

MAGE, Models and Algorithms for Genome Evolution, August 24-26 2013

The MAGE conference was held at Hotel Chateau-Bromont, in Bromont, in beautiful Eastern-Townships, in Québec. It gathered a diverse audience of 80 graduate students, post-doctoral fellows, young and senior faculty with backgrounds in mathematics, statistics, computer science, and life sciences, including some of the most prominent computational biologists of the last thirty years, such as Gene Myers, Ron Shamir or Pavel Pevzner.

It served well its intended purposes of reflecting on the past and future of computational comparative and evolutionary genomics, and to celebrate 50 years of scientific contributions by David Sankoff, a founding father of these fields. The program included 5 keynote talks by Gene Myers, Tandy Warnow, Joseph Nadeau, Pavel Pevzner and Ron Shamir, 3 short talks celebrating various aspects of David Sankoff's career, by Anne Bergeron, Joe Felsenstein and Jotun Hein (the last two were given from away by video), 16 contributed talks, all given by well established researchers and presenting either surveys of important topics or perspectives on recent results and future directions, and finally two lively poster sessions featuring 30 posters. Moreover, all along the three days the conference lasted, the cozy environment of the Hotel Chateau-Bromont favored informal small groups discussions on a variety of topics, that are likely to have served as starting points of several research collaborations.

The topics that were discussed in the talks ranged from very theoretical ones to very applied. Among the highlights of the conference, the very first keynote talk, by Gene Myers, described the mathematical questions that he investigated in order to design, in the mid-1980s, the BLAST (Basic Local Alignment Search Tool) software that is still today the most used tool to mine the NCBI sequences databases. This provided a new light on BLAST that showed the impact of mathematical research on tools that are now used by most life scientists on a daily basis. Along the same lines, Pavel Pevzner showed in his keynote talk that models of graphs initially developed for different purposes, breakpoint graphs (used to compute genomic distances) and de Bruijn graphs (used in genome assembly), share striking similarities, an observation that might have an important impact to integrate genome assembly and evolutionary genomics. At the other end of the spectrum, Joseph Nadeau presented fascinating applied results on the impact of epigenetic heritage in the adaption to disease causing conditions, that showed clearly the need to integrate epigenetic in evolutionary studies, a problem that is likely to generate several fundamental mathematical and computational questions in the very near future.

All along the four days, keynote and contributed talks reminded the audience of the lasting impact of the work of David Sankoff in many fields of computational biology, especially in establishing fundamental techniques such as dynamic programming, or developing the field of genome rearrangement algorithms.

The MAGE conference also included the release of a book published by Springer in the «Computational Biology» series, that is now available on Springer website and contains 14 chapters written by participants to the conference, offering both a retrospective view on the development computational genomics, its current achievements, and challenges the field will likely meet in the near future.

Cedric Chauve, Department of Mathematics, Simon Fraser University, October 7, 2013.