

Cornell University Computational Biology Services Unit



Cornell University's Computational Biology Service Unit uses Red Barn compute clusters to provide research, software and hardware support for computational biology applications.

The Customer: Dr. Jaroslaw Pillardy @ CBSU, Bioinformatics Facility

Computational Biology Service Unit is Cornell University's core facility for computational biology and bioinformatics. CBSU's mission is to provide research and computational support for life sciences research through training and research collaboration and to bring advanced computational tools and techniques to life sciences investigators. Since 2001, CBSU has been developing and maintaining a web-based interface to provide scientists in the field user-friendly and affordable access to a high-performance computing environment. Through the project BioHPC, researchers can log in from any computer and submit jobs to a suite of computational biology applications running on the CBSU compute clusters. Using the advanced computing resources available through BioHPC Computing Lab and BioHPC Web portal “[biologists] don't need to deal with parallel job submission, queues, clusters: knowing the application, parameters, and input is all that is required.”



The System: “...new large memory machines from Red Barn are used for memory intensive applications in bioinformatics...”

To keep up with CBSU's specialized computational demands, the unit's facility utilizes a platform based on Red Barn HPC servers each with 64 cores, 512GB of memory and 18TB of local storage. CBSU Director and Senior Research Associate since 2004, Jaroslaw Pillardy details some of the specific uses of the compute clusters:

“The new large memory machines from Red Barn are used for memory intensive applications in bioinformatics; the most demanding being de novo genome assembly from next-generation sequencing data. This application becomes more common with the advance of sequencing technologies and large memory machines are essential there. The Red Barn servers are also being used for wide array of other computations related to genetic diversity studies with next-generation sequencing data. In particular, the machines are used in our collaborative projects: genetic architecture of maize and teosinte; a systems approach to the development and function of C4 photosynthesis; high-resolution map of recombination in maize; accelerating grape cultivar improvement via phenotyping centers and next-generation markers, and many other small projects.”

Why Red Barn: Red Barn has been building HPC products for over 15 years, and has the experience and expertise to provide a solution for any size project.

Dr. Pillardy writes:

“Red Barn is our preferred source of high-end computing servers since it offers very affordable and highly configurable systems, coupled with excellent support in the server design stage. The people from Red Barn are very knowledgeable, friendly and helpful with all our questions and concerns. As a customer, I feel a personal connection with the company. We recommended Red Barn to several groups from Cornell University, all the systems purchased by us and others perform very well, and a few small problems were addressed fast and professionally by Red Barn staff.”

At Red Barn, we approach each project individually and design systems tailored to the customer's specific requirements. We work with our clients during every step from concept to completion to make sure every objective is met.

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