

How IRP Lab Tools and Biowulf Help Sequence the Human Genome

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[Biowulf](#), a high-performance computing resource managed and supported by the [High-Performance Computing Services](#) team (HPC) at the NIH's Center for Information Technology (CIT), is designed to help sequence large sets of biomedical data. The IRP's "I Am Intramural" Blog recently highlighted how Adam Phillippy, Ph.D., and his investigative lab team developed new computational tools to interpret the data generated by Biowulf [to help complete our genetic blueprints](#), and understand how different illnesses develop.

Dr. Phillippy is head of the Genome Informatics Section and a principal investigator in the [Computational and Statistical Genomics Branch at the National Human Genome Research Institute](#)(NHGRI).

Biowulf makes DNA sequencing faster and easier by allowing Dr. Phillippy and his team to focus on the accuracy of results produced by their algorithms as opposed to the efficiency of those algorithms.

"Biowulf is just a tremendous force multiplier for us," Dr. Phillippy told the IRP Blog. "There are things we can do here that we wouldn't be able to do if we were somewhere else, where we didn't have access to these analysis resources. One of my most pleasant surprises joining the NIH intramural program is how well-run that resource is and how much of a fantastic resource it is for my group."

For more information about Dr. Phillippy's work with Biowulf, and how long-read sequencing may dramatically expand scientists' understanding of how such illnesses develop, visit the? [I Am Intramural Blog](#).