Proceedings of the “Bamako 2009 Conference on the Bioinformatics of Infectious Diseases” - Editorial
Manuel Corpas, Seydou Doumbia, Olivier Gascuel, Nicola Mulder

To cite this version:
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 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
  
  Ghoulia 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* (tsetsse 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 nilli*, one of the major (but neglected) malaria vectors. Population analysis of *An. nilli* females collected in Burkina Faso revealed the presence of two highly polymorphic inversions on the 2R chromosomal arm. Comparative mapping suggests that *An. nilli* is, at least, as diverged from *A. gambiae* as *A. 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. discussed the mechanisms involved in gene regulation of *Plasmodium falciparum* and the relationship 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.

3. Conclusion

The ISCB Africa ASCB 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.

Steering Committee

Manuel Corpas (co-chair), Nicola Mulder (co-chair), Seydou Doumbia (co-chair), Ezekiel Adebiyi, Alia Benkahlia, Segun Fatumo, Olivier Gasuel, Winston Hide, Janet Kelso, Daniel Masiga, BJ Morrison McKay, Burkhard Rost

Scientific Committee

Ezekiel Adebiyi, Alia BenKahla, Manuel Corpas, Appolinaire Dijkeng, Olivier Gasuel, Winston Hide, Raphael Isokpehi, Bo Jin, Beatrice Kiel, Daniel Masiga, Nicola Mulder, Julia Ponomarenko, Burkhard Rost, Reinhard Schneider, Anna Tramontano

Fundraising Committee

Alia Benkahlia (chair), Manuel Corpas, Appolinaire Dijkeng, Seydou Doumbia, Olivier Gasuel, Daniel Masiga, BJ Morrison McKay, Nicola Mulder, Guilherme Oliveira, Sheila Ommeh, Burkhard Rost, Reinhard Schneider

Student Committee

Arun Gupta, Sheila Ommeh, Kavisha Ramdayal

Acknowledgements

We are grateful to the Malaria Research and Training Center, the Faculty of Medicine of University of Bamako, the National Agency of Telemedicine and Medical Informatics of Mali (ANTIM), the Government of Mali and its Ministry of Health, KAUST, EMBnet, the Centre National de la Recherche Scientifique (CNRS), the Office of...
Cyber Infrastructure and Computational Biology of NIAID, US Embassy in Bamako, Wellcome Trust and SANBI for their generous support.

Manuel Corpas Guest Editor
Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK

Seydou Doumbia Guest Editor
Malaria Research and Training Center, University of Bamako, Mali

Olivier Gascuel Guest Editor*
Méthodes et algorithmes pour la Bioinformatique, LIRMM, CNRS – Université Montpellier 2, France

Nicola Mulder Guest Editor
Computational Biology Group, Dept Clinical Laboratory Sciences, University of Cape Town, South Africa

*Corresponding author.
E-mail addresses: mc@manuelcorpas.com (M. Corpas)
sdoumbi@icermali.org (S. Doumbia)
gascuel@lirmm.fr (O. Gascuel)
Nicola.Mulder@uct.ac.za (N. Mulder)