



Volunteer Computing & Project Briefings



Benefiting scientific research through distributed computational analysis.

BOINC Client Software

Overview of the BOINC software

Berkeley Open Infrastructure for Network Computing

BOINC is a software platform for volunteer computing and desktop grid computing. Features include:

Multi-Project Participation

The BOINC client allows participation in multiple projects. Resources can be divided among many different projects. When a project is down or has no work, the resources are divided among the remaining projects. Multi-core machines can run multiple projects simultaneously, while single core machines dedicate blocks of time specifically to one project.

Multiple Computer Setup

BOINC can run on multiple computers operating under one account. Each computer has a separate host ID and RPC Sequence number, which is created upon contacting a scheduling server. The Host ID and RPC sequence number are stored in the client's `client_state.xml` file.

Security

Hashes of downloaded files guard against accidental corruption. Official builds are digitally signed by the University of California based on public-key encryption to protect against the distribution of viruses.

Credit for Work Done

Once the computer completes a result, BOINC determines a claimed credit through processor time or application specific credit. Once validated granted credit is awarded to the account.

Teams

Participants in a project can form teams. Participants can join up to a maximum of one team. Team attributes include name, description, type, URL, founder, and list of members.

Updating

Different projects may require different versions of the BOINC client. There is a minimum version setting for all projects, however most projects work with a range of client software. Normally installing a new version of the BOINC client will leave the work units intact.



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General System Requirements

Operating System – Windows 98 or later

Hardware – Pentium 233MHz, 64MB RAM, 20MB Disk Space

Project Descriptions

Astronomy/Physics/Chemistry		
uFluids@home	Purdue University	The uFluids project simulates two-phase fluid behavior in microgravity and microfluidics problems. Our goal is to design better satellite propellant management devices and address two-phase flow in microchannel and MEMS devices.
Spinhenge@home	Bielefeld University of Applied Sciences	The study of molecular magnets and controlled nanoscale magnetism. These magnetic molecules may be used to develop tiny magnetic switches, with applications in medicine (such as local tumor chemotherapy) and biotechnology.
Einstein@home	Univ. of Wisconsin – Milwaukee, Albert Einstein Institute	Search for spinning neutron stars (also called pulsars) using data from the LIGO and GEO gravitational wave detectors. Einstein@Home is a World Year of Physics 2005 project supported by the American Physical Society (APS) and by a number of international organizations.
SETI@home	U.C. Berkeley Space Science Laboratory	SETI (Search for Extraterrestrial Intelligence) is a scientific area whose goal is to detect intelligent life outside Earth. One approach, known as radio SETI, uses radio telescopes to listen for narrow-bandwidth radio signals from space. Such signals are not known to occur naturally, so detection would provide evidence of extraterrestrial technology.
Quantum Monte Carlo at Home	University of Muenster	Study the structure and reactivity of molecules using Quantum Chemistry.

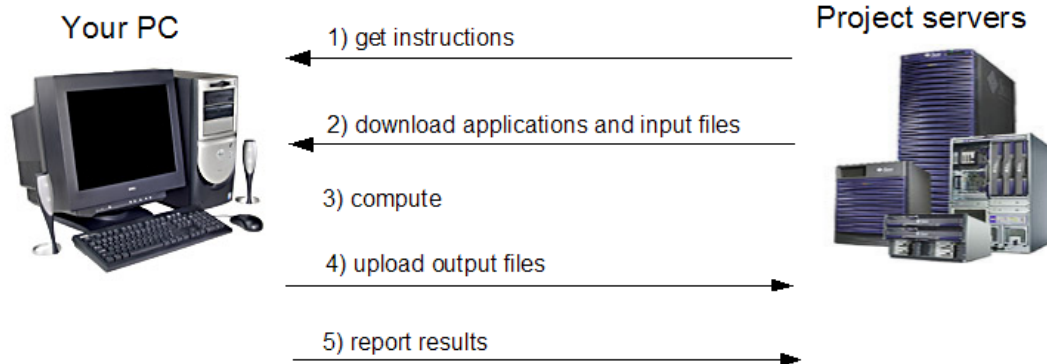
LHC@home	CERN (European Organization for Nuclear Research) University of London	The Large Hadron Collider is a particle accelerator which is being built at CERN, the European Organization for Nuclear Research, the world's largest particle physics laboratory. LHC@home simulates particles traveling around the LHC to study the stability of their orbits.
Earth Sciences		
Climate Prediction.net	Oxford University	To investigate the approximations that have to be made in state-of-the-art climate models. By running the model thousands of times we hope to find out how the model responds to slight tweaks to these approximations – slight enough to not make the approximations any less realistic. This will allow us to improve our understanding of how sensitive our models are to small changes and also to things like changes in carbon dioxide and the sulphur cycle. This will allow us to explore how climate may change in the next century under a wide range of different scenarios.
Biology/Medicine		
Malaria Control.net	The Swiss Tropical Institute	Simulation models of the transmission dynamics and health effects of malaria are an important tool for malaria control. They can be used to determine optimal strategies for delivering mosquito nets, chemotherapy, or new vaccines which are currently under development and testing. Such modeling is extremely computer intensive, requiring simulations of large human populations with a diverse set of parameters related to biological and social factors that influence the distribution of the disease.
SIMAP	Technical University of Munich	Calculate similarities between proteins. SIMAP provides a public database of the resulting data, which plays a key role in many bioinformatics research projects.

Tanpaku	Tokyo University of Science	To predict protein structure and function from genetic sequences, using the 'Brownian Dynamics' (BD) method. This method enables us to simulate more efficiently than conventional methods.
Rosetta@home	University of Washington	Determine the 3-dimensional shapes of proteins in research that may ultimately lead to finding cures for some major human diseases. By running Rosetta@home you will help us speed up and extend our research in ways we couldn't possibly attempt without your help. You will also be helping our efforts at designing new proteins to fight diseases such as HIV, Malaria, Cancer, and Alzheimer's.
World Community Grid	IBM Corporate Community Relations	Humanitarian research on new and infectious disease, natural disasters and hunger. To further critical non-profit research on some of humanity's most pressing problems by creating the world's largest volunteer computing grid. Research includes HIV/AIDS, cancer, muscular dystrophy, dengue fever, and many more.
Predictor@home	Scripps Research Institute	Protein structure prediction starts from a sequence of amino acids and attempts to predict the folded, functioning, form of the protein. Predicting the structure of an unknown protein is a critical problem in enabling structure-based drug design to treat new and existing diseases.
NanoHive@home	NanoRex, Inc. Bloomfield Hills, Michigan	Perform a large-scale nanosystems simulation and analysis that is otherwise too intensive to be calculated via normal means, and thereby enable further scientific study in the field of nanotechnology.

BOINC Client & Project Interaction

Taken from: http://boinc-wiki.ath.cx/index.php?title=Getting_Started

When you run the BOINC Client Software on your PC, it works as follows (see below):



1. Your PC gets a set of instructions from the Project's Scheduling Server. The instructions depend on your PC: for example, the Server won't give it work that requires more RAM than you have. The instructions may include multiple pieces of work. Projects can support several Science Applications, and the Server may send you work from any of them.
2. Your PC downloads executable and input files from the Project's Data Server. If the Project releases new versions of its applications, the executable files are downloaded automatically to your PC.
3. Your PC runs the Science Application programs, producing output files.
4. Your PC uploads the output files to the Data Server.
5. Later (up to several days later, depending on your Preference Settings; see: "Preferences in the BOINC System") your PC reports the completed results to the Scheduling Server, and gets instructions for more work.

This cycle is repeated indefinitely. The BOINC Client Software does this all automatically; you don't have to do anything.

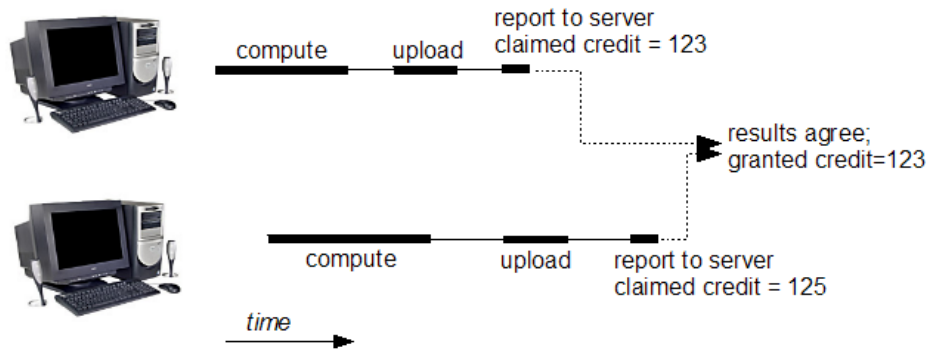
Credit

The Project's BOINC Database keeps track of how much work your computer has done; this is called Credit. To ensure that Credit is granted fairly, most BOINC Powered Projects work as follows:

- Each Work Unit may be sent to several computers.
- When a computer reports a Result, it claims a certain amount of Credit, based on how much CPU Time was used.
- When at least three Results have been returned, the server compares them. In general, it will use the middle value (or the average of the middle values if there are 4 or more Results) of the Claimed Credits, throwing away the top and bottom claim. The Participants are granted this average of the middle of the Claimed Credits.

Note:

This is a *simplification* of the rules. They are covered in depth in the topics on Credit.



Please keep in mind:

- There may be a delay of several days between when your computer reports a Result and when it is Granted Credit for the Result. The "Your Account" Page shows you how much Credit is 'pending' (claimed but not granted).
- The credit-granting process starts when your computer reports a Result to the Scheduling Server (not when it finishes computing the Result or uploading the output files).
- In rare cases (e.g. if errors occur on one or more computers) you may never receive Credit for a computation.