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XtremWeb-CH Towards a true P2P Computing Platform

Towards a true Peer-To-Peer Platform for High Performance Computing: *XtremWeb-CH* (www.xtremwebch.net)

XtremWeb-CH is an applied research project carried out at the University of Applied Sciences, Western Switzerland. ***XtremWeb-CH*** aims at building an effective Peer-To-Peer Large Scale Distributed System for high performance needs. A typical *XtremWeb-CH* platform is composed of one coordinator and several workers (remote resources). The coordinator is a three-tier layer allowing "connection" between the users of high performance applications and the workers.

XtremWeb-CH supports five functionalities:

1. Volatility of workers: When a worker voluntarily or involuntarily disappears, the task allocated to it is automatically assigned to another worker.
2. Automatic execution of Parallel and Distributed Applications: a high performance application is generally composed of a set of communicating tasks. *XtremWeb-CH* insures the automatic transfer of data between workers executing communicating tasks.
3. Direct communication between workers: Communication between tasks can take place without passing through the coordinator. The coordinator keeps only the responsibility of assigning tasks to workers.
4. Load balancing: *XtremWeb-CH* optimizes the granularity of the application according to the "state" of the platform. During the "compilation" step, the number of tasks and the workload (quantity of data to be processed) of each task are fixed according to the number of the available workers and their performance. During execution, a scheduling algorithm assigns tasks to workers according to the workload of the former and the performance of the latter.
5. *XtremWeb-CH* provides a set of monitoring tools allowing users to visualize the execution of their applications: tasks allocation, execution progression, step by step execution, etc.

XtremWeb-CH is evaluated in a real case of a CPU time consuming phylogenetic application: PHYLogeny Inference Package (PHYLIP). The parallelized version of PHYLIP is used by the virology laboratory of Geneva Hospital in order to generate phylogenetic tree related to HIV virus.

XtremWeb-CH worker module can be downloaded from www.xtremwebch.net