

agement of bollworm resistance in *Bt* cotton. He proposed a stochastic model 'Bt-adapt' to trace the resistance development in *H. armigera* over the generations against *Bt* cotton. V. Kalia highlighted the importance of refuges for IRM in *Bt* cotton. R. N. Padaria presented the *ex ante* assessment on adoption and socio-economics of *Bt* cotton in India.

The third technical session was chaired and co-chaired by D. Russel and S. Mauria respectively. Shantaram elaborated the global overview of the biosafety and environmental impacts of GM

crops expressing *Bt* genes. He also traced the history of biosafety aspects of genetically modified organism (GMO) in USA. Mauria highlighted the Indian regulatory system on GM crops. A. Raybould discussed the probability aspects of regulatory decision making for transgenic crops. In the last lecture, Manjunath covered the safety and benefits of *Bt* and *Bt* cotton in India.

Swapan K. Datta conducted the panel discussion and valedictory session. The panel discussed the issues related to release of *Bt* crops after the success of *Bt*

cotton in India. The panelists and the participants of the session were more concerned about the delay in regulatory approvals of *Bt* crops in India and suggested possible ways and means to convince the anti-GMO activists in deployment of GM crops.

Akshaya K. Biswal, S. M. Balachandran, A. P. Padmakumari, M. Mohan and B. C. Viraktamath*, Directorate of Rice Research, Rajendranagar, Hyderabad 500 030, India.

*e-mail: pdrice@drircar.org

MEETING REPORT

Influence of virtual conferences on bioinformatics in India and developing nations*

Geographically, the Indian subcontinent is nearly the size of the United States or Western Europe, but there are very few conventional conferences organized there for bioinformatics. Additionally, the on-site conferences that do exist require prohibitively expensive overhead charges, which include the costs of the venue, labour, and providing accommodations for speakers invited from other countries. With the internet burgeoning and online networking becoming commonplace, it seemed feasible that a virtual conference on bioinformatics would work in India. And, even though the bandwidth and network stability needed for an online conference would be much better in Western nations, the advantages in cost, time and energy savings were thought to outweigh the potential technical difficulties. For example, the venue would save time and money for participants, particularly students, who are not always, provided travel grants. Furthermore, it was apparent that the techniques that would be employed to overcome these challenges could be utilized elsewhere in India for virtual meetings and conferences.

Recently, the first Indian Virtual Conference on Bioinformatics 2010 (Inbix'10) was well-received by the student and scientific community across India.

To our best knowledge, this was the first time that a virtual conference on bioinformatics was organized for an Indian audience, featuring talks through online video that was streamed as well as pre-recorded. On day one, the conference began with a keynote presentation from G. P. S. Raghava (IMTECH, Chandigarh) on protein secondary structure prediction. Raghava threw light on various computational protein structure prediction methods and illustrated the structure and fold prediction tools APSSP2, BetatPred2, GammaPred and AlphaPred, which their group developed. Raghava's talk was well-received, even as the audience tried to become acclimated to being virtual attendees. The talk was followed by a presentation given by Tin Wee Tan (National University of Singapore, Singapore), on how sequence diversity in emerging infectious agents can be used for rational vaccine design and for developing other diagnostic tools. The case study was carried out on West Nile Virus, wherein Asif M. Khan and Tan found conserved sequences that are immune-relevant. The talk was complemented by several questions from the audience, and Tan gracefully answered all the questions posed. He further concluded that the same protocol could be extended to other viruses.

The second session of the day began with a talk by Shoba Ranganathan (Macquarie University, Australia) on the role of the Asia Pacific Bioinformatics Network (APBioNet.org) and the impact it

has made in the region. In the pre-recorded version of her talk, she points the need for cloud computing and open-source software (e.g. Knoppix Linux) to accelerate research and education in the biological sciences. According to Ranganathan, the impact that these open-access tools make would first reach the field of systems biology. Tan, who is also involved with APBioNet, then answered several questions about the organization and discussed the issues and initiatives being worked on by the APBioNet team. One of the much awaited topics in Inbix'10 was the talk on 'Virtual embryo: HTS data to multicellular models' by Thomas Knudsen (US Environmental Protection Agency, USA). His presentation resulted in some interesting discussions online, especially on developing mathematical models for the simulation of multicellular virtual tissues. The work that was described aimed to test the toxicity of chemical substances on 'virtual tissues', consequently expediting the process of drug discovery as a cost-effective tool. Russell Thomas' (The Hamner Institute, USA) pre-recorded talk then explored the use of genomic expression data and metabolite pathway information to predict the 'tumorigenic potential of chemicals'. The work, which was presented from the Hamner Institute, involved statistical techniques, machine learning and clustering techniques as well as K-means clustering, RBF function, PLS, etc. to find genetic signatures used as biomarkers for the detection of

*A report on the first 'Indian Virtual Conference on Bioinformatics' held during 12-13 February 2010. The symposium was organized by Bioclues and the Bioinformatics Organization.

carcinogenicity. Thomas' talk was complemented by David Reif's (National Centre for Computational Toxicology, EPA, USA) on developing 'a computational framework for the profiling and prioritization of environmental chemicals'. Their group has developed a software tool for predicting the toxicity of chemicals by taking several descriptors from multiple sources, such as chemical properties, pathway data, *in vivo* and *in vitro* data, etc. Their system, as described, deals with multiple data from several sources but with a systematic prioritization scheme, the authors have developed a framework with a highly accurate decision making kernel. The questions raised were answered by his collaborator, Amar Singh.

The last talk of the day was by Søren Brunak (Denmark Technical University). A full house attended the talk, which was on 'a large-scale analysis of tissue-specific pathology and gene expression of human disease genes'. Brunak couldn't make it for the live presentation, and so his pre-recorded talk was aired. The talk was on creating, annotating and analysing a pool of genetic data pertaining to human disease and the pathways associated with these genes.

The second day kicked off with a quick recap of day one, followed by Anshu Bhardwaj's talk on 'Open source

drug discovery (OSDD) – an open collaborative drug discovery model for tuberculosis'. She focused on the OSDD, emphasizing on the models developed for tuberculosis. The process of joining the OSDD for budding graduates was discussed, and she mentioned how the growth of these groups has increased in the last couple of years.

This was followed by the 'virtual poster session'. For this session, each poster was displayed on screen for four minutes and was open for discussion. The attendees were asked to contact the poster authors for further discussions using a dedicated forum at bioinformatics.org. The poster session was then followed by a group discussion, which was observed by over 20 participants. The topic was 'Bioinformatics to systems biology in India: grand challenges; how to improve bioinformatics skills to match the expectations of the international community', and it was moderated by Andrew Lynn (Jawaharlal Nehru University, New Delhi) with the help of Raghava.

With Indian graduate students and scientists currently experiencing a great deal of exposure to the discipline via the internet, most of the student communities unlike the Western nations seldom get a chance to interact with distinguished scientists in real-time. With this event, we

have shown how a virtual conference can be organized with low-cost logistics and how such conferences can become a promising enterprise. MegaMeeting.com was used to host the speaker presentations as well as the hubs, while the free service Livestream.com was used to stream the video from MegaMeeting.com and other sources. Such virtual conferences can experience some technical glitches, and Inbix'10 was no exception, but there is promise that in time we will learn to overcome them.

It is in fact a part of the function of education to help us escape, not from our own time – for we are bound by that – but from the intellectual and emotional limitations of our time.

– T. S. Eliot

Prashanth Suravajhala* and **Jeffrey W. Bizzaro**, Bioinformatics Organization, Hudson, Massachusetts, USA; **Pritish Varadwaj**, Bioinformatics Division, Indian Institute of Information Technology, Allahabad 201 301, India; **Tiratha Raj Singh**, School of Biotechnology, and **Arun Gupta**, School of Computer Science and Information Technology, Devi Ahilya University, Indore 452 001, India.

*e-mail: prash@bioclues.org

Toads as astrologers of earthquakes

Toads can foretell earthquakes by changing their behaviour, suggests a research article published in the *Journal of Zoology*¹. Rachel Grant and Tim Halliday of The Open University, UK carried out this research at L'Aquila, Italy in 2009. According to this study, five days prior to the earthquake of magnitude >4.5, activity of male common toads (*Bufo bufo*) in the breeding sites declined by 96%. This pattern persisted for 10 days after the earthquake in the breeding site, which was 74 km from the epicentre. Even breeding pairs (both male and female together in amplexus) responded similarly, with 100% decline on the day of earthquake. There was no egg laying process (spawning) during the earthquake period.

Researchers correlated the change in toads' behaviour to perturbations in the ionosphere due to large earthquakes.

Ionosphere is the uppermost electromagnetic layer of the atmosphere, between 85 and 600 km from the ground, ionized by solar radiation. Perturbations in the ionosphere due to earthquake are detected at very low frequency and the low frequency electromagnetic signals emitted by them.



Common toad (*Duttaphrynus melanostictus*).

Although there are anecdotal reports on response of animals (be it ant, spider, fish, birds or mammals) to earthquakes. For rarity and unpredictability of earthquake events, this particular study is perhaps the only one specifically monitoring the effects before, during and after the earthquake and that too in amphibians. More importantly, toads can be used as a form of earthquake early warning system.

1. Grant, R. A. and Halliday, T., *J. Zool.*, 2010, 1–9.

K. V. Gururaja, Centre for Infrastructure, Sustainable Transportation and Urban Planning, and Centre for Ecological Sciences, Indian Institute of Science, Bangalore 560 012, India.
e-mail: gururajakv@gmail.com