

New supercomputer to aid genomics research

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The National Center for Supercomputing Applications (NCSA) has gifted the Institute for Genomic Biology (IGB) a highly parallel shared memory supercomputer named Ember. Originally funded by the NSF, Ember will be managed by the High-Performance Biological Computing (HPCBio) group.

"We've been using Ember for a while now through the NCSA, mainly in computational genomics," said Victor Jongeneel, Director of HPCBio. "It can perform a lot of tasks that our existing systems just can't. Having it under our own management will allow us better access and faster results."

The Ember [computing system](#) has become part of the IGB biocluster, adding 1536 cores and eight terabytes of memory spread across four nodes.

Ember was installed in the server room at the IGB after its October 1st decommission by the NCSA. It would cost two million to purchase today, and is only two years old. Ember will be available to anyone on campus for a service fee, which will be placed in a fund to replace the infrastructure as it becomes dated.

For ease of use, Ember runs a Linux operating system, and can be used in many applications including chemistry, fluid mechanics, and imaging. However, its most called for use at the IGB will likely be in genomics and transcriptomics research.

Currently, the Carver Biotechnology Center sequences DNA in short segments of around 250 base pairs. These thousands of segments, however, overlap and are distributed randomly, making it difficult to see the "big picture" of the genome. Ember's very large shared memory—2 terabytes in a single system—will enable the applications to run much more efficiently as they organize and connect these segments, and has already facilitated several projects.

"It will be a wonderful addition to our research community," said Jongeneel. "In the past, some projects like these were left incomplete, or spent thousands of dollars on computer time. This will enable larger projects that we've had trouble with in the past, and easier [genome](#) and transcriptome assemblies."

Provided by University of Illinois at Urbana-Champaign

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