Proceedings of the "Bamako 2009 Conference on the Bioinformatics of Infectious Diseases" - Editorial

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Editorial

Bamako 2009 Conference on the Bioinformatics of Infectious Diseases

The International Society for Computational Biology (ISCB) and the African Society for Bioinformatics and Computational Biology (ASBCB) teamed up to organize a major meeting in Africa (30 November–3 December 2009) focused on the "Bioinformatics of Infectious Diseases: Pathogens, Hosts and Vectors". The meeting, held in Bamako (Mali), was a new ISCB and ASBCB venture and a follow-up of the 2007 ASBCB meeting in Nairobi (special issue of *Infection, Genetics and Evolution*, 2009, 9(3)). The Mali event was hosted by the Malaria Research and Training Center, an internationally recognized facility for malaria research in Western Africa. Although the meeting had an obvious African focus, it aspired to become a full-fledged international event, encompassing scientists and students from institutions in the US, Latin America, Europe and Africa. One of our main goals since the outset was to stimulate local efforts for cooperation and dissemination of leading research techniques to combat major African diseases.

The meeting was able to provide 40 full travel fellowships, mainly to African students, thanks to the support of KAUST, CNRS, The Wellcome Trust and ISCB. A world-class Scientific Committee evaluated submissions and carefully selected abstracts for oral or poster presentation. A total of 37 oral presentations and 47 posters were shown at the conference (the distribution of accepted presentations by country is displayed in Fig. 1). Awards were given to the best presentation of the day and the best poster.

1. Conference program and papers selected for this special issue

The meeting consisted of a four-day conference followed by two days of practical workshops. The first three days of the meeting
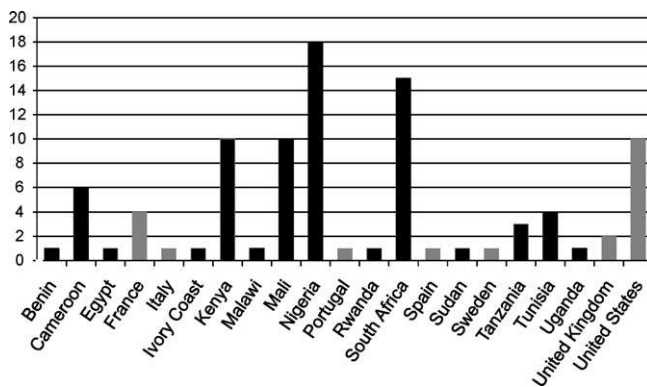
Fig. 1. Distribution of accepted presentations by country.

included six keynote presentations by international invited speakers:

- Charles Rotimi (Director of the Center for Research on Genomics and Global Health, US): "Engaging African scientists in the genomic revolution to ensure that tomorrow's biotechnology and medicine will work for African people"
- Erik Bongcam-Rudloff (Chair of EMBNet Board, Uppsala University, Sweden): "Annotating next-sequencing data: new opportunities for worldwide collaborative work"
- Burkhard Rost (Columbia University, US): "Evolution teaches protein prediction"
- Karine Leroch (University of California Riverside, US): "Unraveling gene regulation mechanisms in the human malaria parasite: insights into chromatin remodeling"
- David Roos (University of Pennsylvania, US): "Designing and mining pathogen genome databases"
- Mike Tartakovsky and Yentram Huyen (NIAID, US): "Building a sustainable bioinformatics program"

The last day of the conference was a dedicated KAUST day focusing on "Systems view of biological organisms". Workshops were given by Jeff Skinner and Sudhir Varma: "Microarray analysis using R and Bioconductor", David Roos: "PlasmoDB", Erik Bongcam-Rudloff: "Sequence analysis using EMBOSS", Christine Orengo: "Structural Bioinformatics", and Neil Lobo and Karyn Megy: "VectorBase".

Abstracts selected for oral presentation were invited to submit full papers for this special issue. Submitted papers underwent an independent review process carried out by *Infection, Genetics and Evolution* before acceptance for this issue. Here we briefly introduce accepted papers classified according to the session in which they were presented at the conference.

- *Functional, structural and comparative genomics of pathogens*

    Ghouila et al. presented EuPathDomains, an extended database of protein domains belonging to ten major eukaryotic human pathogens (including Plasmodium, Leishmania and Trypanosomes) along with the gene ontology functional annotations derived from these domains.
- *Search and design of vaccines and drugs*

    Fatumo et al. aimed at predicting new drug targets in silico. To achieve this goal, several automatically inferred metabolic networks and enzyme sets were compared using a comprehensive list of known drug targets for *Plasmodium falciparum*.

- *Host/pathogen systems biology*

   The paper by Ponts et al. discussed the mechanisms involved in gene regulation of *Plasmodium falciparum* and the relationships between nucleosome positioning and gene regulation. New results were shown on the mechanisms whereby a transcriptionally permissive organization of chromatin can control the parasite's progression through its life cycle. Mazandu et al. created an interactome network for *Mycobacterium tuberculosis* using microarray data, proposing a novel method for generation of organism-level co-expression networks.

- *Database and resource development for infectious disease research*

   Kwofie et al. presented Dragon, a comprehensive biomedical text-mining based online web resource for hepatitis C virus (HCV). ~30,000 PubMed abstracts were processed to enable retrieval of information related to HCV using specific concepts, keywords and phrases.

- *Molecular epidemiology and evolution of vectors, pathogens and hosts*

   Mwangi et al. analyzed in detail immune-related CLIP domain serine proteases in *G. morsitans* (tsetse flies), establishing its evolutionary relationship in other host species. They found that in a similar way to *D. melanogaster*, *G. morsitans* does not contain expansions in their CLIP-domain serine protease and serpin families, which could explain the low prevalence of infection by trypanosomes. Sharakhova et al. present a high resolution cytogenetic map for *Anopheles nili*, one of the major (but neglected) malaria vectors. Population analysis of *An. nili* females collected in Burkina Faso revealed the presence of two highly polymorphic inversions on the 2R chromosomal arm. Comparative mapping suggests that *An. nili* is, at least, as diverged from *An. gambiae* as *An. stephensi*.

- *Bioinformatics education*

   Ojo et al. reviewed the meaning, history and development of bioinformatics worldwide, with a focus on prospects and challenges facing bioinformatics education. They also provided an overview of efforts performed to introduce bioinformatics in Nigeria, suggesting strategies for effective education in this complex multidisciplinary domain.

The last day of the conference or KAUST day had two sessions on "Systems views of biological organisms". Several presentations were selected from this day for papers in this issue. Adebiyi et al. computationally identified two signalling pathways of interest that may have an effect on *Plasmodium falciparum*'s resistance to chloroquine and an additional pathway that may be involved in the start of red blood cell invasion signalling. Baber et al. described a Python module that normalizes microarray data by the quantile adjustment method for visualization. This software is able to display data before and after normalization and to subtract background noise before normalization. Guedira et al. predicted in silico the regulatory network of Leishmania-infected human macrophages. Based on this construction, they identified the key role the Irak1 pathway has in their gene expression regulation. Cho-Ngwa et al. presented several antigens with diagnostic potential for Onchocerciasis, among which OV1FC may offer great promise as a marker candidate.

2. Inauguration of five African Regional Student Groups

Regional Student Groups (RSGs) are a very active part of both ISCB and ASCB. Initially they were set up as part of an ISCB Student Council to serve the local needs and interests of specific geographical regions. An RSG Africa was inaugurated in 2007 at the Conference on "Bioinformatics of African Pathogens and Vectors" in Nairobi, Kenya. Since then, the number of student members for this RSG steadily grew to reach more than 500 members including many countries on the African continent. At Bamako RSG Africa split into five new RSGs divided according to their geographical location in the African continent: Eastern, Western, Southern, Northern and Central countries. Forming part of any RSG does not require any formal membership to ISCB or ASBCB. This free approach of commitment has been pivotal in Africa for the involvement of students who otherwise would not be able to afford a society membership and would thus be impaired from participating in the local developments of their nascent bioinformatics community.

3. Conclusion

The ISCB Africa ASBCB Joint Conference on "Bioinformatics of Infectious Diseases: Pathogens, Hosts and Vectors" provided an international forum for discussion and fostering of potential new collaborations at the heart of Africa. We believe that by bringing the science to this continent we were able to encourage the development of this nascent field in Africa. We also hope that this opportunity was a key event for promoting effective networking and research initiatives involving groups based on this continent. A key objective for the conference organizers was to provide opportunities for improving regional training by sharing techniques and relevant material on the Bioinformatics of Hosts, Pathogens and Vectors. The two days of workshops for students and trainers were specifically designed to spread as much as possible technical expertise and knowledge directly from leading scientists. The meeting was set up to enable an optimal venue for nurturing new links between young and emerging scientists from Africa. The launching event for five new Regional Student Groups was extremely well attended by not only students, but also senior international scientific figures.

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