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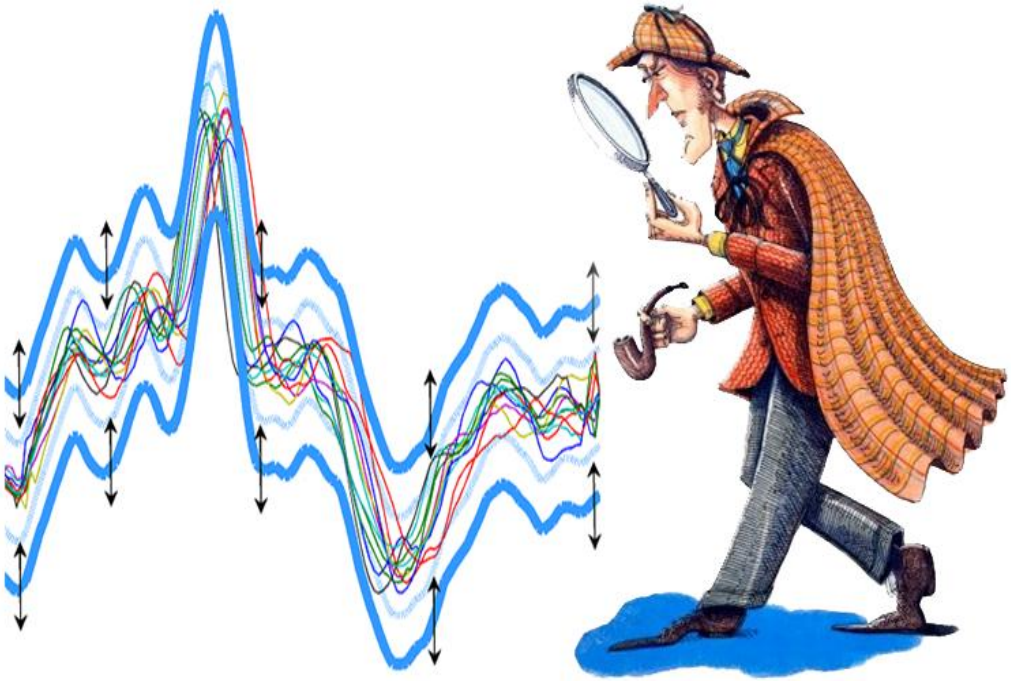
Time Series Motifs Statistical Significance



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Roadmap

I. Introduction
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II. Approach
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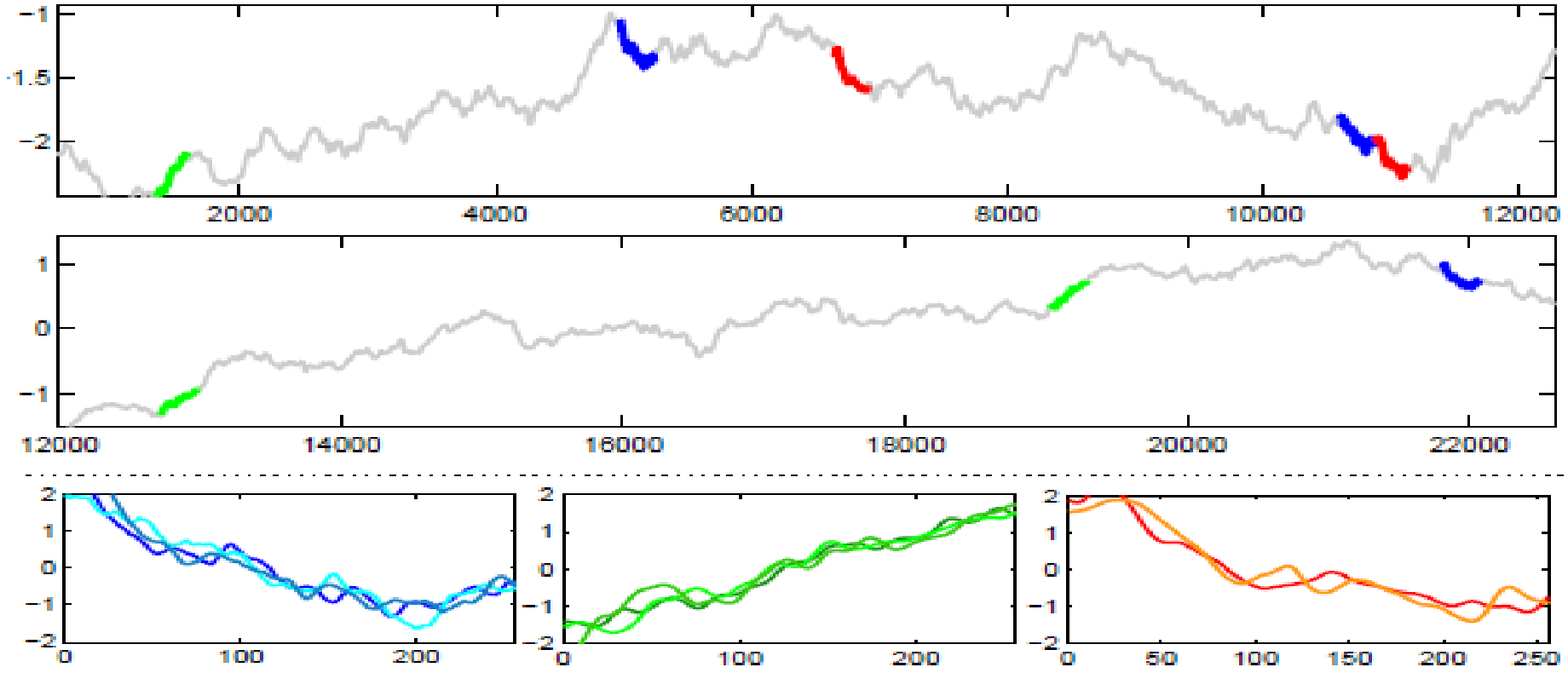
Motif Definition

- **Motifs**, also known as “recurrent patterns”, “frequent patterns”, “repeated subsequences”, or typical shapes” are **previously unknown** patterns in **time series**



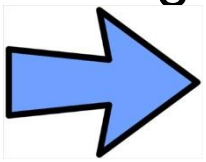
Motivation

- Finding motifs is an important task:
  - Describe the time series at hand
  - Help summarize/represent the database
  - Provide useful insight to the domain expert

- Examples of motifs:
  - Patterns that typically precede a seizure in EEG
  - DNA subsequence preserved through evolution
  - Bursts in telecommunication traffic

Problem

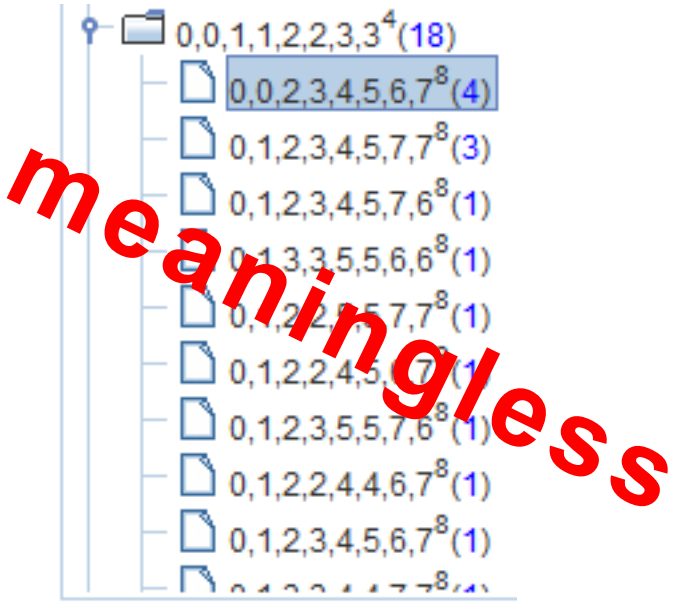
- A large number of proposals recently introduced on "how to efficiently **mine** motifs"
- Very **few** works on how to **evaluate** the motifs
- Motifs are typically evaluated by *humans*
  - Subjective
  - Slow
- **Unfeasible** for real-world datasets (**Terabytes** of data)
  - A large number of patterns are returned by motif mining algorithms

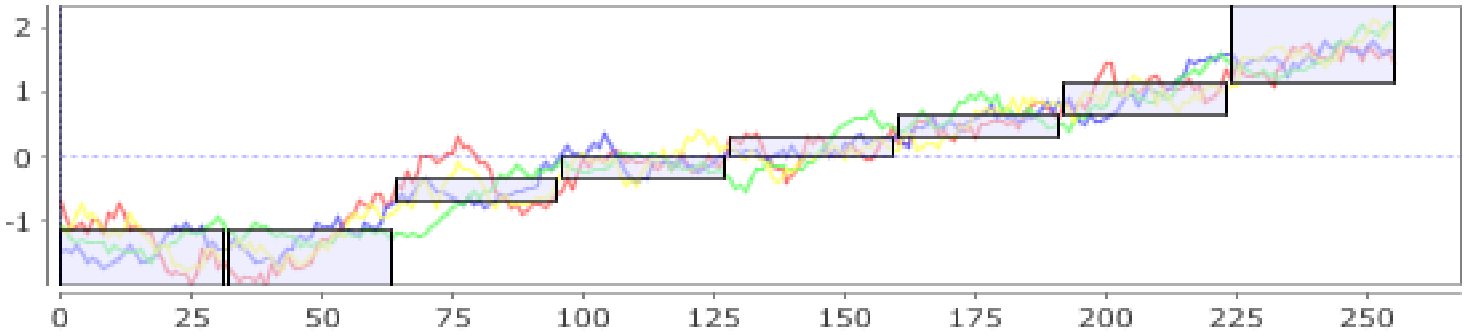


Automatic evaluation measures are necessary.

Example

- Randomly generated dataset with 65536 time series of length 256
- 65 motifs were discovered
- Most frequent motif: 4 repetitions
- Average motif count: 2.17





Solution

- Statistical tests are widely used data mining
  - In bioinformatics, to detect DNA segments with unexpected frequency
  - In networks mining, to find significant subgraphs
  - In itemsets mining, to discard redundant rules

- They aim to answer the question:
  - "Can this pattern occur so many times just by chance?"

- We intend to compare a motif's **expected** and **observed** count using statistical tests

Contribution

- To present an approach to assess the statistical significance of time series motifs:

calculate each **motif**'s **p-value**

II – Our approach

- Motifs are extracted from the database

- Motif's expected count is calculated

- Statistical hypothesis tests are applied to assess each motif's p-value

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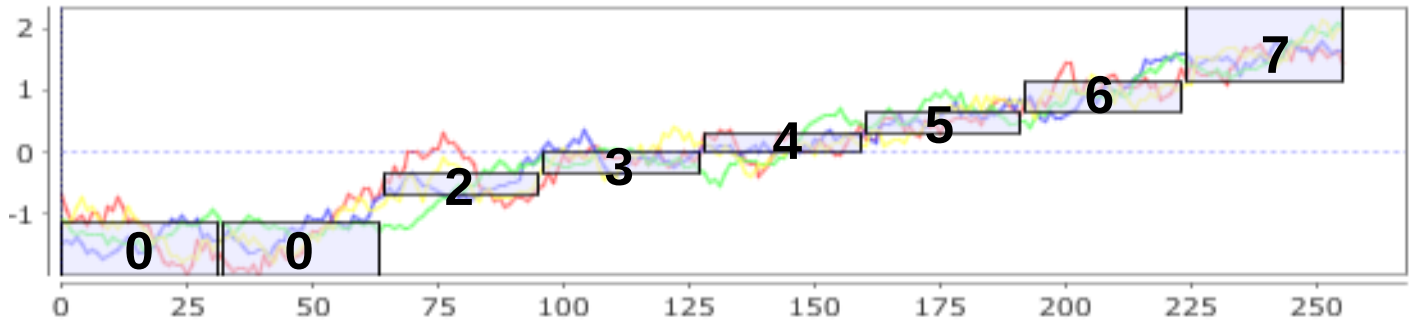
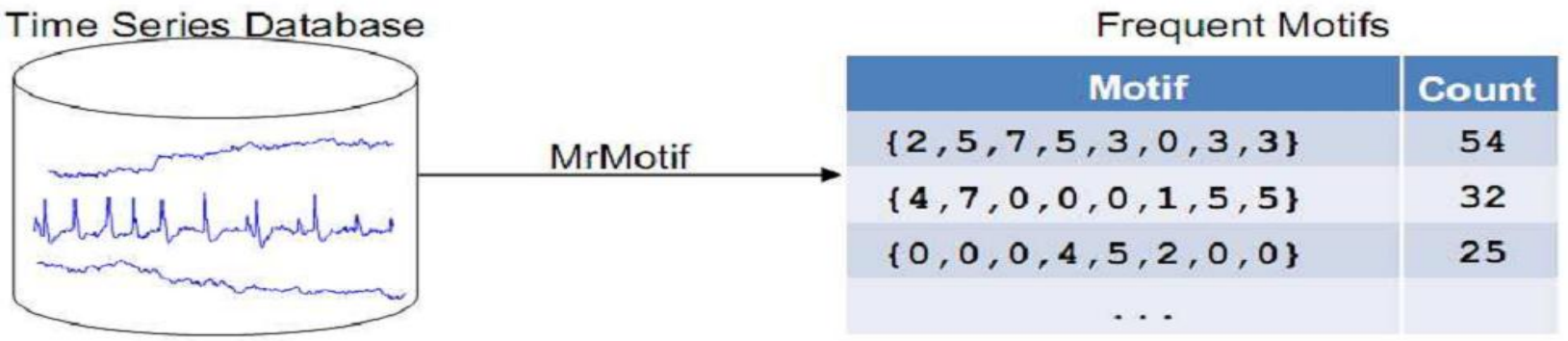
Extracting motifs

- In order to leverage existing work from the bioinformatics, we are interested in **symbolic** motifs
- A symbolic motif is the representation of a motif using symbols (integers, letters)
- For example, the motif { 0, 0, 2, 3, 4, 5, 6, 7 }:



Extracting motifs (cont.)

- Frequent motifs are extracted using a motif discovery algorithm and symbolized using iSAX*



* Shieh, J. and Keogh, E., *iSAX: indexing and mining terabyte sized time series*, in Proceedings of the 14th ACM SIGKDD international Conference on Knowledge Discovery and Data Mining (2008), pp. 623-631.

- Motifs are extracted from the database

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Expected counts

- Frequency by its own does not guarantee that motifs are significant
- A better approach is to consider the difference between the motif **expected count** and its **observed count**
- The expected count is the number of repetitions of a motif we should expect in random sequences that are similar to our database

Expected counts (cont.)

- We use Markov Chain Models to estimate a motif's probability of occurrence
- For a motif, we consider its **subword** count
- For example, the motif "baccdfah":

$$\text{M6} \;\Big|\; \mu = \frac{N(baccdfa)\, N(accdfah)}{3n\, N(accdfa)}$$

- Expected count: $\hat{N}_m(w) = n\,\mu$

II – Approach

- Motifs are extracted from the database

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Statistical Significance

- We intend to calculate the motifs p-values:
  - P-value is the probability of the **motif count** to be *at least as large* as the **observed count**, just by chance.
  - We assume the motif count in time series is Binomial, therefore

$$\mathbb{P}(\mathcal{B}(n,\mu) \geq N^{obs}(w)) = 1 - \sum_{k=0}^{N(w)-1} \binom{n}{k} \mu^k (1-\mu)^{n-k}$$

  - If P ≤ α, we say the pattern is accepted as significant
    - α calculated using the Holm method
  - Otherwise, pattern is rejected

Multiple hypothesis testing problem

- The significance level (**α**) is typically fixed to **0.05**
- Since we apply a test for **each** distinct motif, in a dataset with **100000** motifs we expect to have **5000** significant motifs by chance alone
- The higher the number of simultaneously executed tests, the higher the chance to find at least one that **incorrectly** rejects the null hypothesis

Multiple hypothesis testing problem

- Bonferroni adjustment
  - $\alpha' = \alpha / n$
    - e.g. $\alpha' = 0.05 / 65 = 0{,}00077$
  - too strict

- Holm procedure
  - all p-values are sorted increasingly from p_1 until p_n
  - the first one to reject $\mathbf{p_j \leq \alpha / (n-j+1)}$ becomes α'

III – Experimental Analysis

- We test our approach on data from a **wide** range of applications and **sizes**
- **52** publicly available datasets from a variety of sources are used
- The **MrMotif** algorithm is used to extract **symbolic** motifs from the time series database
- The significance level (**α**) is automatically calculated using the **Holm** procedure

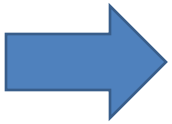
Results

sequence length | distinct motifs | nr. significant motifs | adjusted cutoff | % accepted

Dataset	n	N_d	NSM	α'	%
ERP	47616	2628	95	1.97E-05	3.61
eog	67493	5882	95	8.64E-06	1.62
rateeg	576694	100438	95	4.98E-07	0.09
lightcurves	5327	376	70	0.000163	18.62
cl2	4310	54	36	0.002632	66.67
sasa	81280	754	29	6.89E-05	3.85
koskiecg	2394	360	24	0.000148	6.67
mallat	803	30	18	0.003846	60.00
motor	420	60	7	0.000926	11.67
stocks	18000	1394	7	3.6E-05	0.50
arrowheads	1231	161	5	0.000318	3.11
pen	510	46	4	0.001163	8.70
burstin	1310	221	4	0.000229	1.81
powerdata	1838	295	4	0.000171	1.36
shapemixed	160	14	2	0.003846	14.29
10000	10000	754	2	6.64E-05	0.27
TEK	180	51	1	0.00098	1.96
eegheartrate	373	85	1	0.000588	1.18
leaf	442	72	1	0.000694	1.39
network	1121	36	1	0.001389	2.78
insect	1471	77	1	0.000649	1.30
chaotic	109	4	0	0.0125	0
random	1718	65	0	0.000769	0
fortune	500	9	0	0.005556	0
logistic	2000	181	0	0.000276	0
packet	2332	187	0	0.000267	0
tide	2906	6	0	0.008333	0
eeg	62700	2767	0	1.81E-05	0

Pruning power

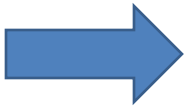
- Our approach **prunes** most of the false discoveries
- For some datasets, **all** frequent motifs were **discarded**
- Using statistical tests in time series motif discovery can act as a **filter**, pruning *meaningless* motifs



This seems to support the **need** for statistical tests in time series motif discovery.

Number of parameters

- Pruning the prohibitively large output of pattern discovery algorithms is typically done by **support** or (top) **K** parameters
- Unintuitive parameters
- Can only be optimized by experimentation
  - May be unfeasible for some datasets to re-run the algorithm with a new parameter setting



Using our approach **avoids** the use of unintuitive parameters, since the adjusted cutoff value (α') is automatically derived

Motif ranking

- Motifs can be **ranked** according to their statistical significance, i.e. p-value
- To be able to rank motifs is important: a ranking yields a smooth way to select the most representative and relevant motifs
- For example, for the domain expert it is better to manually analyze 5 motifs, than 754
- In some cases, when the number of motifs makes the manual analysis very difficult, p-value based rankings may become a requirement

Motif ranking (cont.)

Motif count

Motif Probability

Datasets	Motif	$N(w)$	μ	Expected	p-value
sasa	gggfcbbb	17	3.9E-05	3.172479	4.77E-08
	hggdcbbb	8	8.79E-06	0.7143	8.93E-07
	bbbbgggg	14	3.37E-05	2.735099	1.19E-06
	bbbcggfg	10	1.67E-05	1.354194	1.68E-06
	abbdgggg	7	7.16E-06	0.58183	2.7E-06
eog	aacefggg	31	8.79E-05	5.932245	3.69E-13
	caacfggh	11	6.36E-06	0.429089	1.54E-12
	babbeggh	12	8.78E-06	0.592607	2.27E-12
	dbdgggfa	11	7.38E-06	0.497955	7.41E-12
	gabdeggd	12	1.03E-05	0.695669	1.2E-11
cl2	heddddbe	74	0.00193	8.319006	3.98E-13
	hecdccdf	37	0.001998	8.613394	7.54E-13
	hedcdccd	645	0.049903	215.0832	9.33E-13
	hedddcce	80	0.006069	26.1573	1.06E-12
	hedddccd	64	0.004855	20.92584	1.23E-12
koskiecg	gddddddbg	40	0.002734	6.544641	2.37E-12
	dddddbfh	34	0.00299	7.157086	2.88E-12
	heddddddb	43	0.006027	14.42812	7.89E-10
	dddddbgh	22	0.001817	4.350855	1.49E-09
	dbggdddd	45	0.00719	17.21198	1.55E-08
mallat	dgbcdche	90	0.03608	28.97219	6E-13
	cgbcdche	97	0.041707	33.49079	6.16E-13
	dgbbdche	92	0.038283	30.74089	6.57E-13
	dgbcdcge	59	0.024542	19.70757	7.29E-13
	dhbcdcge	137	0.056988	45.76165	7.92E-13

IV – Conclusions

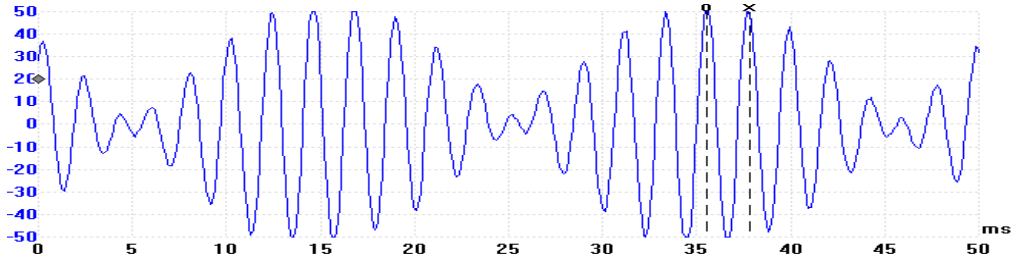
- We proposed an approach to compute the p-values of time series motifs

- A motif is accepted if it passes a statistical hypothesis test
  - i.e. p-value ≤ significance level.

Conclusions (cont.)

- Our approach:
  - Significantly **reduces** the number of returned patterns
  - Avoids the use of unintuitive support or top-K **parameters**
  - Allows to **rank** motifs according to their significance
  - Provides researchers and practitioners with an important technique to **evaluate** the degree of **relevance** of each pattern
- We aim to **highlight** the **importance** of motif evaluation, since we believe it is **crucial** to make motif mining an useful task in practice

Thank you for your attention!



- Contact: castro@di.uminho.pt
- Paper web site (executable, source code and datasets):

  www.di.uminho.pt/~castro/stat

Future work

- Extend work to other statistical tests
- Integrate the approach in the motif discovery process (currently applied as post-processing)

Extra

Multiple hypothesis problem

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