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Bibliographic Notes for Chapter 8 Mining Stream, Time-Series, and Sequence Data

Stream data mining research has been active in recent years. Popular surveys on stream data systems and stream data processing include Babu and Widom [BW01], Babcock, Babu, Datar, et al. [BBD⁺02], Muthukr-ishnan [Mut03], and the tutorial by Garofalakis, Gehrke, and Rastogi [GGR02].

There have been extensive studies on stream data management and the processing of continuous queries in stream data. For a description of synopsis data structures for stream data, see Gibbons and Matias [GM98]. Vitter introduced the notion of reservoir sampling as a way to select an unbiased random sample of n elements without replacement from a larger ordered set of size N, where N is unknown [Vit85]. Stream query or aggregate processing methods have been proposed by Chandrasekaran and Franklin [CF02], Gehrke, Korn, and Srivastava [GKS01], Dobra, Garofalakis, Gehrke, and Rastogi [DGGR02], and Madden, Shah, Hellerstein, and Raman [MSHR02]. A one-pass summary method for processing approximate aggregate queries using wavelets was proposed by Gilbert, Kotidis, Muthukrishnan, and Strauss [GKMS01]. Statstream, a statistical method for the monitoring of thousands of data streams in real time, was developed by Zhu and Shasha [ZS02, SZ04].

There are also many stream data projects. Examples include Aurora by Zdonik, Cetintemel, Cherniack, et al. [ZCC⁺02], which is targeted towards stream monitoring applications; STREAM, developed at Stanford University by Babcock, Babu, Datar, et al. aims at developing a general purpose Data Stream Management System (DSMS) [BBD⁺02]; and an early system called Tapestry by Terry, Goldberg, Nichols, and Oki [TGNO92], which used continuous queries for content-based filtering over an append-only database of email and bulletin board messages. A restricted subset of SQL was used as the query language in order to provide guarantees about efficient evaluation and append-only query results.

A multidimensional stream cube model was proposed by Chen, Dong, Han, et al. [CDH⁺02] in their study of multidimensional regression analysis of time-series data streams. MAIDS (Mining Alarming Incidents from Data Streams), a stream data mining system built on top of such a stream data cube, was developed by Cai, Clutter, Pape, et al. [CCP⁺04].

For mining frequent items and itemsets on stream data, Manku and Motwani proposed sticky sampling and lossy counting algorithms for approximate frequency counts over data streams [MM02]. Karp, Papadimitriou and Shenker proposed a counting algorithm for finding frequent elements in data streams [KPS03]. Giannella, Han, Pei, et al. proposed a method for mining frequent patterns in data streams at multiple time granularities [GHP+04].

For stream data classification, Domingos and Hulten proposed the VFDT algorithm, based on their Hoeffding tree algorithm [DH00]. CVFDT, a later version of VFDT, was developed by Hulten, Spencer, and Domingos [HSD01] to handle concept drift in time-changing data streams. Wang, Fan, Yu and Han proposed an ensemble classifier to mine concept-drifting data streams [WFYH03]. Aggarwal, Han, Wang and Yu developed a k-nearest neighbor-based method for classify evolving data streams [AHWY04b].

Several methods have been proposed for clustering data streams. The k-median based STREAM algorithm was proposed by Guha, Mishra, Motwani, and O'Callaghan [GMMO00] and by O'Callaghan, Mishra, Meyerson, et al. [OMM⁺02]. Aggarwal, Han, Wang, and Yu proposed CluStream, a framework for clustering evolving data streams [AHWY03], and HPStream, a framework for projected clustering of high dimensional data streams [AHWY04a].

Statistical methods for time-series analysis have been proposed and studied extensively in statistics, such as in Chatfield [Cha03], Brockwell and Davis [BD02], and Shumway and Stoffer [SS05]. StatSoft's Electronic Textbook (www.statsoft.com/textbook/stathome.html) is a useful online resource that includes a discussion on time-series data

analysis. The ARIMA forecasting method is described in Box, Jenkins, and Reinsel [BJR94]. Efficient similarity search in sequence databases was studied by Agrawal, Faloutsos, and Swami [AFS93]. A fast subsequence matching method in time-series databases was presented by Faloutsos, Ranganathan, and Manolopoulos [FRM94]. Agrawal, Lin, Sawhney, and Shim [ALSS95] developed a method for fast similarity search in the presence of noise, scaling, and translation in time-series databases. Language primitives for querying shapes of histories were proposed by Agrawal, Psaila, Wimmers, and Zait [APWZ95]. Other work on similarity-based search of time-series data includes Rafiei and Mendelzon [RM97], and Yi, Jagadish, and Faloutsos [YJF98]. Yi, Sidiropoulos, Johnson, Jagadish, et al. [YSJ⁺00] introduced a method for on-line mining for coevolving time sequences. Chen, Dong, Han, et al. [CDH⁺02] proposed a multidimensional regression method for analysis of multidimensional time-series data. Shasha and Zhu present a state-of-the-art overview of the methods for high performance discovery in time series [SZ04].

The problem of mining sequential patterns was first proposed by Agrawal and Srikant [AS95]. In the Aprioribased GSP algorithm, Srikant and Agrawal [SA96] generalized their earlier notion to include time constraints, a sliding time window, and user-defined taxonomies. Zaki [Zak01] developed a vertical format-based sequential pattern mining method called SPADE, which is an extension of vertical-format-based frequent itemset mining methods, like Eclat and Charm [Zak98, ZH02]. PrefixSpan, a pattern growth approach to sequential pattern mining, and its predecessor, FreeSpan, were developed by Pei, Han, Mortazavi-Asl, et al. [HPMA+00, PHMA+01, PHMA+04]. The CloSpan algorithm for mining closed sequential patterns was proposed by Yan, Han, and Afshar [YHA03]. BIDE, a bidirectional search for mining frequent closed sequences was developed by Wang and Han [WH04].

The studies of sequential pattern mining have been extended in several different ways. Mannila, Toivonen, and Verkamo [MTV97] consider frequent episodes in sequences, where episodes are essentially acyclic graphs of events whose edges specify the temporal before-and-after relationship but without timing-interval restrictions. Sequence pattern mining for plan failures was proposed in Zaki, Lesh, and Ogihara [ZLO98]. Garofalakis, Rastogi, and Shim [GRS99] proposed the use of regular expressions as a flexible constraint specification tool that enables user-controlled focus to be incorporated into the sequencial pattern mining process. The embedding of multidimensional, multilevel information into a transformed sequence database for sequential pattern mining was proposed by Pinto, Han, Pei, et al. [PHP⁺01]. Pei, Han, and Wang studied issues regarding constraint-based sequential pattern mining [PHW02]. CLUSEQ is a sequence clustering algorithm, developed by Yang and Wang [YW03]. An incremental sequence indexing by frequent and discriminative analysis of sequential patterns, was studied by Cheng, Yan, and Han [CYH05]. A method for parallel mining of closed sequential patterns was proposed by Cong, Han, and Padua [CHP05].

Data mining for periodicity analysis has been an interesting theme in data mining. Özden, Ramaswamy, and Silberschatz [ORS98] studied methods for mining periodic or cyclic association rules. Lu, Han, and Feng [LHF98] proposed intertransaction association rules, which are implication rules whose two sides are totally ordered episodes with timing-interval restrictions (on the events in the episodes and on the two sides). Bettini, Wang, and Jajodia [BWJ98] consider a generalization of intertransaction association rules. The notion of mining partial periodicity was first proposed by Han, Dong, and Yin, together with a max-subpattern hit set method [HDY99]. Ma and Hellerstein [MH01] proposed a method for mining partially periodic event patterns with unknown periods. Yang, Wang, and Yu studied mining asynchronous periodic patterns in time-series data [YWY03].

Methods for the analysis of biological sequences have been introduced in many textbooks, such as Waterman [Wat95], Setubal and Meidanis [SM97], Durbin, Eddy, Krogh and Mitchison [DEKM98], Baldi and Brunak [BB01], Krane and Raymer [KR03], Jones and Pevzner [JP04], and Baxevanis and Ouellette [BO04]. BLAST was developed by Altschul, Gish, Miller, et al. [AGM⁺90]. Information about BLAST can be found at the NCBI Web site www.ncbi.nlm.nih.gov/BLAST/. For a systematic introduction of the BLAST algorithms and usages, see the book "BLAST" by Korf, Yandell, and Bedell [KYB03].

For an introduction to Markov chains and hidden Markov models from a biological sequence perspective, see Durbin, Eddy, Krogh, and Mitchison [DEKM98], and Jones and Pevzner [JP04]. A general introduction can be found in Rabiner [Rab89]. Eddy and Krogh have each respectively headed the development of software packages for hidden Markov models for protein sequence analysis, namely HMMER (pronounced "hammer", available at *http://hmmer.wustl.edu/*) and SAM (*www.cse.ucsc.edu/research/compbio/sam.html*).

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