Contribution ID: **66**   Type: **Poster**

Virtualisation of Bioinformatics Applications on STRATUS LAB Cloud

The bioinformatics community is facing a deluge of data. The challenge is to analyze these data with the relevant applications and a good efficiency. Some bioinformatics algorithms like BLAST, FastA or ClustalW are daily used and usually classified as data-intensive. They are processing gigabytes of data stored in flat-file databases like UNIPROT, EMBL or PDBseq. To give an insight to this challenge, we have built two virtual bioinformatics appliances in the context of the StratusLab project (www.stratuslab.org). Bioinformaticians need access to the international reference databases recording biological resources such as protein or gene sequences and associated data, protein structures or complete genomes. We have built a virtual appliance that acts as a proxy between the internet where all the reference databases are published and the cloud instances that will compute the bioinformatics analyses. To import and maintain the required biological databases, we use the BioMaJ system. Bioinformaticians are combining regularly multiple software packages to analyze their data. We have built a virtual machine with bioinformatics software pre-installed with the help of a script system, called 'bioapps' developed in our team. This tool downloads the application package from the reference site, compiles and installs the binary on the machine. Because bioinformatics applications require access to reference data to process their analyses, this bioinformatics compute appliance is linked to the biological databases repository appliance, and mounts the exported volumes containing the biological databases. The adoption of clouds for bioinformatics applications will be strongly correlated to the capability of cloud infrastructures to provide ease-of-use and access to reference biological data and applications. In that sense, StratusLab is collaborating with the French Bioinformatics Network RENABI (www.renabi.fr) and its infrastructure GRISBI (www.grisbio.fr) to help solving the requirements from the Bioinformatics community.

Primary authors: Dr LOOMIS, Charles (CNRS LAL); Dr BLANCHET, Christophe (CNRS IBCP); Mr GAUTHEY, Clément (CNRS IBCP)

Presenter: Dr BLANCHET, Christophe (CNRS IBCP)