omit portions of the database that are guaranteed not to contain the candidate we want to count. The proposed solution is inspired by (Zaki 2000) that introduced the *vertical data format* for itemset mining and later applied it for sequential pattern mining (Zaki 2001).

Let us associate every frequent RTP P with a list of identifiers of all MSS in D_y for which P is an RTP (Definition 5):

$$P.RTP\text{-}list = \langle i_1, i_2, ..., i_n \rangle : Z_{i_j} \in D_y \wedge R_g(P, Z_{i_j}) \text{ for } j = 1, ..., n.$$

Clearly, $RTP\text{-}sup_g(P, D_y) = |P.RTP\text{-}list|$.

Let us also associate every state S with a list of identifiers for all MSS that contain S (Definition 3):

$$S.list = \langle q_1, q_2, ..., q_m \rangle : Z_{q_j} \in D_y \wedge S \in Z_{q_j}$$

Now, when we generate candidate P' by backward extending RTP P with state S, we define the potential list (***p-RTP-list***) of P' as follows:

$$P'.p\text{-}RTP\text{-}list = P.RTP\text{-}list \ \cap \ S.list$$

Proposition 2 *If P' be a b-extension of RTP P with state S and $P'.p\text{-}RTP\text{-}list = P.RTP\text{-}list \ \cap \ S.list$, then $P'.RTP\text{-}list \subseteq P'.p\text{-}RTP\text{-}list$.*

Proof Assume Z_i is an MSS for which P' is an RTP: $R_g(P', Z_i)$. By definition, $i \in P'.RTP\text{-}list$. We know that $R_g(P', Z_i) \implies P' \in Z_i \implies S \in Z_i \implies i \in S.list$. Also, we know that $Suffix(P, P') \implies R_g(P, Z_i)$ (according to Proposition 1) $\implies i \in P.RTP\text{-}list$. Therefore, $i \in P.RTP\text{-}list \cap S.list = P'.p\text{-}RTP\text{-}list$. □

Putting it all together, we compute the *RTP-lists* in the *counting phase* (based on the true matches) and the *p-RTP-lists* in the *candidate generation phase*. The key idea is that when we count candidate P', we only need to check the instances in its *p-RTP-list* because according to Proposition 2: $i \notin P'.p\text{-}RTP\text{-}list \implies i \notin P'.RTP\text{-}list \implies P'$ is not an RTP for Z_i. This offers a lot of computational savings because the *p-RTP-lists* get smaller as the size of the patterns increases, making the counting phase much faster.

Algorithm 2 outlines the candidate generation. Line 4 generates coherent candidates according to Algorithm 1. Line 6 computes the *p-RTP-list* for each candidate. Note that the cost of the intersection is *linear* in the length of the lists because the lists are always sorted according to the order of the instances in the data. Line 7 applies *additional pruning* to remove candidates that are guaranteed not to be frequent according to the following implication of Proposition 2:

$$|P'.p\text{-}RTP\text{-}list| < \sigma_y \implies |P'.RTP\text{-}list| = RTP\text{-}sup_g(P', D_y) < \sigma_y \implies P' \text{is not frequent}$$

Algorithm 2: A high-level description of candidate generation.

```
   Input: All frequent k-RTPs: $\mathbf{F_k}$; all frequent states: $L$
   Output: Candidate (k+1)-patterns: $Cand$, with their p-RTP-lists
1  $Cand = \Phi$;
2  foreach $P \in \mathbf{F_k}$ do
3      foreach $S \in L$ do
4          $C = extend\_backward(P, S)$;     (Algorithm 1)
5          for $q = 1$ to $| C |$ do
6              $C[q].p\text{-}RTP\text{-}list = P.RTP\text{-}list \cap S.list$;
7              if ( $| C[q].p\text{-}RTP\text{-}list | \geq \sigma_y$ ) then
8                  $Cand = Cand \cup \{C[q]\}$;
9              end
10         end
11     end
12 end
13 return $Cand$
```

5 Mining Minimal Predictive Recent Temporal Patterns

Although RTP mining focuses the search on temporal patterns that are potentially useful for predicting the labels (e.g., whether or not the adverse medical event would happen), not all frequent RTPs are as important for prediction.

In this section, we describe our approach for selecting the most predictive RTPs. First, we describe the Bayesian score for evaluating the predictiveness of patterns (Section 5.1). After that, we argue that scoring each RTP individually and selecting the top scoring ones often leads to spurious patterns (Section 5.2). Then we describe the concept of Minimal Predictive Recent Temporal Patterns (MPRTP) which considers the relations between patterns to filter out spurious patterns (Section 5.3). Finally, we present an efficient mining algorithm that integrates MPRTP evaluation with frequent RTP mining and applies efficient pruning techniques to speed up the mining (Section 5.4).

5.1 The Bayesian Score

The Bayesian score we describe here allows us to evaluate how predictive is an RTP P for label y compared to a more general group of instances G (e.g., G might be the entire dataset). We denote this score by $\boldsymbol{BS(P \Rightarrow y, G)}$.

Let G_P denote the group of instances (MSS) in G for which P is an RTP:

$$G_P = \{Z_i : Z_i \in G \ \wedge \ R_g(P, Z_i)\}$$

Intuitively, the score of $P \Rightarrow y$ compared to G should be high if there is a strong evidence to support the hypothesis that the probability of observing label y in G_P is higher than the probability of observing y in G: $\Pr(y|G_P) > \Pr(y|G)$.

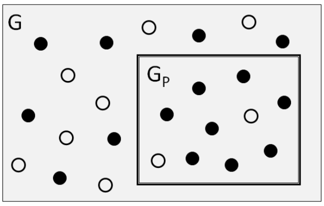


Fig. 7 Evaluating the predictiveness of $P \Rightarrow y$ compared to more general group G: $G_P \subset G$. The instances with label y are denoted by $\bullet$ and the instances without y are denoted by $\circ$.

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The main idea behind the Bayesian score is to apply Bayesian inference and treat the estimated probabilities as uncertain random variables, which is done by modeling the posterior distribution of the estimated probabilities and integrating over all possible values. We have originally proposed this score in (Batal, Cooper & Hauskrecht 2012) in the context of mining predictive itemset patterns (for atemporal data). The Bayesian score was shown to be more robust compared to classical rule evaluation scores (see (Geng & Hamilton 2006)), which only rely on point estimation and cannot model the uncertainty of the estimation.

To introduce the Bayesian score, we first define the following three competeing models (hypothesis):

1. M_e conjectures that the probability of y is the ***same*** for all instances in G.
2. M_h conjectures that the probability of y in G_P is ***higher*** than the probability of y outside G_P $(G \setminus G_P)$.
3. M_l conjectures that the probability of y in G_P is ***lower*** than the probability of y outside G_P.

We define $BS(P \Rightarrow y, G)$ to be the posterior probability of model M_h (the hypothesis of interest):

$$BS(P\Rightarrow y, G) = \frac{\Pr(G|M_h) \cdot \Pr(M_h)}{\Pr(G|M_e) \cdot \Pr(M_e) + \Pr(G|M_h) \cdot \Pr(M_h) + \Pr(G|M_l) \cdot \Pr(M_l)} \tag{1}$$

To be "non-informative", we might simply assume that all three models are equally likely a-priori: $\Pr(M_e) = \Pr(M_h) = \Pr(M_l) = \frac{1}{3}$.

In order to solve Equation 1, we need to compute the marginal likelihood of all models: $\Pr(G|M_e)$, $\Pr(G|M_h)$ and $\Pr(G|M_l)$. The likelihood of each model given the values of its parameters follows the binomial distribution, while the prior distribution on the parameters is a beta distribution (the beta distribution is a conjugate prior to the binomial distribution, which makes the Bayesian computation tractable). If we do not have prior knowledge about the parameters, we simply use uniform beta distributions.

In the Appendix, we derive the closed form solutions for all three marginal likelihoods. We also demonstrate that the complexity of computing the Bayesian score is $O(min(N_{11}, N_{12}, N_{21}, N_{22}))$, where N_{11} is the number of instances in G_P with label y, N_{12} is the number of instances in G_P without label y, N_{21} is the number of instances in $G \setminus G_P$ (the instances of G outside G_P) with label y and N_{21} is the number of instances in $G \setminus G_P$ without label y.

5.2 Spurious RTPs

A straightforward approach for selecting the most predictive RTPs is to score each RTP by itself and then select the top scoring ones. However, this approach is not effective because it leads to many spurious RTPs, as we explain in the following example.

Example 7 Assume that having elevated creatinine level is an important indicator of chronic kidney disease (CKD). If we denote this pattern by P =*(Creatinine, High)*, we expect the probability of CKD in G_P (the group of instances for which P is an RTP) to be significantly higher than the probability of CKD in the entire population of patients D: $\Pr(\text{CKD}|G_P) > \Pr(\text{CKD}|D)$.

Now consider a pattern P' that is a *b-extension* of P, for example, P': *(Cholesterol, Normal) before (Creatinine, High)*. We know that $G_{P'} \subseteq G_P$ according to Proposition 1. Assume that observing P' does not change our belief about the presence of CKD compared to observing P: $\Pr(\text{CKD}|G_{P'}) \approx \Pr(\text{CKD}|G_P)$. In other words, the instances in $G_{P'}$ can be seen as a random subsample of the instances in G_P with respect to the labels of CKD.

The problem is that if we score P' by comparing it to the entire data D (whether using our Bayesian score or using another rule evaluation score (Geng & Hamilton 2006)), we may conclude that P' is important for predicting CKD because $\Pr(\text{CKD}|G_{P'})$ is significantly higher than $\Pr(\text{CKD}|D)$. However, P' is redundant given the real predictive pattern P.

In general, spurious RTPs are formed by extending predictive RTPs with additional irrelevant states. Having spurious RTPs in the result is undesirable for knowledge discovery because they overwhelm the domain expert and prevent him/her from understanding the real patterns in data. It is also undesirable for prediction because they lead to many redundant and highly correlated features, which might hurt the prediction performance. In order to filter out spurious RTPs, we present the concept of *Minimal Predictive Recent Temporal Patterns.*

5.3 Minimal Predictive Recent Temporal Patterns

Definition 9 A temporal pattern P is a **Minimal Predictive Recent Temporal Pattern** (**MPRTP**) for label y if RTP P predicts y significantly better than all of its suffix subpatterns.

$$\forall S \text{ such that } \text{Suffix}(S, P): \; BS(P \Rightarrow y, G_S) \geq \delta$$

Where BS is the Bayesian score, G_S is the group of instances for which S is an RTP and δ is a user specified significance parameter. Note that, by definition, the empty pattern Φ is a suffix subpattern of any temporal pattern and G_Φ is the entire data D.

This definition means that if P is an MPRTP for y, then there is a strong evidence in the data not only to conclude that P improves the prediction of y compared to the entire data, but also compared to the data matching any of its suffix subpatterns. We call such patterns "minimal predictive" because they are more predictive than all of their simplifications, i.e., they do not contain redundant states. Note that a spurious RTP (such as the one described in Example 7) is not going to be an MPRTP because its effect on the class distribution can be explained by a simpler suffix subpattern that covers a larger population.

5.4 The Mining Algorithm

The algorithm presented in Section 4.2 describes how to mine all frequent RTPs for label y using D_y (the MSS in the data that belong to y). In order to mine MPRTPs for y, the algorithm requires another input: $D_{\neg y}$, the MSS in the data that do not have label y (in order to score the predictiveness of patterns).

The most common way for applying pattern mining in the supervised setting is to use the **two-phase** approach as in (Cheng et al. 2007, Webb 2007, Xin et al. 2006, Kavsek & Lavrač 2006, Exarchos et al. 2008, Deshpande et al. 2005, Li et al. 2001). This approach first generates *all* frequent patterns (the first phase) and then evaluates them in order to select the predictive patterns (the second phase). If we were to apply the two-phase approach to mine MPRTPs for y, we would perform the following two phases:

1. Phase I: Mine *all* of the frequent RTPs: $\Omega = \{P_1, ..., P_m : \textit{RTP-sup}_g(P_i, D_y) \geq \sigma_y\}$.
2. Phase II: For each $P_i \in \Omega$, output rule $P_i \Rightarrow y$ if P_i is an MPRTP for y (i.e., P_i satisfies Definition 9).

In contrast to the two-phase approach, our algorithm *integrates pattern evaluation with frequent RTP mining.* This allows us to apply effective pruning techniques that are not applicable in the two-phase approach. In our context, we say that an RTP is pruned if we do not explore any of its b-extensions. Note that in frequent RTP mining (Section 4.2), we prune an RTP if it is not frequent because we know that none of its b-extensions would be frequent. The techniques presented here utilize the *predictiveness* of patterns to further restrict the search space of the algorithm. In the following, we present two pruning techniques: The first one is *lossless* and the second is *lossy.*

5.4.1 lossless pruning

The MPRTP definition can help us to prune the search space. The idea is that we can *prune* a frequent RTP P, i.e., we do not further extend P backward in time, if we guarantee that none of its backward-extension superpatterns is going to be an MPRTP. We know that for any P' that is a *b-extension* of P, the following holds according to Corollary 1:

$$\textit{RTP-sup}_g(P', D_y) \leq \textit{RTP-sup}_g(P, D_y) \wedge \textit{RTP-sup}_g(P', D_{\neg y}) \leq \textit{RTP-sup}_g(P, D_{\neg y})$$

We now define the *optimal b-extension* of P with respect to y, denoted as P^*, to be a hypothetical pattern that is an RTP in *all* and *only* the instances of G_P that have class label y:

$$\textit{RTP-sup}_g(P^*, D_y) = \textit{RTP-sup}_g(P, D_y) \;\wedge\; \textit{RTP-sup}_g(P^*, D_{\neg y}) = 0$$

Clearly, P^* is the best possible *b-extension* of P for predicting y (as it covers all instances from y and none of the other instances). Now, we *safely* prune P if P^* does not satisfy the MPRTP definition because then we guarantee that no *b-extension* of P is going to be an MPRTP (hence the technique is lossless).

5.4.2 lossy pruning

This technique performs *lossy* pruning, which means that it speeds up the mining, but at the risk of missing some MPRTPs. The idea is that if we are mining MPRTPs for y, we prune a frequent RTP P if we have evidence that the underlying probability of y in G_P is lower than the probability of y in the data D. To do so, we apply the Bayesian score to evaluate rule $P \Rightarrow y$ compared to D and we prune P if model M_l (the model that assumes the probability of y in G_P is lower that outside G_P) is the most likely model. The rationale for this heuristic is that for any P' that is a *b-extension* of P, we know that $G_{P'} \subseteq G_P$ (Proposition 1). So if $\Pr(Y = y | G_P)$ is relatively low, we also expect $\Pr(Y = y | G_{P'})$ to be low as well. Thus, P' is unlikely to be an MPRTP for y. Note that this heuristic only extends promising RTPs and prunes unpromising ones.

6 Experimental Evaluation

This section presents our experimental evaluation. We first describe the two real-world EHR datasets we used in the experiments (Section 6.1). Then we compare RTP and MPRTP with other baselines for the task of detecting adverse medical events (Section 6.2). After that, we show the top patterns that MPRTP extracted from the data (Section 6.3). Finally, we compare the efficiency of our algorithms with other time-interval pattern mining algorithms (Section 6.4).

6.1 Temporal Datasets

6.1.1 Diabetes Dataset

This data consist of 13,558 electronic health records of adult diabetic patients (both type I and type II diabetes). The task is to learn models that can detect various types of disorders that are frequently associated with diabetes.

Each patient's record consists of time series of 19 different lab values, including blood glucose, creatinine, glycosylated hemoglobin, blood urea nitrogen, liver function tests, cholesterol, etc. In addition, we have access to time series of ICD-9 diagnosis codes reflecting the diagnoses made for the patient over time. Overall, the database contains 602 different ICD-9 codes. These codes were grouped by a medical expert into the following eight major disease categories:

- Cardiovascular disease (**CARDI**).
- Renal disease (**RENAL**).
- Peripheral vascular disease (**PERIP**).
- Neurological disease (**NEURO**).
- Metabolic disease (**METAB**).
- Inflammatory (infectious) disease (**INFLM**).
- Ocular (ophthalmologic) disease (**OCULR**).
- Cerebrovascular disease (**CEREB**).

Our objective is to learn models that are able to accurately diagnose each of these major diseases. For each disease, we divide the data into positive instances and negative instances as follows:

- The positives are records of patients with the target disease and they include clinical information up to the time the disease was *first* diagnosed.
- The negatives are records of patients without the target disease and they include clinical information up to a randomly selected time point in the patient's record.

To avoid having uninformative data, we discard instances that contain less than 10 total lab measurements or that span less than 3 months (short instances). To make the datasets balanced, we choose the same number of negatives as the number of positives for each category (by randomly sub-sampling the negatives).

For each instance, we consider both the laboratory tests and the disease categories. Note that the diagnosis of one or more disease categories may be predictive of the (first) occurrence of another disease, so it is important to include them as features. Laboratory tests are numeric time series, so we convert them into time-interval state sequences using value abstractions (see Section 3.1). Disease categories, when used as features, are represented as intervals that start at the time of the diagnosis and extend until the end of the record. For these variables, we simply use temporal abstractions that indicate whether or not the patient has been diagnosed with the disease.

Table 1 summarizes the characteristics of the diabetes datasets, where a different dataset is defined for each of the 8 major diseases. For all of these datasets, we use value abstractions (very low, low, normal, high and very high) for the laboratory variables and one abstraction for the disease categories. Hence, the abstraction alphabet size ($|\Sigma|$) is 6. Since we have 19 laboratory variables and 7 disease variables (the 8 major diseases minus the one we are predicting), we have 26 temporal variables per instance. The last column shows the total number of state intervals for each dataset.

Dataset	# Instances	# Variables	Alphabet Size	# Intervals
CARDI	$5,486$	26	6	$235,990$
RENAL	$6,710$	26	6	$327,957$
PERIP	$6,740$	26	6	$325,872$
NEURO	$4,386$	26	6	$240,572$
METAB	$1,936$	26	6	$118,378$
INFLM	$4,788$	26	6	$264,541$
OCULR	$4,490$	26	6	$227,708$
CEREB	$5,648$	26	6	$319,695$

Table 1 Characteristics of the Diabetes datasets.

6.1.2 HIT Dataset

This data are acquired from a database that contains electronic health records of post cardiac surgical patients (Hauskrecht et al. 2010, 2012). The task is to learn a model that can detect the onset of *Heparin Induced Thrombocytopenia* (*HIT*), which is a pro-thrombotic disorder induced by heparin exposure with subsequent thrombocytopenia (low platelet in the blood) and associated thrombosis (blood clot). HIT is a life-threatening condition if it is not detected and managed properly. Hence, it is very important to detect its onset.

Patients who are at risk of HIT were selected using information about the *Heparin Platelet Factor 4 antibody* (*HPF4*) test, which is ordered for a patient when the physician suspects that he/she is developing HIT. Therefore, an HPF4 test order is a good surrogate for the *HIT-risk* label. Our dataset contains 220 positive instances (*HIT-risk*) and we randomly select 220 negative instances (*no HIT-risk*). The positives include clinical information up to the time HFP4 was first ordered. The negatives were selected from the remaining patients and they include clinical information up to a randomly selected time point in the patient's record.

For each instance, we consider 5 clinical variables: platelet counts (PLT), activated partial thromboplastin time (APTT), white blood cell counts (WBC), hemoglobin (Hgb) and heparin orders. PLT, APTT, WBC and Hgb (laboratory variables) are numeric time series, so we convert them into time-interval state sequences using both trend abstractions and value abstractions (see Section 3.1). Heparin orders (already in an interval-based format) specify the time period during which the patient was taking heparin. For this variable, we simply use temporal abstractions that indicate whether or not the patient is currently on heparin.

6.2 Classification Performance

In this section, we test the ability of RTP and MPRTP in representing and capturing temporal patterns that are important for the event detection task.

6.2.1 Compared Methods

We compare several feature construction methods, which create different feature-vector representations of EHR data in order to apply a standard classifier. We did not compare with other time series classification methods such as (Blasiak & Rangwala 2011, Li et al. 2010, Batal & Hauskrecht 2009, Weng & Shen 2008, Vail et al. 2007, Ratanamahatana & Keogh 2005, Yang & Shahabi 2004) because these methods are not directly applicable to the multivariate irregularly sample EHR data[6].

In particular, we compare the performance of the following methods:

1. ***Last-abs:*** The features are the most recent abstractions of each clinical variable. For example, the most recent trend abstraction for platelet counts is "*decreasing*", the most recent value abstraction for platelet counts is "*low*", and so on.

2. ***TP:*** The features correspond to all frequent temporal patterns.

$$\{P_1, ..., P_m : \ sup(P_i, D_y) \geq \sigma_y\}$$

   where $sup(P, D_y) = |\ \{Z_i : Z_i \in D_y \ \wedge \ P \in Z_i\}\ |$ (see Definition 3)

3. ***TP-IG:*** The features correspond to the top **50** frequent temporal patterns, where the patterns are scored using Information Gain (IG) as in (Patel et al. 2008*b*).

4. ***RTP:*** The features correspond to all frequent RTPs.

$$\{P_1, ..., P_k : \ RTP\text{-}sup_g(P_i, D_y) \geq \sigma_y\}$$

   where $RTP\text{-}sup_g(P, D_y) = |\ \{Z_i : Z_i \in D_y \ \wedge \ R_g(P_j, Z_i)\}\ |$ (see Definition 5)

5. ***RTP-IG:*** The features correspond to the top **50** frequent RTPs, where the RTPs are scored using IG.

[6] The observations of the clinical variables are irregular in time because they are measured asynchronously at different time moments.

6. ***MPRTP:*** The features correspond to the top **50** frequent RTPs, where only the RTPs that satisfy the MPRTP definition (Definition 9 using a significance parameter $\delta = 0.95$) are retained and they are scored according to the Bayesian score (see Section 5.1).

The first method (*Last-abs*) is *atemporal* and only considers the most recent abstractions for defining the classification features. On the other hand, methods (2-6) use temporal patterns (built using temporal abstractions and temporal relations) to define features for classification, where a different binary feature is defined for each temporal pattern in the result.

When defining the binary representation of an instance (MSS) Z_i for TP-based methods (*TP* and *TP-IG*), the feature value is set to one if the corresponding temporal pattern is observed anywhere during the instance (Definition 3), and is set to zero otherwise:

$$Z_i \rightarrow x'_i \text{ where } x'_{i,j} = 1 \text{ if } P_j \in Z_i \text{ and } x'_{i,j} = 0 \text{ otherwise.}$$

When defining the binary representation of an instance Z_i for RTP-based methods (*RTP*, *RTP-IG* and *MPRTP*), the feature value is set to one if the corresponding temporal pattern is observed recently in the instance (Definition 5), and is set to zero otherwise:

$$Z_i \rightarrow x'_i \text{ where } x'_{i,j} = 1 \text{ if } R_g(P_j, Z_i) \text{ and } x'_{i,j} = 0 \text{ otherwise.}$$

It is important to note that although patterns generated by *TP* subsume the ones generated by *RTP* (by definition, every frequent RTP is also a frequent temporal pattern), the induced binary features are different. For example, a temporal pattern may be very discriminative only when observed recently (close to the end of the temporal instance).

We use methods *TP-IG*, *RTP-IG* and *MPRTP* in the evaluation because we want to compare the ability of *TP* and *RTP* in representing the classifier using only a limited number of temporal patterns. Moreover, we want to compare using standard univariate scoring (scoring each pattern individually by information gain) with our *MPRTP* approach, which considers the structure of patterns to filter out spurious RTPs.

We judged the quality of the different feature representations in terms of their induced classification performance. More specifically, we use the features extracted by each method to learn a *linear SVM* classifier and evaluate its performance using the area under the ROC curve (AUC).

All classification results are reported using averages obtained via *10-fold cross-validation*, where the same train/test splits are used for all compared methods. To evaluate the statistical significance of performance difference, we apply paired t-tests at 0.05 significance level[7].

[7] We apply statistical significance testing with k-fold cross validation. In this setting, the testing sets are independent of each other, but the training sets are not. Even though this does not perfectly fit the iid assumption, the significance results are still of great help in comparing different learning methods (Mitchell 1997).

6.2.2 Results on Diabetes Data

For all temporal pattern mining methods (*TP*, *TP-IG*, *RTP*, *RTP-IG* and *MPRTP*), we set the local minimum supports (σ_y) to 15% of the number of instances in the class[8]. For *RTP*, *RTP-IG* and *MPRTP*, we set the maximum gap parameter (see Definition 5) to 6 months, which was suggested by our medical expert.

Table 2 shows the AUC for each classification task (major disease). We show the best performing method in boldface and we show all methods that are statistically significantly inferior to it in grey. Note that features based on temporal patterns (*TP*, *RTP* and *MPRTP*) are beneficial for classification since they outperform features based on only most recent abstractions (*last-abs*). We can see that for most tasks, *RTP* is the best performing method. Note that although *MPRTP* does not perform as well as *RTP*, it mostly outperforms *RTP-IG* because of its ability to filter out spurious patterns (see for example the performance on the *NEURO* dataset in Table 2).

	Last-abs	*TP*	*TP-IG*	*RTP*	*RTP-IG*	*MPRTP*
CARDI	77.52 ∗	80.03	77.28 ∗	**80.04**	78.74 ∗	79.43
RENAL	83.28 ∗	84.97 ∗	73.38 ∗	**86.27**	83.65 ∗	84.41 ∗
PERIP	75.11 ∗	76.03 ∗	73.53 ∗	**77.95**	75.72 ∗	75.82 ∗
NEURO	72.20 ∗	74.46 ∗	72.03 ∗	**76.23**	71.89 ∗	74.33 ∗
METAB	80.81 ∗	**83.05**	80.17 ∗	81.65 ∗	80.76 ∗	82.59
INFLM	72.21 ∗	73.20 ∗	70.93 ∗	**74.49**	72.52 ∗	73.19 ∗
OCULR	73.71 ∗	**76.65**	74.92 ∗	75.52	74.74 ∗	75.23 ∗
CEREB	72.69 ∗	75.22	72.53 ∗	**76.3**	73.34 ∗	73.66 ∗

Table 2 Diabetes dataset: The area under ROC of the compared feature representation methods for the eight major diabetes diseases (Section 6.1.1). The best performing method is shown in bold and all methods that are statistically inferior to it are marked by ∗. SVM is used for classification.

6.2.3 Results on HIT Data

For all temporal pattern mining methods (*TP*, *TP-IG*, *RTP*, *RTP-IG* and *MPRTP*), we set the local minimum supports (σ_y) to 10% of the number of instances in the class. For *RTP*, *RTP-IG* and *MPRTP*, we set the maximum gap parameter (see Definition 5) to 2 days, which was suggested by our medical expert. Note that the HIT data are inpatient data and have much finer time granularity than the outpatient diabetes data.

Table 3 shows the AUC on the HIT dataset. We can see that *RTP* and *MPRTP* are the best performing methods.

6.3 Knowledge Discovery

In this section, we test the ability of *MPRTP* in finding predictive and non-spurious RTPs that can concisely describe the predicted medical event.

[8] As discussed in Section 4.2, we mine frequent patterns for the positives and negatives separately using the local minimum supports.

	Last-abs	*TP*	*TP-IG*	*RTP*	*RTP-IG*	*MPRTP*
AUC	87.18 $*$	90.87	87.79 $*$	**91.99**	88.58 $*$	91.57

Table 3 **HIT dataset**: The area under ROC (AUC) of the compared feature representation methods. The best performing method is shown in bold and all methods that are statistically inferior to it are marked by $*$. SVM is used for classification.

6.3.1 Results on Diabetes Data

Table 4 shows some of the top MPRTPs according to the Bayesian score on the diabetes data[9]. Patterns P_1, P_2 and P_3 are predicting renal (kidney) disease. These patterns relate the risk of renal problems with very high values of the BUN (Blood Urea Nitrogen) test (P_1), an increase in creatinine levels from normal to high (P_2), and high values of BUN co-occurring with high values of creatinine (P_3). P_4 shows that an increase in glucose levels from high to very high may indicate a metabolic disease. Finally, P_5 shows that patients who were previously diagnosed with cardiovascular disease and exhibit an increase in glucose levels are prone to develop a cerebrovascular disease. These patterns, extracted automatically from data without incorporating prior clinical knowledge, are in accordance with the medical diagnosis guidelines.

MPRTP	*Precision*	*Recall*
P_1: *BUN=VH* ⇒ *Dx=RENAL*	0.97	0.17
P_2: *Creat=N before Creat=H* ⇒ *Dx=RENAL*	0.96	0.21
P_3: *BUN=H co-occurs Creat=H* ⇒ *Dx=RENAL*	0.95	0.21
P_4: *Gluc=H before Gluc=VH* ⇒ *Dx=METAB*	0.79	0.24
P_5: *Dx=CARDI co-occurs (Gluc=N before Gluc=H)* ⇒ *Dx=CEREB*	0.71	0.22

Table 4 **Diabetes dataset**: The top MPRTPs with their precision and recall. Abbreviations: *Dx*: diagnosis code (one of the 8 major categories described in Section 6.1.1); *BUN*: Blood Urea Nitrogen; *Creat*: creatinine; *Gluc*: blood glucose. Value abstractions: *BUN=VH*: >49 mg/dl; *BUN=H*: >34 mg/dl; *Creat=H*: >1.8 mg/dl; *Creat=N*: [0.8-1.8] mg/dl; *Gluc=VH*: >243 mg/dl; *Gluc=H*: >191 mg/dl.

6.3.2 Results on HIT Data

Table 5 shows the top 5 MPRTPs according to the Bayesian score on the HIT data. Patterns P_1, P_2, P_3 and P_4 describe the main patterns used to detect HIT and are in agreement with the current HIT detection guidelines (Warkentin 2000). P_5 relates the risk of HIT with an increasing trend of APTT (activated partial thromboplastin time). This relation is not obvious from the HIT detection guidelines. However it has been recently discussed in the literature (Pendelton et al. 2006). Hence this pattern requires further investigation.

[9] Most of the highest scores MPRTPs are predicting the RENAL category because it is the easiest prediction task. So to diversify the patterns, we show the top 3 predictive MPRTPs for RENAL and the top 2 MPRTPs for other categories.

MPRTP	*Precision*	*Recall*
P_1: *PLT=L ⇒ HIT-risk*	78.3	84.79
P_2: *PLT=VL ⇒ HIT-risk*	89.31	65.44
P_3: *PLT=L before PLT=VL ⇒ HIT-risk*	91.13	52.07
P_4: *PLT=D co-occurs PLT=L ⇒ HIT-risk*	86.33	55.3
P_5: *APTT=I before PLT=L ⇒ HIT-risk*	88.24	41.47

Table 5 HIT dataset: The top 5 MPRTPs with their precision and recall. Abbreviations: *PLT*: platelet count; *APTT*: activated partial thromboplastin time. Trend abstractions: *PLT=D*: decreasing trend in *PLT*; *APTT=I*: increasing trend in *APTT*. Value abstractions: *PLT=VL* (Very Low): $<76\times10^9$ per liter; *PLT=L* (Low): $<118\times10^9$ per liter.

6.4 Mining Efficiency

In this section, we study the efficiency of different temporal pattern mining algorithms.

6.4.1 Compared Methods

We compare the running time of the following methods:

1. ***TP_Apriori:*** Mine frequent temporal patterns by extending the Apriori algorithm (Agrawal & Srikant 1994, 1995) to the time-interval domain.
2. ***TP_lists:*** Mine frequent temporal patterns by applying the vertical data format (Zaki 2000, 2001) to the time-interval domain as in (Batal et al. 2011, 2013).
3. ***RTP_no-lists:*** Mine frequent RTPs as described in Section 4.2, but without applying the id-list indexing in Section 4.2.3 to speed up the counting. That is, this method scans the entire dataset for each generated candidate in order to compute its *RTP-sup*.
4. ***RTP:*** Our method for mining frequent RTPs as described in Section 4.2 which also applies the id-list indexing.
5. ***MPRTP:*** Our method for mining MPRTPs which applies all optimizations used by the RTP method and also the pruning techniques described in Section 5.4.1 and Section 5.4.2.

To make the comparison fair, *all methods apply the techniques we propose in Section 4.2.2 to avoid generating incoherent candidates.* Note that if we do not remove incoherent candidates, the execution time for all methods greatly increases.

The experiments are conducted on a Dell Precision T1600 machine with an Intel Xeon 3GHz CPU and 16GB of RAM.

6.4.2 Results on Diabetes Data

Figure 8 shows the execution time (on logarithmic scale) of the compared methods on all major diagnosis datasets. Similar to the previous settings (Section 6.2.2), we set the local minimum supports to 15% and the maximum gap parameter to 6 months (unless stated otherwise).

We can see that *RTP* and *MPRTP* are much more efficient than the other temporal pattern mining methods. For example, on the *INFLM* dataset, *RTP* is around 5 times faster than *TP_lists*, 10 times faster than *RTP_no-lists* and 30 times faster than *TP_Apriori*. Furthermore, *MPRTP* is more efficient than *RTP* for all datasets.

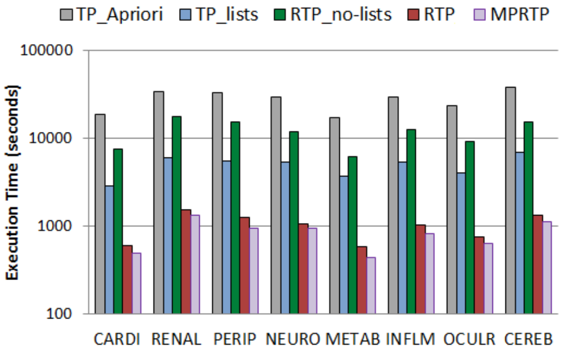

Fig. 8 Diabetes dataset: The mining time (in seconds) of the compared temporal pattern mining methods (Section 6.4.1) for the eight major diabetes diseases. The local minimum support is 15%.

Figure 9 compares the execution time of the different methods on the *CARDI* dataset for different minimum support thresholds.

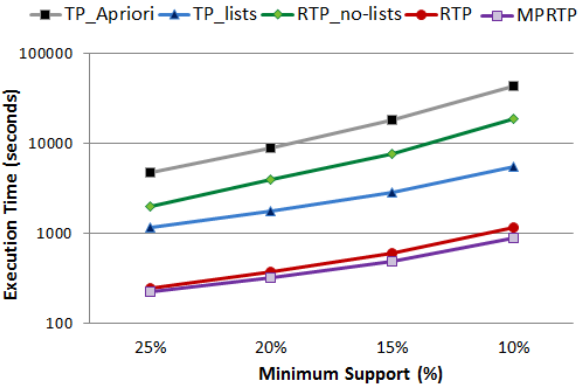

Fig. 9 Diabetes dataset (CARDI): The mining time (in seconds) of the compared temporal pattern mining methods (Section 6.4.1) on the CARDI diabetes dataset for different values of the minimum support.

Finally, we examine the effect of the maximum gap parameter (g) on the efficiency of recent temporal pattern mining methods (*RTP_no-lists*, *RTP* and *MPRTP*). Figure 10 shows the execution time on the *CARDI* dataset for different values of g (the execution time of *TP_Apriori* and *TP_lists* does not depend of g).

Clearly, the execution time of *RTP_no-lists*, *RTP* and *MPRTP* increase with g because the search space becomes larger (more temporal patterns become RTPs). We can see that when g is more than 18 months, *RTP_no-lists* becomes slower than *TP_Apriori*. The reason is that for large values of g, applying the Apriori pruning in candidate generation (pruning a candidate *k-pattern* if it contains an infrequent *(k-1)-subpattern*) becomes more efficient (generates less candidates) than the backward extension of temporal patterns (see Example 5). On the other hand, the execution time of *RTP* and *MPRTP* increase much slower with g and they maintain their efficiency advantage over *TP_Apriori* and *TP_lists* for larger values of g.

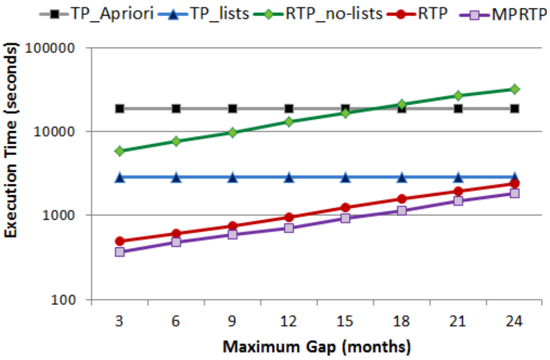

Fig. 10 Diabetes dataset (CARDI): The mining time (in seconds) of the compared temporal pattern mining methods (Section 6.4.1) on the CARDI diabetes dataset for different values of the maximum gap parameter.

6.4.3 Results on HIT Data

Figure 11 shows the execution time (on logarithmic scale) of the compared methods. Similar to the previous settings for the HIT data (Section 6.2.3), we set the local minimum supports to 10% and the maximum gap parameter to 2 days. Again, we see that *RTP* and *MPRTP* are more efficient than the other temporal pattern mining methods.

7 Conclusion

The increasing availability of large temporal data prompts the development of scalable and more efficient mining methods. Methods for mining sequential patterns (time-point patterns) were first introduced in the literature (Agrawal & Srikant

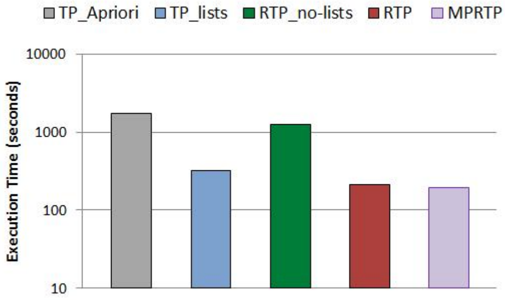

Fig. 11 **HIT dataset**: The mining time (in seconds) of the compared temporal pattern mining methods (Section 6.4.1). The local minimum support is 10%.

1995, Zaki 2001, Pei et al. 2001, Yan et al. 2003). Later on, these methods have been extended to mine data for which the events have time durations (time-interval patterns) (Kam & Fu 2000, Höppner 2001, Papapetrou et al. 2005, Moerchen 2006*a*, Sacchi et al. 2007, Winarko & Roddick 2007, Wu & Chen 2007, Moskovitch & Shahar 2009). However, mining the entire set of frequent patterns (whether sequential patterns or time-interval patterns) from large-scale data is inherently a computationally expensive task. To alleviate this problem, previous research (Srikant & Agrawal 1996, Pei et al. 2007) introduced several temporal constraints to scale up the mining, such as restricting the total pattern duration or restricting the permitted gap between consecutive states in a pattern. This paper proposed a new class of temporal constraints for finding recent temporal patterns (RTP), which we argued is appropriate for event detection problems. We presented an efficient algorithm that mines time-interval patterns backward in time, starting from patterns related to most recent observations. We also presented the minimal predictive recent temporal patterns (MPRTP) framework for selecting predictive and non-spurious RTPs.

We tested and demonstrated the usefulness of our methods on two clinical event detection tasks. The results showed the following benefits of our methods:

1. RTP and MPRTP are able to learn accurate event detection classifiers for real-world clinical tasks.
2. MPRTP is effective for selecting predictive and non-spurious RTPs, which makes it a useful tool for knowledge discovery.
3. Mining RTPs or MPRTPs is much more scalable than mining all frequent time-interval patterns.

A The Bayesian Score: Mathematical Derivation and Computational Complexity

In Section 5.1, we briefly introduced the Bayesian score of RTP P for predicting class label y compared to a more general group G: $G_P \subset G$. In this appendix, we derive the marginal likelihood for models M_e, M_h and M_l, which are required for computing the Bayesian score (solving Equation 1). Section A.1 describes the closed form solution for computing $P(G|M_e)$, which is the marginal likelihood for model M_e (the probability of y is the same inside and outside G_P). Section A.2 derives the closed form solution for computing $P(G|M_h)$, which is the marginal likelihood for model M_h (the probability of y in G_P is higher than outside G_P). Section A.3 shows the four equivalent formulas for computing $P(G|M_h)$. Section A.4 illustrates how to obtain the marginal likelihood for model M_l (the probability of y in G_P is lower than outside G_P) directly from the solution to $P(G|M_h)$. Finally, Section A.5 analyzes the overall computational complexity for computing the Bayesian score.

A.1 The Closed-form Solution of the Marginal Likelihood for Model M_e

Let us start by defining the marginal likelihood for model M_e. This model assumes that all instances in G have the same probability of having label $Y = y$. Let us denote this probability by θ. To represent our uncertainty about θ, we use a beta distribution with parameters α and β. Let N_{*1} be the number of instances in G with $Y = y$ and let N_{*2} be the number of instances in G with $Y \neq y$ (i.e., instances that do not have class label y). The marginal likelihood for model M_e is as follows:

$$Pr(G|M_e) = \int_{\theta=0}^{1} \theta^{N_{*1}} \cdot (1-\theta)^{N_{*2}} \cdot beta(\theta;\alpha,\beta) d\theta$$

The above integral yields the following well known closed-form solution (Heckerman et al. 1995):

$$Pr(G|M_e) = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha+N_{*1}+\beta+N_{*2})} \cdot \frac{\Gamma(\alpha+N_{*1})}{\Gamma(\alpha)} \cdot \frac{\Gamma(\beta+N_{*2})}{\Gamma(\beta)} \tag{2}$$

where Γ is the gamma function.

A.2 Deriving a Closed-form Solution of the Marginal Likelihood for model M_h

Now let us now define the marginal likelihood for model M_h. This model assumes that the probability of $Y = y$ for the instances in G_P, denoted by θ_1, is higher than the probability of $Y = y$ for the instances of G that are outside G_P ($G \setminus G_P$), denoted by θ_2. To represent our uncertainty about θ_1, we use a beta distribution with parameters α_1 and β_1. To represent our uncertainty about θ_2, we use a beta distribution with parameters α_2 and β_2. Let N_{11} and N_{12} be the number of instances in G_P with $Y = y$ and with $Y \neq y$, respectively. Let N_{21} and N_{22} be the number of instances outside G_P with $Y = y$ and with $Y \neq y$, respectively (see Figure 12).

The marginal likelihood for model M_h ($Pr(G|M_h)$) is defined as follows:

$$\frac{1}{k}\int_{\theta_1=0}^{1}\int_{\theta_2=0}^{\theta_1} {\theta_1}^{N_{11}} \cdot (1-\theta_1)^{N_{12}} \cdot {\theta_2}^{N_{21}} \cdot (1-\theta_2)^{N_{22}} \cdot beta(\theta_1;\alpha_1,\beta_1) \cdot beta(\theta_2;\alpha_2,\beta_2) d\theta_2 d\theta_1$$

$$= \underbrace{\frac{1}{k}\int_{\theta_1=0}^{1} {\theta_1}^{N_{11}} \cdot (1-\theta_1)^{N_{12}} \cdot beta(\theta_1;\alpha_1,\beta_1)}_{f_1} \underbrace{\int_{\theta_2=0}^{\theta_1} {\theta_2}^{N_{21}} \cdot (1-\theta_2)^{N_{22}} \cdot beta(\theta_2;\alpha_2,\beta_2) d\theta_2}_{f_2} d\theta_1 \tag{3}$$

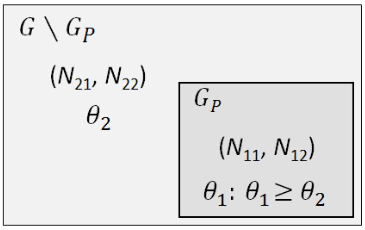

Fig. 12 A diagram illustrating model M_h.

where k is a normalization constant for the parameter prior. Note that we do not assume that the parameters are independent, but rather we constrain θ_1 to be higher than θ_2.

To solve Equation 3, we first show how to solve the integral over θ_2 in closed form, which is denoted by f_2 in Equation 3. We then expand the function denoted by f_1, multiply it by the solution to f_2, and solve the integral over θ_1 in closed form to complete the integration.

We use the regularized incomplete beta function (Abramowitz & Stegun 1964) to solve the integral given by f_2, which is as follows:

$$\int_{\theta=0}^{x} \theta^{a-1} \cdot (1-\theta)^{b-1} d\theta = \frac{\Gamma(a) \cdot \Gamma(b)}{\Gamma(a+b)} \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a+b)}{\Gamma(j+1) \cdot \Gamma(a+b-j)} \cdot x^j \cdot (1-x)^{a+b-1-j} \quad (4)$$

where a and b should be natural numbers.

Note that when $x = 1$ in Equation 4, the solution to the integral in that equation is simply the following:

$$\int_{\theta=0}^{1} \theta^{a-1} \cdot (1-\theta)^{b-1} d\theta = \frac{\Gamma(a) \cdot \Gamma(b)}{\Gamma(a+b)} \quad (5)$$

We now solve the integral given by f_2 in Equation 3 as follows:

$$f_2 = \int_{\theta_2=0}^{\theta_1} {\theta_2}^{N_{21}} \cdot (1-\theta_2)^{N_{22}} \cdot beta(\theta_2; \alpha_2, \beta_2) d\theta_2$$

$$= \int_{\theta_2=0}^{\theta_1} {\theta_2}^{N_{21}} \cdot (1-\theta_2)^{N_{22}} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2) \cdot \Gamma(\beta_2)} \cdot \theta_2^{\alpha_2-1} \cdot (1-\theta_2)^{\beta_2-1} d\theta_2$$

$$= \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2) \cdot \Gamma(\beta_2)} \int_{\theta_2=0}^{\theta_1} {\theta_2}^{N_{21}+\alpha_2-1} \cdot (1-\theta_2)^{N_{22}+\beta_2-1} d\theta_2$$

$$= \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2) \cdot \Gamma(\beta_2)} \int_{\theta_2=0}^{\theta_1} {\theta_2}^{a-1} \cdot (1-\theta_2)^{b-1} d\theta_2$$

where $a = N_{21} + \alpha_2$ and $b = N_{22} + \beta_2$.

Using Equation 4, we get the following:

$$f_2 = \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2) \cdot \Gamma(\beta_2)} \cdot \frac{\Gamma(a) \cdot \Gamma(b)}{\Gamma(a+b)} \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a+b)}{\Gamma(j+1) \cdot \Gamma(a+b-j)} \cdot \theta_1^j \cdot (1-\theta_1)^{a+b-1-j} \quad (6)$$

We now turn to f_1, which can be expanded as follows:

$$\begin{aligned} f_1 &= \int_{\theta_1=0}^{1} {\theta_1}^{N_{11}} \cdot (1-\theta_1)^{N_{12}} \cdot beta(\theta_1;\alpha_1,\beta_1) \\ &= \int_{\theta_1=0}^{1} {\theta_1}^{N_{11}} \cdot (1-\theta_1)^{N_{12}} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \theta_1^{\alpha_1-1} \cdot (1-\theta_1)^{\beta_1-1} \\ &= \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \int_{\theta_1=0}^{1} {\theta_1}^{c-1} \cdot (1-\theta_1)^{d-1} \end{aligned} \tag{7}$$

where $c = N_{11} + \alpha_1$ and $d = N_{12} + \beta_1$.

Now we combine Equations 6 and 7 to solve Equation 3:

$$\begin{aligned} Pr(G|M_h) &= \frac{1}{k} \cdot f_1 \cdot f_2 \; d\theta_1 \\ &= \frac{1}{k} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \int_{\theta_1=0}^{1} {\theta_1}^{c-1} \cdot (1-\theta_1)^{d-1} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)} \cdot \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)} \\ &\quad \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a+b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \theta_1^{j} \cdot (1-\theta_1)^{a+b-1-j} d\theta_1 \\ &= \frac{1}{k} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)} \cdot \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)} \cdot \int_{\theta_1=0}^{1} {\theta_1}^{c-1} \cdot (1-\theta_1)^{d-1} \\ &\quad \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a+b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \theta_1^{j} \cdot (1-\theta_1)^{a+b-1-j} d\theta_1 \\ &= \frac{1}{k} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)} \cdot \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)} \\ &\quad \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a+b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \int_{\theta_1=0}^{1} {\theta_1}^{(c+j)-1} \cdot (1-\theta_1)^{(a+b+d-1-j)-1} d\theta_1 \end{aligned}$$

which by Equation 5 is

$$\begin{aligned} Pr(G|M_h) &= \frac{1}{k} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)} \cdot \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)} \\ &\quad \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a+b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \frac{\Gamma(c+j)\cdot\Gamma(a+b+d-1-j)}{\Gamma(a+b+c+d-1)} \\ &= \frac{1}{k} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)} \\ &\quad \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \frac{\Gamma(c+j)\cdot\Gamma(a+b+d-1-j)}{\Gamma(a+b+c+d-1)} \end{aligned} \tag{8}$$

where $a = N_{21} + \alpha_2$, $b = N_{22} + \beta_2$, $c = N_{11} + \alpha_1$ and $d = N_{12} + \beta_1$.

We can solve for k (the normalization constant for the parameter prior) by solving Equation 3 (without the k term) with $N_{11} = N_{12} = N_{21} = N_{22} = 0$. Doing so is equivalent to applying Equation 8 (without the k term) with $a = \alpha_2$, $b = \beta_2$, $c = \alpha_1$ and $d = \beta_1$. Note that $k = \frac{1}{2}$ if we use uniform priors on both parameters by setting $\alpha_1 = \beta_1 = \alpha_2 = \beta_2 = 1$.

A.3 Four Equivalent Solutions of the Marginal Likelihood for Model M_h

In the previous section, we showed the full derivation of the closed-form solution of the marginal likelihood for model M_h. It turned out that there are four equivalent solutions to Equation 3. Let us use the notations introduced in the previous section: $a = N_{21} + \alpha_2$, $b = N_{22} + \beta_2$, $c = N_{11} + \alpha_1$ and $d = N_{12} + \beta_1$. Also, let us define C as follows:

$$C = \frac{1}{k} \cdot \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)} \cdot \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)} \tag{9}$$

The marginal likelihood of M_h (Equation 3) can be obtained by solving any of the following four equations:

$$C \cdot \sum_{j=a}^{a+b-1} \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \frac{\Gamma(c+j)\cdot\Gamma(a+b+d-j-1)}{\Gamma(a+b+c+d-1)} \tag{10}$$

which is the solution we derived in the previous section.

$$C \cdot \sum_{j=d}^{d+c-1} \frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(j+1)\cdot\Gamma(c+d-j)} \cdot \frac{\Gamma(b+j)\cdot\Gamma(c+d+a-j-1)}{\Gamma(a+b+c+d-1)} \tag{11}$$

$$C \cdot \left(\frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)} \cdot \frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(c+d)} - \sum_{j=b}^{a+b-1} \frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(j+1)\cdot\Gamma(a+b-j)} \cdot \frac{\Gamma(d+j)\cdot\Gamma(a+b+c-j-1)}{\Gamma(a+b+c+d-1)} \right) \tag{12}$$

$$C \cdot \left(\frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)} \cdot \frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(c+d)} - \sum_{j=c}^{c+d-1} \frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(j+1)\cdot\Gamma(c+d-j)} \cdot \frac{\Gamma(a+j)\cdot\Gamma(c+d+b-j-1)}{\Gamma(a+b+c+d-1)} \right) \tag{13}$$

A.4 Deriving a Closed-form Solution of the Marginal Likelihood for Model M_l

Lastly, let us define the marginal likelihood for model M_l, which assumes that the probability of $Y = y$ for the instances in G_P (θ_1) is lower than the probability of $Y = y$ for the instances of G that are outside G_P (θ_2). The marginal likelihood for M_l is similar to Equation 3, but integrates θ_2 from 0 to 1 and constrains θ_1 to be integrated from 0 to θ_2 (forcing θ_1 to be smaller than θ_2) as follows:

$$\frac{1}{k}\underbrace{\int_{\theta_2=0}^{1} {\theta_2}^{N_{21}} \cdot (1-\theta_2)^{N_{22}} \cdot beta(\theta_2;\alpha_2,\beta_2)}_{f_1} \underbrace{\int_{\theta_1=0}^{\theta_2} {\theta_1}^{N_{11}} \cdot (1-\theta_1)^{N_{11}} \cdot beta(\theta_1;\alpha_1,\beta_1) d\theta_1\, d\theta_2}_{f_2} \tag{14}$$

By solving the integral given by f_2, we get:

$$f_2 = \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)}\int_{\theta_1=0}^{\theta_2} {\theta_1}^{c-1}\cdot(1-\theta_1)^{d-1} d\theta_2$$

$$= \frac{\Gamma(\alpha_1+\beta_1)}{\Gamma(\alpha_1)\cdot\Gamma(\beta_1)}\cdot\frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(c+d)}\cdot\sum_{j=c}^{c+d-1}\frac{\Gamma(c+d)}{\Gamma(j+1)\cdot\Gamma(c+d-j)}\cdot\theta_2^j\cdot(1-\theta_2)^{c+d-1-j}$$

where, as before, $c = N_{11} + \alpha_1$ and $d = N_{12} + \beta_1$.

By solving f_1, we get:

$$f_1 = \frac{\Gamma(\alpha_2+\beta_2)}{\Gamma(\alpha_2)\cdot\Gamma(\beta_2)}\int_{\theta_2=0}^{1} {\theta_2}^{a-1}\cdot(1-\theta_2)^{b-1}$$

where, as before, $a = N_{21} + \alpha_2$ and $b = N_{22} + \beta_2$.

Now we can solve Equation 14:

$$Pr(G|M_l) = C\cdot\sum_{j=c}^{c+d-1}\frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(j+1)\cdot\Gamma(c+d-j)}\cdot\frac{\Gamma(a+j)\cdot\Gamma(c+d+b-1-j)}{\Gamma(a+b+c+d-1)} \tag{15}$$

where C is the same constant we defined by Equation 9 in the previous section.

Notice that Equation 15 (the solution to $Pr(G|M_l)$) can be obtained from Equation 13 (one of the four solutions to $Pr(G|M_h)$) as follows:

$$Pr(G|M_l) = C\cdot\frac{\Gamma(a)\cdot\Gamma(b)}{\Gamma(a+b)}\cdot\frac{\Gamma(c)\cdot\Gamma(d)}{\Gamma(c+d)} - Pr(G|M_h) \tag{16}$$

It turns out that no matter which formula we use to solve $Pr(G|M_h)$, we can use Equation 16 to obtain $Pr(G|M_l)$.

A.5 Computational Complexity

Since we require that N_{11}, N_{12}, N_{21}, N_{22}, α_1, β_1, α_2 and β_2 be natural numbers, the gamma function simply becomes a factorial function: $\Gamma(x) = (x-1)!$. Since such numbers can become very large, it is convenient to use the logarithm of the gamma function and express Equations 2, 10, 11, 12, 13 and 16 in logarithmic form in order to preserve numerical precision. The logarithm of the integer gamma function can be pre-computed and efficiently stored in an array as follows:

```
$lnGamma[1] = 0$
For $i = 2$ to $n$
    $lnGamma[i] = lnGamma[i-1] + ln(i-1)$
```

We then can use *lnGamma* in solving the above equations. However, Equations 10, 11, 12 and 13 include a sum, which makes the use of the logarithmic form more involved. To deal with this issue, we can define function *lnAdd*, which takes two arguments x and y that are in logarithmic form and returns $ln(e^x + e^y)$. It does so in a way that preserves a good deal of numerical precision that could be lost if $ln(e^x + e^y)$ were calculated in a direct manner. This is done by using the following formula:

$$lnAdd(x, y) = x + ln(1 + e^{(y-x)})$$

Now that we introduced functions *lnGamma* and *lnAdd*, it is straightforward to evaluate Equations 2, 10, 11, 12, 13 and 16 in logarithmic form.

Let us now analyze the overall computational complexity for computing the Bayesian score for a specific rule (solving Equation 1). Doing so requires computing $Pr(M_e|G)$, $Pr(M_h|G)$ and $Pr(M_l|G)$. $Pr(M_e|G)$ can be computed in $O(1)$ using Equation 2. $Pr(M_h|G)$ can be computed by applying Equation 10, Equation 11, Equation 12 or Equation 13. The computational complexity of these equations are $O(N_{22} + \beta_2)$, $O(N_{11} + \alpha_1)$, $O(N_{21} + \alpha_2)$ and $O(N_{12} + \beta_1)$, respectively. Therefore, $Pr(M_h|G)$ can be computed in $O(min(N_{11} + \alpha_1, N_{12} + \beta_1, N_{21} + \alpha_2, N_{22} + \beta_2))$. $Pr(M_l|G)$ can be computed from $Pr(M_h|G)$ in $O(1)$ using Equation 16. By assuming that α_1, β_1, α_2, β_2 bounded from above, the overall complexity for computing the Bayesian score is $\boldsymbol{O(min(N_{11}, N_{12}, N_{21}, N_{22}))}$.

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