# Bringing the tools to the data - Providing scientists with personalized and on-demand bioinformatics services on the cloud of the French Institute of Bioinformatics

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Life science researchers, thanks to the continuous improvement of experimental technologies, face a deluge of data whose exploitation requires large computing resources and appropriate software tools. They simultaneously use many of the bioinformatics tools from the arsenal of thousands available from the international community. Usually they combine their data with public data that are too large to be moved easily. So the computational infrastructure need to be tightly connected to public biological databases.

At the French Institute of Bioinformatics (IFB), we developed several bioinformatics cloud services available as cloud appliances. A cloud appliance is a predefined virtual machine that can be run on a remote cloud infrastructure. As cloud appliances have size usually of gigabytes, this is more efficient to moved them where the terabytes of biological data to analyse are stored instead of moving the data. But that requires to have at least few computing resources close to the stored data.
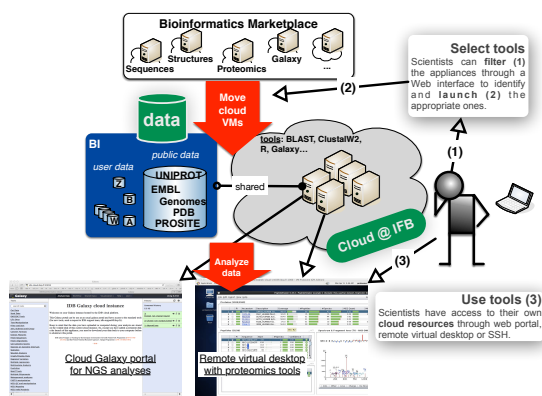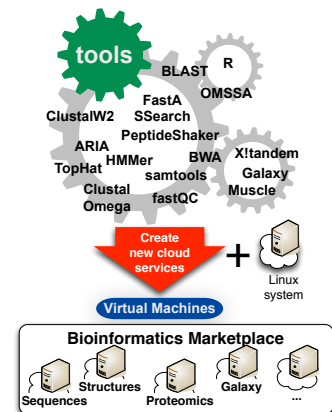
We have created bioinformatics appliances providing, for example, an user-devoted Galaxy portal, a virtual desktop environment for proteomics analysis or a bioinformatics cluster with a lot of standard tools (BLAST, ClustalW2, R, Samtools, Bowtie, TopHat, etc.). Scientists can run their own appliances through an user-adapted web interface. To connect our cloud infrastructure to existing public biological databases, we have configured it to connect automatically all virtual machines to a local repository with public databases like UNIPROT or EMBL.

IFB is currently running an academic cloud infrastructure with the appropriate biological data and bioinformatics tools to meet the needs of the life science community.

French Institute of Bioinformatics - http://www.france-bioinformatique.fr