

World Grid used to study protein folding

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A team of U.S. scientists is using IBM's World Community Grid to be able to predict the structures of key proteins.

The researchers at New York University's Center for Comparative Functional Genomics are starting the second phase of a project designed to shed light on the role of proteins in diseases and offer pathways to cures.

The inter-institutional project will focus on key human and malaria proteins, merging the biomedical and computation fields in carrying out the study.

"Protein folding is a big problem; there are a large number of proteins and a lot of possible shapes/fold," explained NYU Assistant Biology Professor Richard Bonneau. "In spite of the difficulty, it is an important problem, at the heart of deciphering genomes. The sheer amount of computer power needed to carry out this project makes the use of grid computing essential."

The grid consists of the computing power generated during the idle cycles of millions of computers.

The NYU researchers, in collaboration with scientists at Seattle's Institute for Systems Biology, will focus on cancer biomarkers -- proteins expressed during the early stages of several cancers.

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