

Emerging Technology Workshop (Genomics)

18:30-21:00, 2010, July 20

- 19:00-19:10** ***A Few Words About Technology***
Chai-Shian Kua
Co-chair, XTBG - Chinese Academy of Sciences
- 19:10-19:25** ***GenStat Analysis Package***
Liz Jupe
Sponsor, VSN International Ltd., GenStat
- 19:30-19:45** ***1000 Plant and Animal Reference Genome Project***
Yang Bicheng
Sponsor, BGI-Shenzhen
- 19:50-20:10** ***Emerging Trends In Advanced DNA Technology, From Cytometry To Gen3 Sequencing, And How These Can Be Anticipated and Adopted By Tropical Biologists***
David Galbraith
Invited Speaker, University of Arizona
- 20:15-20:35** ***Now-gen DNA Sequencing Technologies And Their Application In Tropical Biology***
Chuck Cannon
Co-chair, XTBG-Chinese Academy of Sciences,
Texas Tech University
- 20:40-21:00** ***Open Discussion***
Cannon

Abstracts:

Liz Jupe (VSN International Ltd., GenStat) :

GenStat analysis package

VSNi believe that research is central to understanding the world's major biological challenges and that the researcher's ability to fund the right tools should not be wealth driven. Man's demands on land, sea, environment continue to grow, placing significant pressure on food production, ecosystems, our climate's predictability and man's way of existence. Our aim is to support all bioscientists, researchers, farmers and agriculturists in their work, even those with no budget, through our successful GenStat for Teaching and GenStat Discovery programmes. GenStat for Teaching is free to educators and students across the globe. GenStat Discovery is provided free to not-for-profit research organisations, charities and educational institutes based in the developing world. In all, every student worldwide, and all but commercial organisations from the world's 101 less wealthy countries, can access first world menu-driven analysis tools absolutely free. VSNi is a prime supplier of data analysis software for the biological and life sciences markets worldwide. We were formed in 2000 as a spin off from Rothamsted Research (RRES) and the Numerical Algorithms Group(NAG). We are backed by UK government through RRES being the largest land-based research institute in the UK and arguably the original home of statistics in biology. As a result we are uniquely placed to provide statistical software to the agricultural and wider biology markets. Our ethos is collaboration and partnership, ingrained within our psychology from our government links.

Yang Bicheng (BGI-Shenzhen, China):

1000 plant and Animal Reference Genome Project

Next-generation DNA sequencing technologies provide ultra-high throughput at a substantially lower cost; however, the data is presented in very short read-length sequences, making de novo assembly extremely challenging. BGI has developed a novel method for de novo assembly of large genomes from short-read sequences and successfully assembled the panda (2.7Gb), cucumber (367Mb), Chinese cabbage (500Mb), and potato (830Mb) genomes. The development of this de novo short-read assembly method creates new opportunities for building reference sequences and carrying out

accurate analyses of unexplored genomes in a cost effective way. Empowered by the capacities, BGI announced the “1000 Plant and Animal Reference Genomes Project” (idl.genomics.org.cn) in January and calls for collaborations from all over the world with the aim to generate reference genomes of a thousand economical and scientific important plant/animal species in two years.

Unraveling whole genome sequences of a species will tremendously accelerate basic research, increase knowledge on the functions of important genes, and facilitate their applications and manipulations. Genetic variations and evolutionary process can be identified through comparative analysis of population and individuals, and finally lead to huge impacts on scientific discoveries and society development.

David Galbraith (University of Arizona):

Emerging trends in advanced DNA technology, from cytometry to Gen3 sequencing, and how these can be anticipated and adopted by tropical biologists.

Advances in microelectronics and computing have revolutionized many scientific fields and disciplines. In general, these advances are a consequence of the validity of “Moore’s Law”, which posited, back in 1965, that the number of transistors that can be placed on an integrated circuit doubles approximately every two years. This exponential trend has persisted for the last 45 years, and its end is not immediately expected. A corollary of Moore’s Law is that computing performance per unit cost increases exponentially, with a similar doubling time.

In biological instrumentation, the impact of Moore’s Law has been particularly noticeable in the areas of DNA sequencing and cytometry. In the first case, the ability to generate, archive, and computationally process DNA sequences has followed exponential increases in sequence production, and corresponding decreases in cost per unit sequence. In the second case, advances in computing power have resulted in a radically decreased physical footprint for cytometers with, at the same time, an increase in performance specifications.

Advances in computational power combined with additional advances in electronics (particularly lasers and light steering and harnessing hardware), and with advances in chemistry and biology of light detection and

transduction (particularly fluorescence-based molecules), has led to an explosion of data in the form of high-throughput analysis of biological organisms, again with exponentially decreasing costs per unit information.

This talk will describe advances in DNA sequencing and cytometric technologies, indicate future trends, describe applications that employ these technologies, and offer suggestions as to how they might best be integrated into Tropical Conservation Biology programs.

Chuck Cannon, (XTBG-CAS, Texas Tech Univ.)

Now-gen DNA sequencing technologies and their application in tropical biology

The development of cheap genomic-level DNA sequencing technology has continued to accelerate over the past few years, promising a radically new perspective on genetics. Biodiversity is one of the great advantages (and challenges) we face as hopeful tropical genomicists. We can make use of this feature of tropical communities to perform powerful comparative studies of closely related species that vary phenotypically or geographically in compelling ways. In this presentation, I will review various analytical techniques and research programs which can bring this technological revolution to the tropics. These examples range from the identification of DNA fingerprints to control and manage the international trade in tropical timbers to whole genomic comparisons among major lineages for patterns in their diversification and similarity. The most obvious concern about this technology is what will we do with all of this data and how can it best be employed for conservation and basic research. The presentation will end with an open discussion about the future of tropical genomics.