



presents Guest Speaker :

Jason Stajich

Dept of Molecular Genetics and Microbiology, Duke University

BioPerl: The evolution of a bioinformatics toolkit □

The BioPerl toolkit has become an invaluable tool for bioinformatics data processing. The project, first started in 1995, has grown and matured over the years and now serves as key components in many bioinformatics tools from simple data parsing scripts in a lab to the Generic Genome Browser. The toolkit provides support for analyses from population genetics to molecular evolution, BLAST parsing to accessing raw sequence traces, querying GenBank to relational databases for sequences and annotations. The project is open source which has allowed many different ideas to be integrated and for community ownership of the software. I'll speak to the experience of developing open source software with developer and user groups of many different experience levels.

Student Presentation (15 mins) :

Obi Griffith, Genome Sciences Centre (Jones lab)

Genomic island analysis: Improved software and insights into an apparent gene pool associated with genomic islands.

Chan Auditorium, CFRI, 4480 Oak St. at 28th

April 13, 2006, 3:30 pm

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