

Data Mining and Computational Creativity

Prof. Hannu Toivonen Discovery Group University of Helsinki and HIIT

Aalto University



Discovery Group

- 1 Prof. Hannu Toivonen
- +1 Alessandro Valitutti, Postdoc (until Dec 2013)
 - Ping Xiao from 2014

Laura Langohr, PhD student

+3 Oskar Gross, PhD student
Jukka Toivanen, PhD student

Affiliate members

Assoc. Prof. Antoine Doucet

(U. Caen, France)

Dr. Tommi Opas (entrepeneour)

- Fang Zhou, PhD 2012
- Mika Timonen, PhD 2013 (VTT, Techn. Res. Centre of Finland)
- Esther Galbrun, PhD 2014 (co-supervised with Mikko Koivisto)

Joonas Paalasmaa, PhD 2014 (Beddit.com Ltd.)



Mission

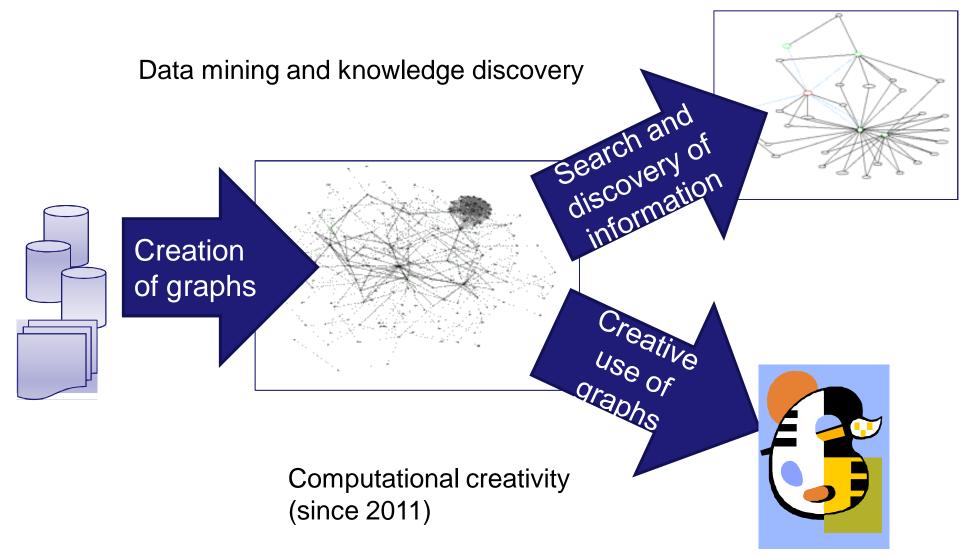
We develop novel methods and tools for data mining and computational creativity.

Algorithms for discovering links and patterns in data
 Their use in creative systems

E.g. poetry generation



Evolution of research topics





Computational creativity

- 1. Creative computers
- 2. Computers supporting human creativity
- 3. Studies of creative computational processes

Why study computational creativity?

- An ultimate Al challenge
- A test bed for AI/ML/DM methods
- Applications: games, user interfaces, creativity support
- An intellectual challenge

International conference ICCC since 2010



Computational poetry

Music swells, accent practises, theatre hears! Her delighted epiphanies bent in her universe: – And then, singing directly a universe she disappears! An anthem in the judgements after verse!



Computational poetry (ICCC 2012, 2013)

No explicit grammars, rules or semantics given

Except for rhymes in this example

- Instead, utilization of existing texts both for the form (syntax) and the content (lexical selection)
- Endless data mining opportunities
 - Analysis of language use beyond simple co-occurrence
 - Analysis of example poetry, learning styles etc.
- Applications e.g. in supporting creativity
 - An interactive tool for playful practice of writing in grammar schools



Future work

Focus on computational creativity

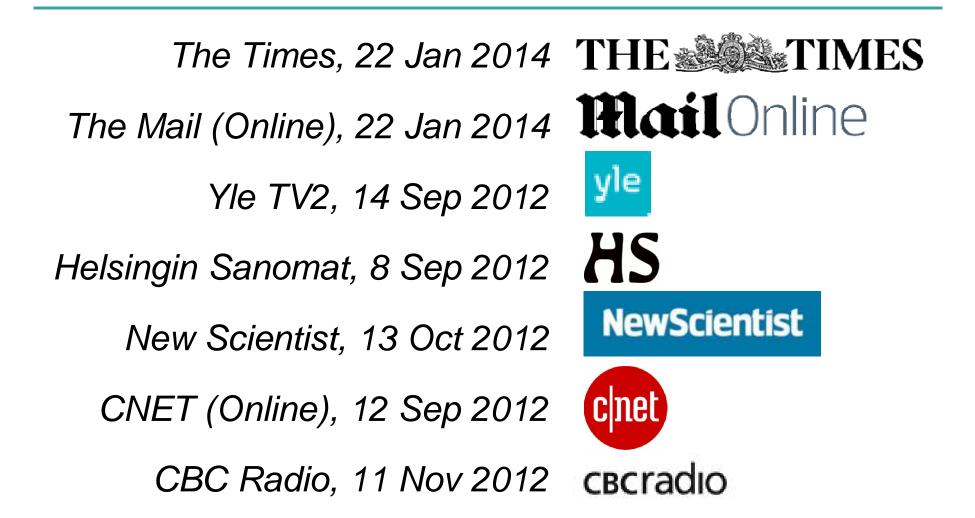
- Using data mining and graph mining
- Learning and adaptive creative systems
- "Concept creation technology", EU FP7, 2013-16
- Establish further contacts and collaboration with scientists in applied fields (e.g. literature, cinema)
 "Promoting scientific exploration of computational creativity", EU FP7 CSA, 2013-16



Societal impact: Contributions to arts



Societal impact: Press





Technical and economical impact

Impact comes from data mining research with companies:

- Collaboration with Finnish media companies on news analysis
- Sleep analysis research commercialized by Beddit Ltd, see the following talk by Joonas Paalasmaa



Publications 2011-2013

Computational creativity

- ICCC (Computational Creativity) x 3
- KICSS (Creativity Support)
- IDA, Frontier award winner
- ACL
- CICLing

Data mining in bioinformatics

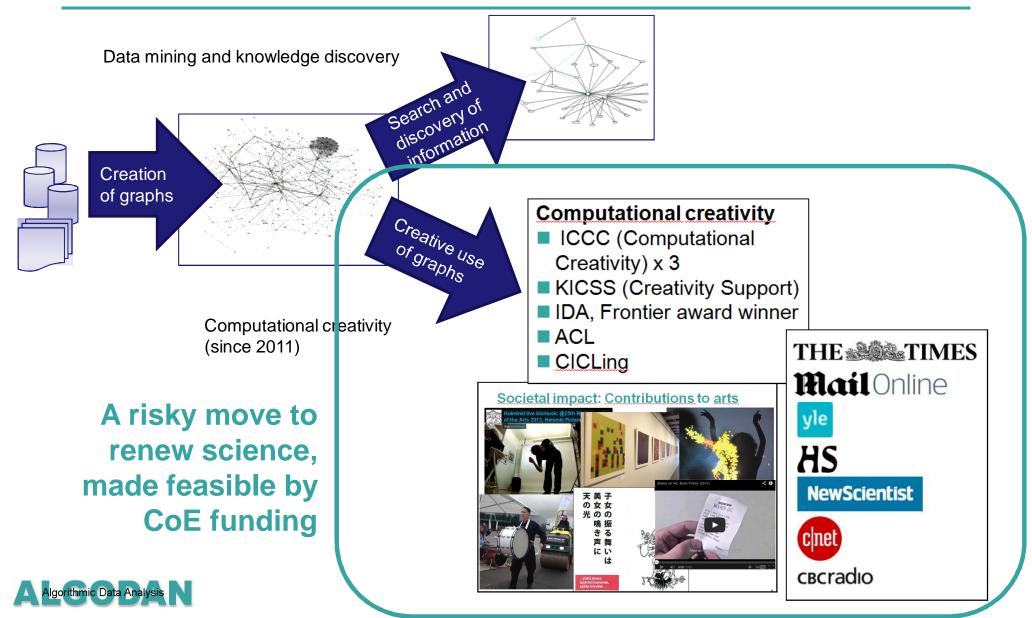
- BMC Bioinformatics x 2
- PloS One
- IEEE EMBS

Data mining

- Machine Learning
- Statistical Analysis and Data Mining
- Computer x 2
- Print Media Technology Research
- SIGKDD x 2
- SDM
- DS
- ASONAM
- Bisociative Knowledge Discovery (book) x 5



Impact of CoE funding





Monitoring Sleep with Force Sensor Measurement

Joonas Paalasmaa

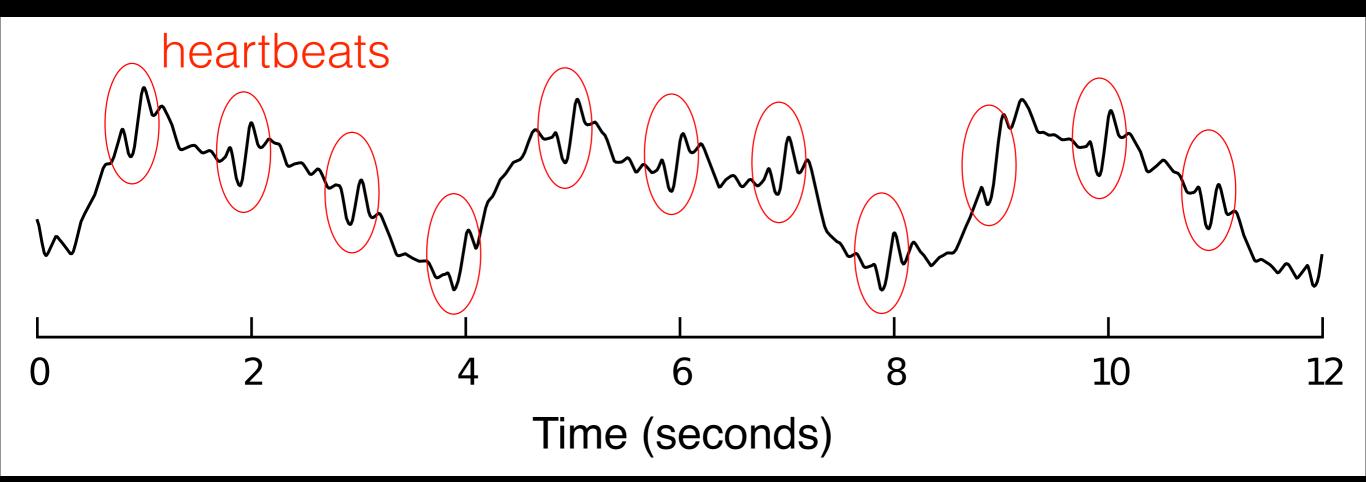




My PhD thesis from last month: Monitoring Sleep with Force Sensor Measurement

Developing sleep measurement signal processing methods for this kind of sleep sensors



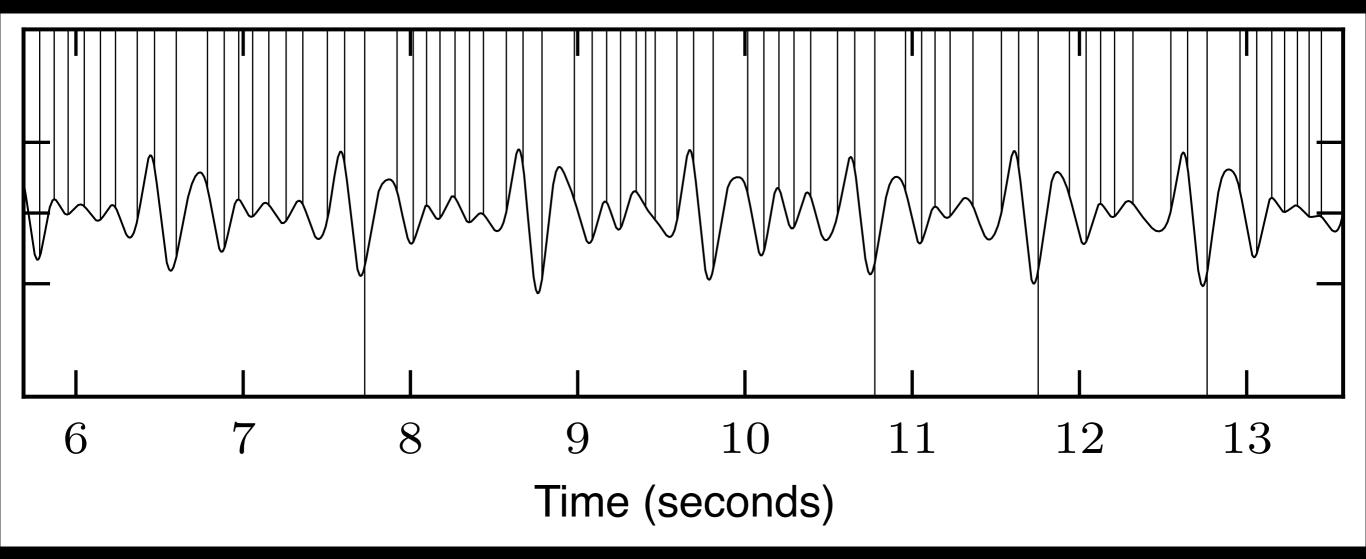


Signal processing problems to solve

- Detect from the signal: heart rate, respiration, movements
- It is very difficult, because signal properties vary by person, bed, etc. **Unsupervised** methods are needed.

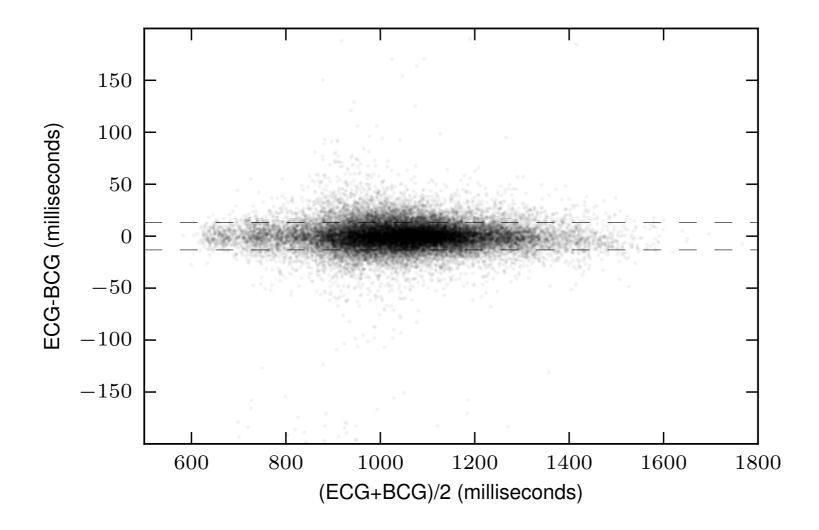
Other machine learning problems to solve

 Based on heart rate, respiration and movements, classify sleep into: sleep stages, sleep cycles, snoring, ...

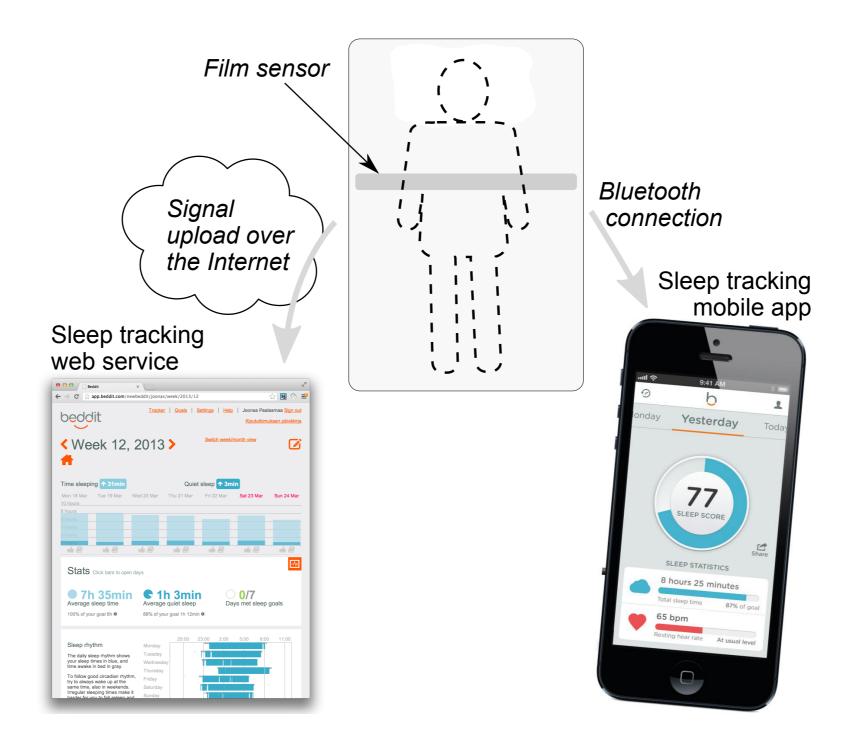


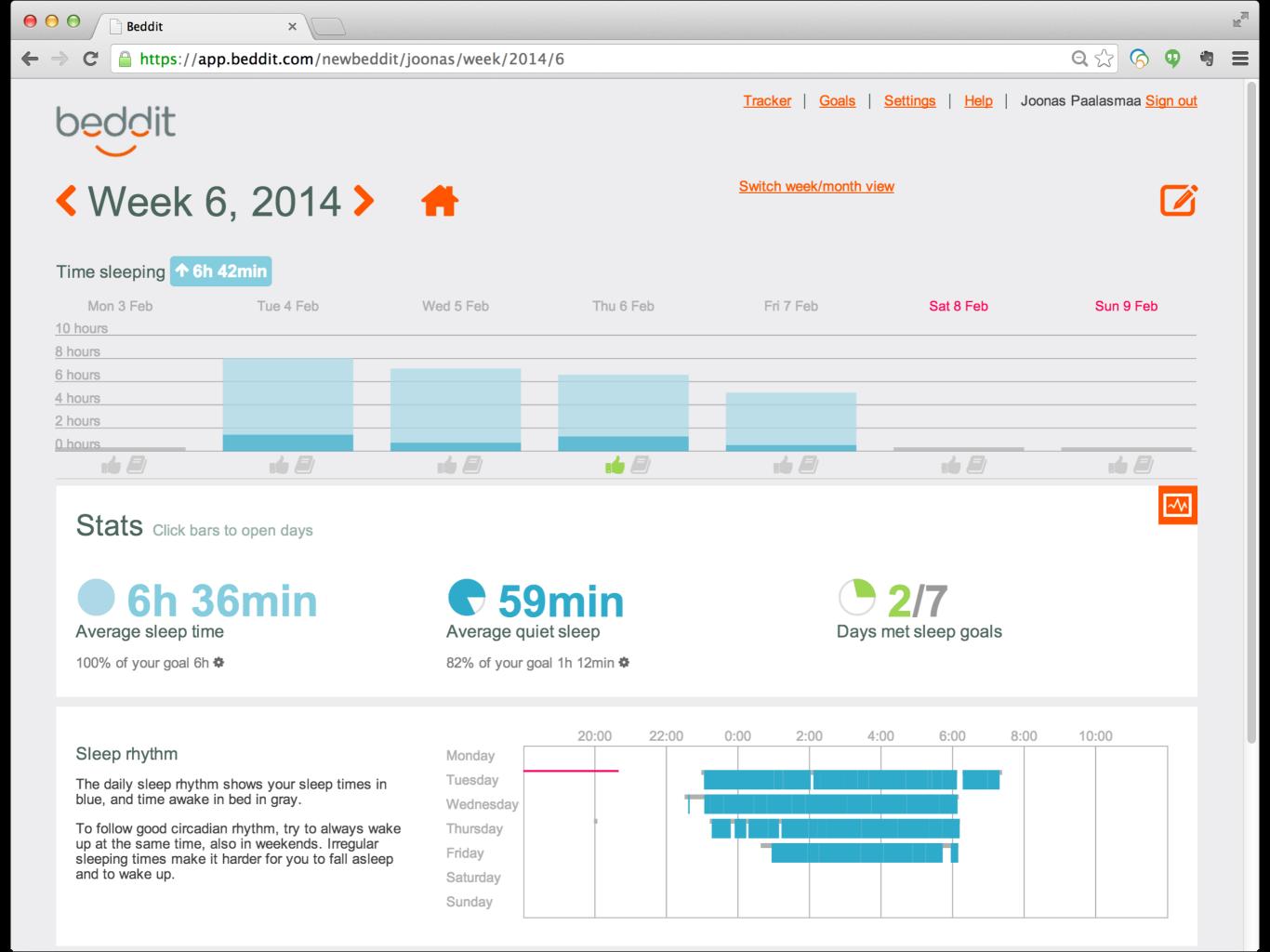
Clinical validation

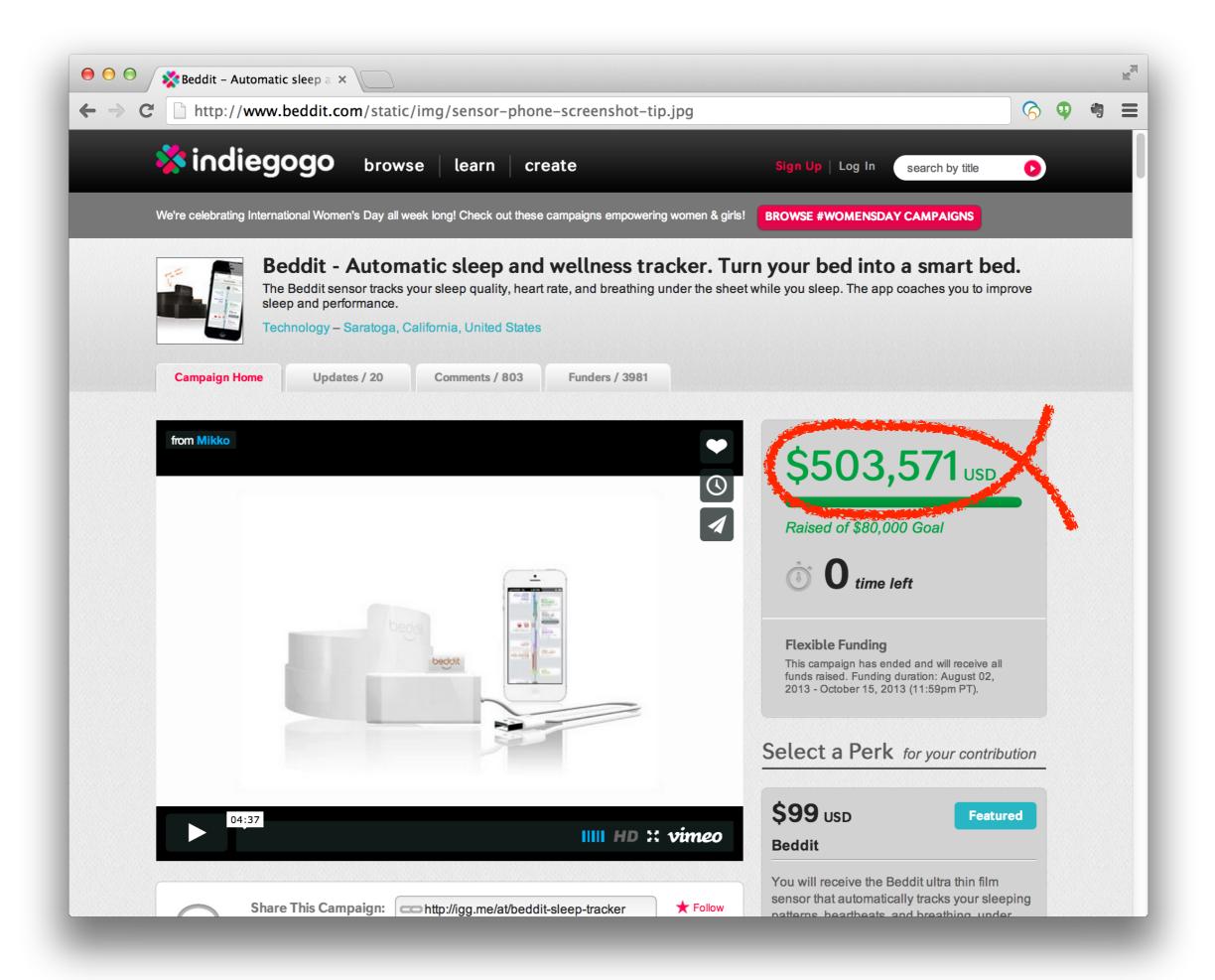
- 40-person clinical study in 2010 (patients at the lab)
- 20-person clinical study in 2012 (volunteers at their homes)



Turning research into business — Beddit Ltd







Summary

- Scientific contributions: signal analysis methods (*Physiological Measurement*, 2010. *IEEE EMBS*, 2011, 2012. *IEEE J-BHI*, under review.)
- Medical contributions: clinical validation of methods
- **Commercial activity**: raised over \$500 000 in a crowdfunding campaign in 10 weeks. 10000 units produced so far.

Exact algorithms

Petteri Kaski Department of Information and Computer Science Aalto University, Helsinki

ALGODAN Scientific Advisory Board 18 March 2014





Combinatorics, Algebra, and Computing (CO-ALCO)

Members

- Mikko Koivisto, Academy Research Fellow (8/2008-10/2013), Professor (1/2013-), Co-leader
- Petteri Kaski, Academy Research Fellow (9/2011-), Professor (1/2012-), Co-leader
- Pekka Parviainen, Doctoral student (-6/2012, PhD 3/2012)
- Janne Korhonen, Doctoral student (PhD 2/2013)
- Juho-Kustaa Kangas, Doctoral student (1/2012-)
- Teppo Niinimäki, Doctoral student

Mission of the group

The group develops and applies combinatorial and algebraic tools for computational problems, focusing on <u>exact deterministic algorithms</u>. Applications range from fundamental combinatorial problems to computational tasks associated with established probabilistic models in machine learning and data mining.

ALGODAN themes F = Foundations of algorithmic data analysis D = Discovery of hidden structure in data

CO-ALCO Highlights, 2011 & beyond

Theme D

- Graphical models from data (exact algorithms for polytrees & for Bayesian networks parameterized by treewidth; AAAI'12, AISTATS'13, JMLR 2013)
- Discovering connected motifs in graphs Theme D (linear-time in the size of the host graph; STACS'13)
- Fast "Fourier analysis" on partially ordered sets Theme F (fast Möbius inversion on lattices, counting thin subgraphs; SODA'12 & SODA'14)

review articles

DOI:10.1145/2428556.2428575

Discovering surprises in the face of intractability.

BY FEDOR V. FOMIN AND PETTERI KASKI

Exact Exponential Algorithms

MANY COMPUTATIONAL PROBLEMS have been shown to be intractable, either in the strong sense that no algorithm exists at all—the canonical example being the undecidability of the Halting Problem—or that no *efficient* algorithm exists. From a theoretical perspective perhaps the most intriguing case occurs with the family of *NP*-complete problems, for which *it is not known* whether the problems are intractable. That is, despite extensive research, neither is an

of non-parameterized instances of intractable problems? At first glance, the general case of an *NP*-complete problem is a formidable opponent: when faced with a problem whose instances

F. V. Fomin & P. Kaski Communications of the ACM March 2013, pp. 80–88.

But what can we say about finding exact solutions

surprises have emerged recently.

80 COMMUNICATIONS OF THE ACM | MARCH 2013 | VOL. 56 | NO. 3



Graph motifs

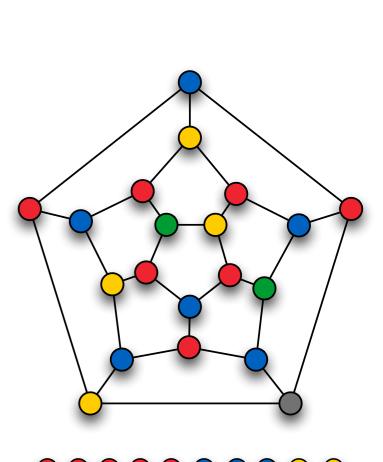
• Input

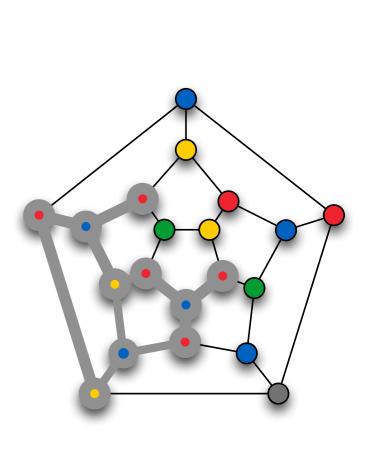
- A vertex-colored host graph H
- A multiset M of colors (**the motif**)

Question

Does H have a *connected* subgraph whose vertex colors agree with M?

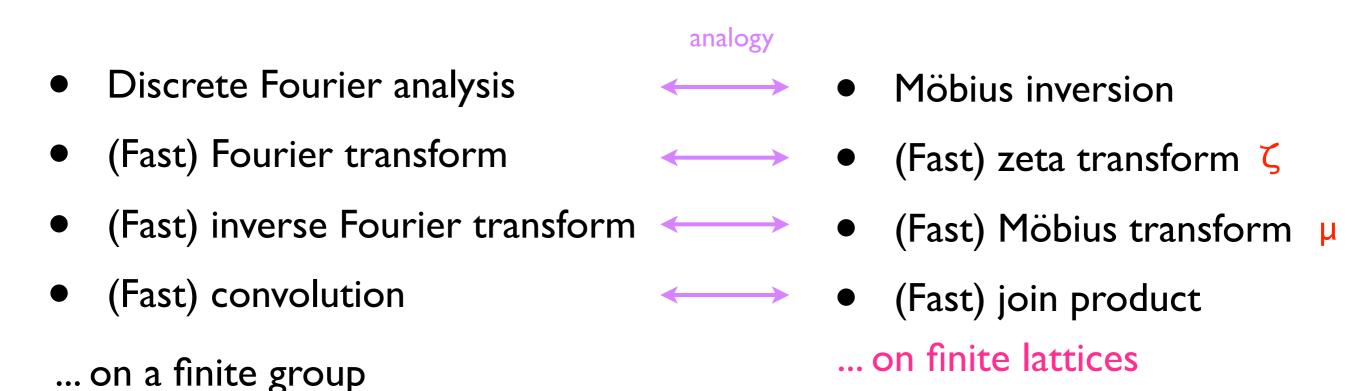
- Main result (Björklund, K., & Kowalik, STACS'13)
 - Let H have *n* vertices and e edges, $e \ge n$
 - Let M have size k
 - There is a randomized algorithm that runs in time O(2^k k³ e) with
 (i) no false positives, and
 (ii) false negatives with probability ≤0.001
 - 1) Linear time in the size e of the host graph 2) NP-hard problem, but exponentiality only in k, k << n3) There is evidence that an O(1.9999^k poly(k,e)) algorithm is unlikely





Fast Möbius inversion ("Fourier analysis") on partially ordered sets

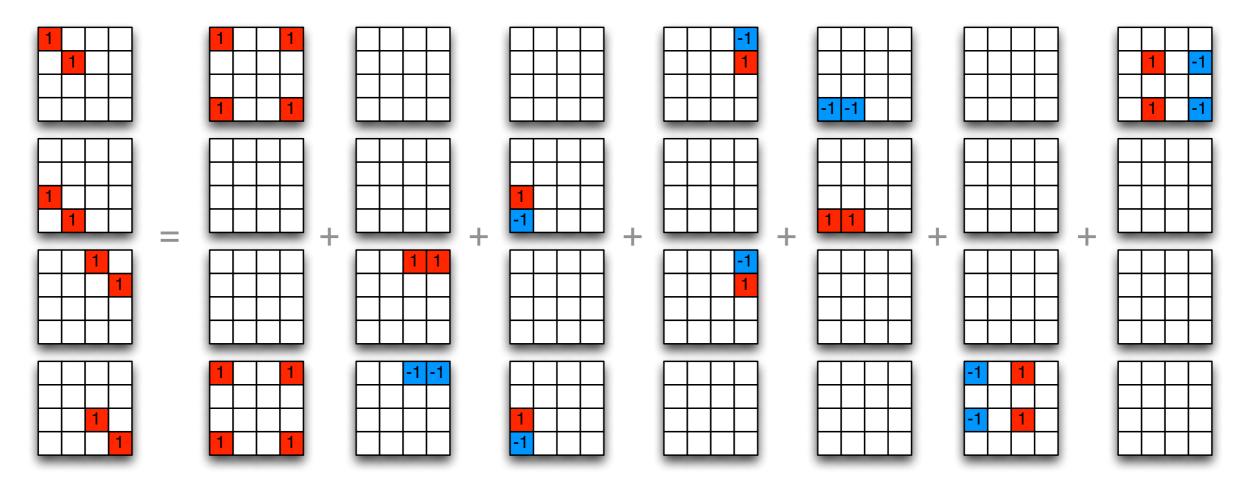
(Björklund, Husfeldt, K., Koivisto, Nederlof, Parviainen; SODA'12 & ACM TALG, to app.)



(e.g. the cyclic group = classical discrete Fourier analysis)

Previous slide summarized: The structural tensor of the join product has "low (tensor) rank"

... but so has the structural tensor of the square matrix product ...



(Strassen's 1969 low-rank tensor decomposition for 2x2 matrix product)

Counting (thin subgraphs) in three parts faster than "meet-in-the-middle" time

(Björklund, K., Kowalik SODA'14)

• Given as input $f, g, h : {\binom{[n]}{k/3}} \to \mathbb{Z}$ with values bounded in bit-length by a polynomial in n, we can in time $O(n^{(1/2-\tau)k+c})$ compute

$$\Delta(f, g, h) = \sum_{\substack{A, B, C \in \binom{[n]}{k/3} \\ A \cap B = \emptyset \\ A \cap C = \emptyset \\ B \cap C = \emptyset}} f(A)g(B)h(C)$$

where $\tau = \begin{cases} \frac{(3-\omega)(1-\alpha)}{36-6(1+\omega)(1+\alpha)} & \text{if } \alpha \le 1/2\\ \frac{1}{18} & \text{if } \alpha \ge 1/2 \end{cases}$

Summary — what next ?

Theme D

- Graphical models from data (exact algorithms for polytrees & for Bayesian networks parameterized by treewidth; AAAI'12, AISTATS'13, JMLR 2013)
- Discovering connected motifs in graphs Theme D (linear-time in the size of the host graph; STACS'13)
- Fast "Fourier analysis" on partially ordered sets Theme F (fast Möbius inversion on lattices, counting thin subgraphs; SODA'12 & SODA'14)

Theory and Practice of Advanced Search and Enumeration

(ERC StG 338077 "TAPEASE")

Petteri Kaski Department of Information and Computer Science Aalto University, Helsinki

(| Feb 2014 – 31 Jan 2019)





erc



Machine Learning for Metabolite Identification

Juho Rousu Department of Information and Computer Science Aalto University





Metabolite identification (MID)

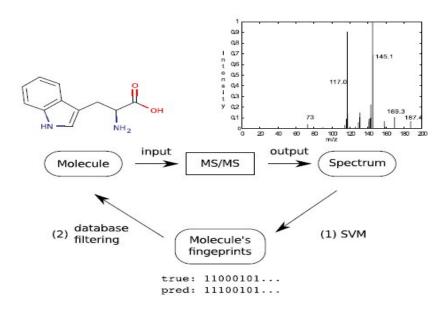
- Given a biological sample, identification of which molecular species are present is a major bottleneck in metabolomics research
- Tandem Mass Spectrometry (MS/MS) is one of the key measurement techniques, but gives a convoluted signal that requires further processing
- The classical approach to MID is spectral matching:
 - look up a most similar spectrum to the query
 - (only) works well if there is a database spectrum of the same molecule, that was measured with same MS/MS type, similar conditions



Our Approach: Machine Learning

Basic idea:

- SVM learning of mappings between MS/MS spectra and molecular features.
- Retrieve molecules with the predicted features from a large molecular database (PubChem)
- First MID approach using modern machine learning (Heinonen et al. 2012)

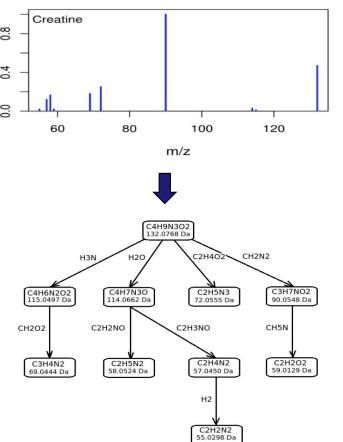


Metabolite identification and molecular fingerprint prediction through machine learning (2012). M Heinonen, H Shen, N Zamboni, J Rousu. Bioinformatics 28 (18), 2333-2341



Adding prior knowledge: Fragmentation Trees (FT)

Fragmentation trees (FT): model the process of 0.4 breakage of the molecule 0.0 inside MS/MS Help molecular formulae identification, not full MID We use FTs to define kernels for MS/MS spectra Collaboration with prof. Sebastian Böcker (Jena)





Huibin Shen, Kai Duehrkop, Sebastian Boecker and Juho Rousu. Metabolite Identification through Multiple Kernel Learning on Fragmentation Trees. ISMB 2014, accepted

Multiple Kernel Learning

Kernels between two trees: count co-occurring labeled nodes, edges, paths, subtrees Edges, nodes: inner product of feature maps Paths, subtrees: dynamic programming Probability Product Kernel for "raw" MS/MS spectra (Heinonen et al .2012) Multiple Kernel Learning: combine the base kernels optimally Uniform combination Lp block-norm approaches Kernel alignment approaches (Cortes et al. 2012)

Non-linear combination



Huibin Shen, Kai Duehrkop, Sebastian Boecker and Juho Rousu. Metabolite Identification through Multiple Kernel Learning on Fragmentation Trees. ISMB 2014, accepted

Prediction performance

Molecular fingerprints

Metabolite Identification

F1 of fingerprint prediction 978 compounds in METLIN 1.0 100 Proportion of dataset (%) 0.8 80 NB/ALIGNF 0.6 60 0.4 40 L₃ MKL NB UNIMKL 0.2 20 ALIGNF NB PPK 0 NUM 0.0 △ ALIGNF 0 0.0 0.2 0.4 0.6 0.8 1.0 2 5 10 20 50 100 PPK Rank (log scale)



Huibin Shen, Kai Duehrkop, Sebastian Boecker and Juho Rousu. Metabolite Identification through Multiple Kernel Learning on Fragmentation Trees. ISMB 2014, accepted

MID Software

- Our algorithms are available for research community
 - Software package (source forge)
- FingerID tool
 - Easy user interface for metabolomics researchers

http://research.ics.aalto.fi/ke

paco/fingerid/

F	ingerID
Exact mass	Device type
174.11168	Number of training spectra listed in bracket.
Precursor	LC-ESI-QTOF-CID (1492) LC-ESI-ITFT-CID (447) LC-ESI-ITFT-HCD (2655) LC-APCI-ITFT-CID (295)
175.12	LC-APCI-ITFT-HCD (882)
Peaks	Mode
83.037743 820.501831	e Positive O Negative
94.951782 6441.830078	
109.981171 192217.531250 110.885223 132.844055	Search PPM
110.885223 132.844055	10
137.928238 1087.422607	

Trail Mode Batch Mode

>>						
Score	Name	Formula	Exact Mass	Structure	Database ID	
0.833	Amino acid(Arg-); Arginine; 2-Amino-5-guanidinovaleric acid	C6H14N4O2	174.1117		C02385	
0.359	D-Arginine; D-2-Amino-5-guanidinovaleric acid	C6H14N4O2	174.1117		C00792	
0.359	L-Arginine; (S)-2-Amino-5-guanidinovaleric acid; L-Arg	C6H14N4O2	174.1117		C00062	



Perspectives on Metabolite Identification

- Current results are state-of-the-art of automatic MID
- Google search analogy: 80% of correct molecular structures within top 5 candidates – already useful in practise!
- Current and future themes:
 - Multilabel and structured output prediction methods for MID
- Joint identification of metabolites from metabolomics samples
 Supported by Academy of Finland grant "Metabolite Identification through Algorithms and Statistical Learning (MIDAS)", 2013-2017



Activities of KEPACO group: see posters

More MID:

 Huibin Shen: Metabolic Identification through Multiple Kernel Learning on Fragmentation Trees (ISMB 2014, to appear)
 Things I did not tell you about:

- Hongyu Su: Random graph ensembles for multilabel learning (ACML 2013)
- Jana Kludas: Protein-protein interactions in the protein transport pathways (BIOLEDGE, FP7 STREP)
- Anna Cichonska: Predicting Drug-Target interactions through KroneckerRLS learning (Collaboration with Finnish Institute for Molecular Medicine, FIMM)

