



CPM2011

22nd Annual Symposium on Combinatorial Pattern Matching
Hotel La Torre, Palermo, ITALY, 27-29 June 2011

PROGRAM

Sunday, June 26th

17.00-19.30: Registration.

19.30-20.30: Welcome Aperitivo, Terrace of Hotel La Torre

Monday, June 27th

8:15-8:45: Registration.

8:45-9:00: Opening.

Invited Talk (Chair Giovanni Manzini)

09.00-10.00: Gad Landau: *Algorithms on Grammar-Compressed Strings.*

CPM and Compressed Text I (Chair Juha Kärkkäinen)

10.00: 10.20: Enno Ohlebusch and Simon Gog. *Lempel-Ziv Factorization Revisited.*

10.20-10.40: Chris Thachuk. *Succincter Text Indexing with Wildcards.*

10.40-11.00: Sebastian Kreft and Gonzalo Navarro. *Self-Indexing Based on LZ77.*

11.00-11.30: *Coffee break*

Combinatorics on Words (Chair Aldo de Luca)

11.30-11.50: Haitao Jiang, Farong Zhong and Binhai Zhu. *Filling Scaffolds with Gene Repetitions: Maximizing the Number of Adjacencies.*

11.50-12.10: David E. Daykin, Jacqueline W. Daykin and William F. Smyth. *String Comparison & Lyndon-Like Factorization Using V-Order in Linear Time.*

12.10-12.30: Antoine Deza, Frantisek Franek and Mei Jiang. *A d-step Approach for Distinct Squares in Strings.*

12.30-12.50: Cedric Chauve, Ján Maňuch, Murray Patterson and Roland Wittler. *Tractability Results for the Consecutive-Ones Property with Multiplicity.*

13.00: *Lunch*

CPM and Computational Biology I (Chair Michal Ziv-Ukelson)

15.00-15.20: Stefanie Schirmer and Robert Giegerich. *Forest Alignment with Affine Gaps and Anchors.*

15.20-15.40: Wolfgang Otto, Peter F. Stadler and Sonja J. Prohaska. *Phylogenetic Footprinting and Consistent Sets of Local Alignments.*

15.40-16.00: Michel Habib and Juraj Stacho. *Unique Perfect Phylogeny is NP-hard.*

16.00-16.20: Daniel G. Brown and Jakub Trzuskowski. *Fast Error-tolerant Quartet Phylogeny Algorithms.*

16.20-16.50: *Coffee break*

Classic String Matching I (Chair Sabrina Mantaci)

16.50-17.10: Dany Breslauer and Zvi Galil. *Real-Time Streaming String Matching*

17.10-17.30: Dany Breslauer, Roberto Grossi and Filippo Mignosi. *Simple Real-Time Constant-Space String-Matching*

17.30-17.50: Raphaël Clifford, Markus Jalsenius, Ely Porat and Benjamin Sach. *Space Lower Bounds for On-line Pattern Matching*

18.00-19.00: *Business Meeting and Best Student Paper Award Ceremony*

Tuesday, June 28th

Invited Talk (Chair Raffaele Giancarlo)

09.00-10.00: Nello Cristianini: *Automatic Discovery of Patterns in Media Content*

CPM and Compressed Text II (Chair Gonzalo Navarro)

10.00-10.20: Travis Gagie and Juha Kärkkäinen. *Counting Colours in Compressed Strings.*

10.20-10.40: German Tischler. *On Wavelet Tree Construction*

10.40-11.00: Markus J. Bauer, Anthony J. Cox and Giovanna Rosone. *Lightweight BWT Construction for Very Large String Collections.*

11.00-11.30: *Coffee break*

Classic String Matching II (Chair Chiara Epifanio)

11.30-11.50: Tomohiro I, Shunsuke Inenaga and Masayuki Takeda. *Palindrome Pattern Matching.*

11.50-12.10: Takashi Uemura and Hiroki Arimura. *Sparse and Truncated Suffix Trees on Variable-Length Codes*

12.10-12.30: Paolo Ferragina. *On the Weak Prefix-Search Problem.*

12.30-12.50: Isaac Goldstein and Moshe Lewenstein. *Quick Greedy Computation for Minimum Common String Partitions.*

13.00: *Lunch*

15.30: *Social Tour*

20.00: *Social Dinner at Grand Hotel Piazza Borsa, Palermo*

Wednesday, June 29th

Invited Talk (Chair Maxime Crochemore)

09.00-10.00: Martin Vingron: *Computational Regulatory Genomics*.

CPM and Compressed Text III (Chair Travis Gagie)

10.00-10.20: Jérémy Barbay, Johannes Fischer and Gonzalo Navarro. *LRM-Trees: Compressed Indices, Adaptive Sorting, and Compressed Permutations*.

10.20-10.40: Philip Bille and Inge Li Gørtz. *Substring Range Reporting*.

10.40-11.00: Takanori Yamamoto, Hideo Bannai, Shunsuke Inenaga and Masayuki Takeda. *Faster Subsequence and Don't-Care Pattern Matching on Compressed Texts*.

11.00-11.30: *Coffee break*

CPM and Computational Biology II (Chair Max Alekseyev)

11.30-11.50: Yassin Refahi, Etienne Farcot, Yann Guédon, Fabrice Besnard, Teva Vernoux and Christophe Godin. *A Combinatorial Model of Phyllotaxis Perturbations in Arabidopsis thaliana*.

11.50-12.10: Laurent Bulteau, Guillaume Fertin, Minghui Jiang and Irena Rusu. *Tractability and Approximability of Maximal Strip Recovery*.

12.10-12.30: Michalis Christou, Maxime Crochemore, Costas S. Iliopoulos, Marcin Kubica, Solon P. Pissis, Jakub Radoszewski, Wojciech Rytter, Bartosz Szreder and Tomasz Walen. *Efficient Seeds Computation Revisited*.

12.30-12.50: Domenico Cantone, Salvatore Cristofaro and Simone Faro. *Efficient Matching of Biological Sequences Allowing for Non-Overlapping Inversions*.

13.00: *Lunch*

Trees and Graphs (Chair Giosuè Lo Bosco)

15.00-15.20: Jesper Nielsen. *A Coarse-to-Fine Approach to Computing the k-best Viterbi Paths.*

15.20-15.40: Riccardo Dondi, Guillaume Fertin and Stéphane Vialette. *Finding Approximate and Constrained Motifs in Graphs.*

15.40-16.00: Kouichi Hirata, Yoshiaki Yamaoto and Tetsuji Kuboyama. *Improved MAX SNP-Hard Results for Finding an Edit Distance between Unordered Trees.*

16.00-16.20: Michael Elberfeld, Danny Segev, Colin R. Davidson, Dana Silverbush and Roded Sharan. *Approximation Algorithms for Orienting Mixed Graphs.*

16.20-16.50: *Coffee break*

Classic String Matching III (Chair Gregory Kucherov)

16.50-17.10: Stéphane Gosselin, Guillaume Damiand and Christine Solnon. *Frequent Submap Discovery.*

17.10-17.30: Tamar Pinhas, Dekel Tsur, Shay Zakov and Michal Ziv-Ukelson. *Edit Distance with Duplications and Contractions Revisited.*

17.30-17.50: Marek Cygan, Marcin Kubica, Jakub Radoszewski, Wojciech Rytter and Tomasz Walen. *Polynomial-Time Approximation Algorithms for Weighted LCS Problem.*

17.50-18.10: Raphaël Clifford, Zvi Gotthilf, Moshe Lewenstein and Alexandru Popa. *Restricted Common Superstring and Restricted Common Supersequence.*