

The Canadian Bioinformatics Resource For Industry (CBRi) presents:

Bioinformatics of Virus Genomes

ABOUT THE COURSE

This hands-on tutorial will provide participants the ability to use bioinformatics software developed for the management and analysis of the DNA/Protein sequences in complete genomes. The focus will be on large viral genomes such as poxviruses and herpesviruses, but the approach is also applicable to bacterial genomes. Upon completion, participants will be able to use readily available bioinformatics software tools for the analysis of viral and bacterial genomes. In addition, they will also be instructed on how to use this software in more advanced ways than commonly used. These tools for sequence data management and analysis have been designed specifically to be user friendly with simple graphical interfaces.

WHO CAN BENEFIT?

- Biotechnology professionals and managers seeking an applied introduction to new user friendly tools for studies using the large amount of data contained in complete genomes
- Researchers interested in expanding their work into the area of bioinformatics of virus and bacterial genomes
- Research technologists, research assistants and graduate students wishing to apply bioinformatics tools to enhance their research and laboratory expertise
- Computer professionals wishing to expand their skills and experience into the growing field of bioinformatics

COURSE CONTENT

When you have completed this course you will have learned a wide variety of topics and subjects including:

- The importance of specialized tools for analyzing virus genomes
- Problems encountered in dealing with a large number of complete virus genomes
- Introduction to software tools: Virus Orthologous Clusters (VOCs), Virus Genome Organizer (VGO), Jdotter, Base-By-Base (BBB), ReHAB, Genome Fingerprint Scanner (GFS)
- Comparisons of large genomes
- Genome Alignment; Searching for distant homologs; Motif searches in VOCs and BBB
- Use of dbEST: database of "Expression Sequence Tags"

ABOUT THE INSTRUCTOR

Dr. Upton is a Virologist in the Department of Biochemistry & Microbiology at the University of Victoria. He is leading the bioinformatics project, *VirGO*; an ongoing investigation aimed at improving the representation of complete viral genomes and the data resulting from database searches. A significant portion of his research involves poxvirus bioinformatics. This includes identification of poxvirus genes with the aid of database search techniques, evolution of poxvirus genomes, and the development of software for the analysis of poxvirus genomes. More recently, he has been developing bioinformatics resources for the SARS Coronavirus, Herpesviruses, Baculoviruses and Adenoviruses.

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COURSE FEE

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Early Bird Discount offered to those who register by Feb. 16, 2005.	\$495.00 (plus GST)
Student Fee	\$395.00 (Plus GST)
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To better gauge the experience of registrants in order to ensure the course suits your background, please attach a brief summary that describes your bioinformatics experience or level.