

KUBIC-NII Joint Seminar on Bioinformatics 2013

organized by
Bioinformatics Center, Institute for Chemical Research, Kyoto University and
National Institute of Informatics

Date

Friday, April 19, 2013

Venue

Kyoto University, Uji, Kyoto 611-0011, Japan
Bioinformatics Center, Institute for Chemical Research,
3F, Seminar Room CB316.

Access

- [Location and Transportation to Uji Campus of Kyoto University.](#)
- [Vicinity of Uji Campus.](#)
- [Uji Campus Map.](#)

Participants (alphabetical)

Tatsuya Akutsu	Institute for Chemical Research, Kyoto University, Japan
Earl Bellinger	Indiana University Bloomington, USA
J.B. Brown	Graduate School of Pharmaceutical Sciences, Kyoto University, Japan
Morihiro Hayashida	Institute for Chemical Research, Kyoto University, Japan
Katsumi Inoue	National Institute of Informatics, Japan
Jesper Jansson	The Hakubi Project, Kyoto University, Japan
Hitoshi Koyano	Institute for Chemical Research, Kyoto University, Japan
Morgan Magnin	Institut de Recherche en Communications et Cybertétique de Nantes (IRCCyN), École Centrale de Nantes, France
Avraham Melkman	Ben-Gurion University of the Negev, Israel
Tenda Okimoto	Transdisciplinary Research Integration Center, Japan
Tony Ribeiro	The Graduate University for Advanced Studies (SOKENDAI), Japan
Alexandre Rocca	Grenoble INP Ensimag, France
Adrien Rougny	University Paris-Sud, France
Takeyuki Tamura	Institute for Chemical Research, Kyoto University, Japan

Programme

9:30 - 10:00	Opening
10:00 - 10:20	Tatsuya Akutsu A Dominating Set Approach to Controllability of Scale-free Networks.
10:20 - 10:50	J.B. Brown Drug discovery and the need for new post-ligation downstream network analysis algorithms incorporating contextualization.
10:50 - 11:10	Avraham Melkman Nested canalyzing SAT-formulae and their satisfaction.
11:10 - 11:20	Break

11:20 - 11:40	Katsumi Inoue*, Tony Ribeiro, Chiaki Sakama Learning from Interpretation Transition and its Applications to Boolean Networks and Cellular Automata.
11:40 - 12:00	Tony Ribeiro*, Katsumi Inoue, Chiaki Sakama Learning from Interpretation Transition Using an Efficient OBDD-Like Structure.
12:00 - 13:30	Lunch
13:30 - 14:00	Morgan Magnin*, Maxime Folschette, Katsumi Inoue, Loic Pauleve, Olivier Roux, Olivier Roux, Gilles Bernot, Jean-Paul Comet, Adrien Richard Inference in Biological Regulatory Networks: From Discrete Parameters to Timing Information.
14:00 - 14:20	Jesper Jansson Computing the Rooted Triplet Distance between Galled Trees by Counting Triangles.
14:20 - 14:40	Hitoshi Koyano Probability theory on the monoid of strings and its application to molecular ecology.
14:40 - 15:00	Coffe Break
15:00 - 15:20	Morihiro Hayashida Predicting protein-RNA residue-base contacts using two-dimensional conditional random field with the lasso.
15:20 - 15:40	Adrien Rougny*, Christine Froidevaux, Katsumi Inoue, Yoshitaka Yamamoto Translating the Systems Biology Graphical Notation to Logic.
15:40 - 16:00	Takeyuki Tamura On the complexity of the maximum common subgraph problem for partial k-trees of bounded degree.
16:00 - 16:20	Coffe Break
16:20 - 16:40	Alexandre Rocca*, Morgan Magnin, Katsumi Inoue CTL and ASP for Model-Checking of Biological Boolean Networks.
16:40 - 17:00	Earl Bellinger*, Hei Chan, Katsumi Inoue Asynchronously Updated Elementary Cellular Automata with Random Perturbations.
17:00 - 17:20	Tenda Okimoto* and Katsumi Inoue A Study for Multi-Objective Distributed Constraint Optimization.

Contact

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