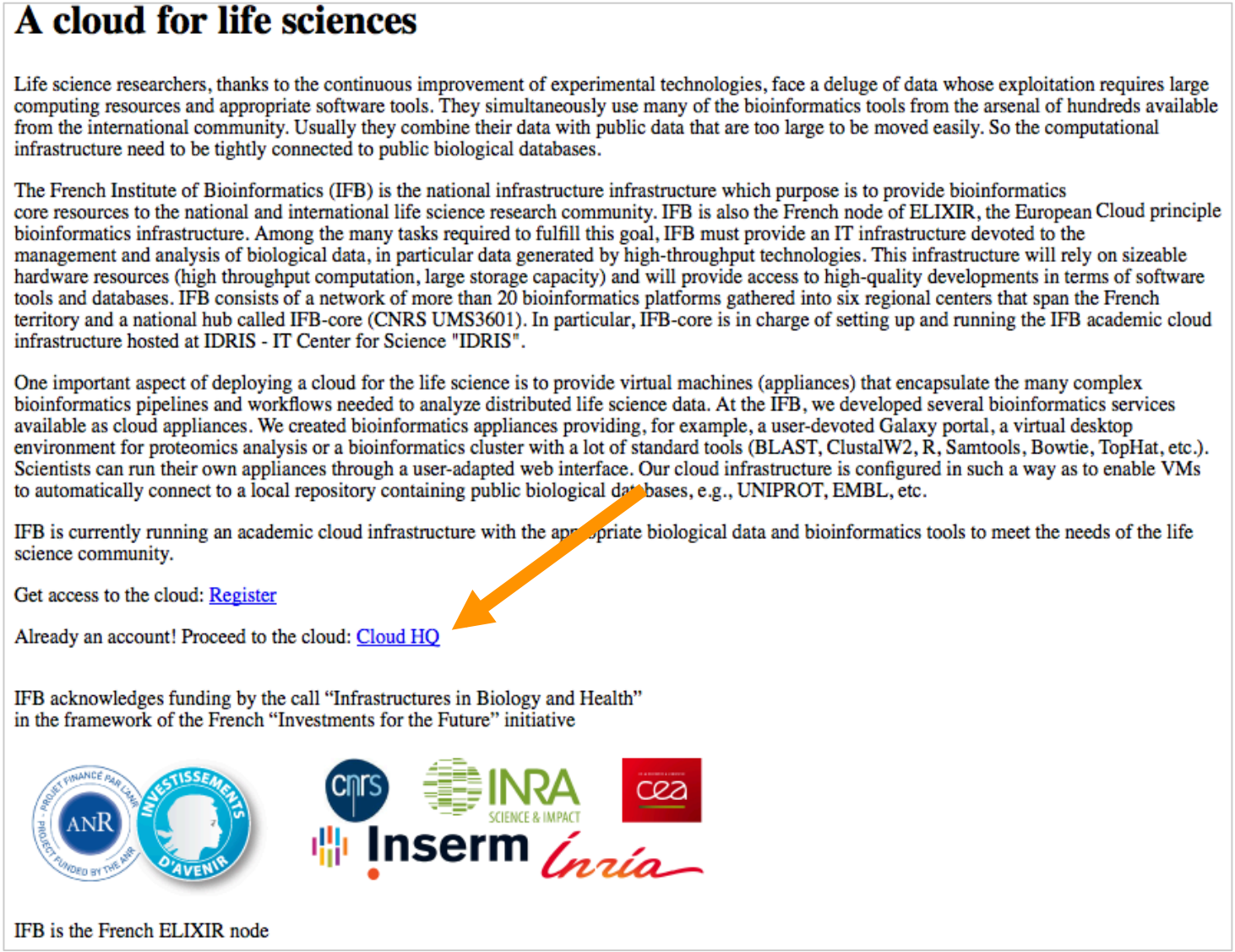
Regulatory Sequence Analysis Tools

Using RSAT Virtual Machine at IFB cloud

(Institut Français de Bioinformatique)

Connection to the IFB cloud (Institut Français de Bioinformatique)

- https://cloud.france-bioinformatique.fr/



A cloud for life sciences

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 hundreds 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.

The French Institute of Bioinformatics (IFB) is the national infrastructure infrastructure which purpose is to provide bioinformatics core resources to the national and international life science research community. IFB is also the French node of ELIXIR, the European Cloud principle bioinformatics infrastructure. Among the many tasks required to fulfill this goal, IFB must provide an IT infrastructure devoted to the management and analysis of biological data, in particular data generated by high-throughput technologies. This infrastructure will rely on sizeable hardware resources (high throughput computation, large storage capacity) and will provide access to high-quality developments in terms of software tools and databases. IFB consists of a network of more than 20 bioinformatics platforms gathered into six regional centers that span the French territory and a national hub called IFB-core (CNRS UMS3601). In particular, IFB-core is in charge of setting up and running the IFB academic cloud infrastructure hosted at IDRIS - IT Center for Science "IDRIS".

One important aspect of deploying a cloud for the life science is to provide virtual machines (appliances) that encapsulate the many complex bioinformatics pipelines and workflows needed to analyze distributed life science data. At the IFB, we developed several bioinformatics services available as cloud appliances. We created bioinformatics appliances providing, for example, a 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 a user-adapted web interface. Our cloud infrastructure is configured in such a way as to enable VMs to automatically connect to a local repository containing public biological databases, e.g., UNIPROT, EMBL, etc.

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.

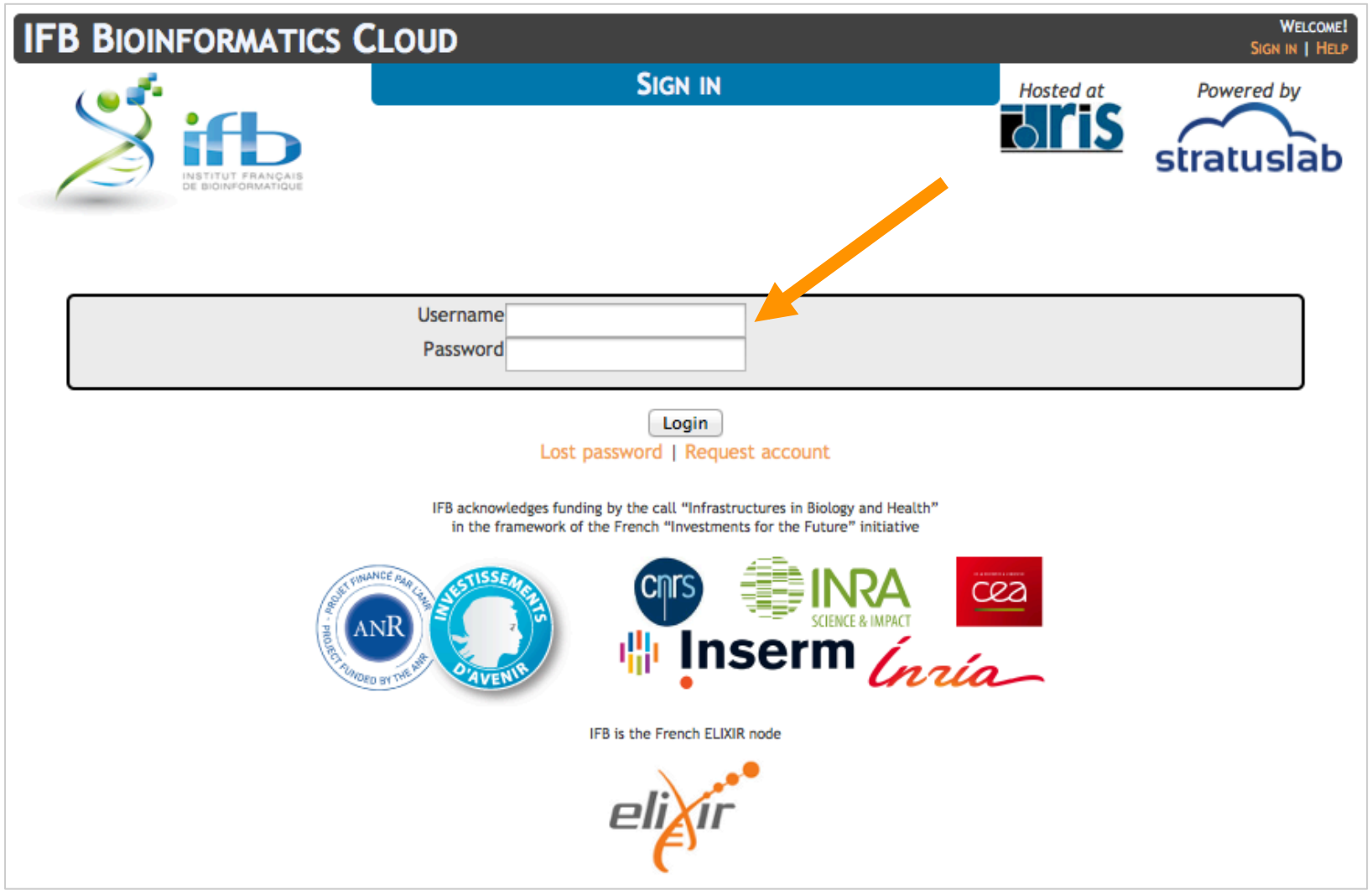
Get access to the cloud: Register

Already an account! Proceed to the cloud: Cloud HQ

IFB acknowledges funding by the call “Infrastructures in Biology and Health”
in the framework of the French “Investments for the Future” initiative

IFB is the French ELIXIR node

Login form


IFB BIOINFORMATICS CLOUD
WELCOME!
SIGN IN | HELP
SIGN IN
Hosted at
iris
Powered by
stratuslab
ifb
INSTITUT FRANÇAIS DE BIOINFORMATIQUE
Username
Password
Login
Lost password | Request account
IFB acknowledges funding by the call "Infrastructures in Biology and Health"
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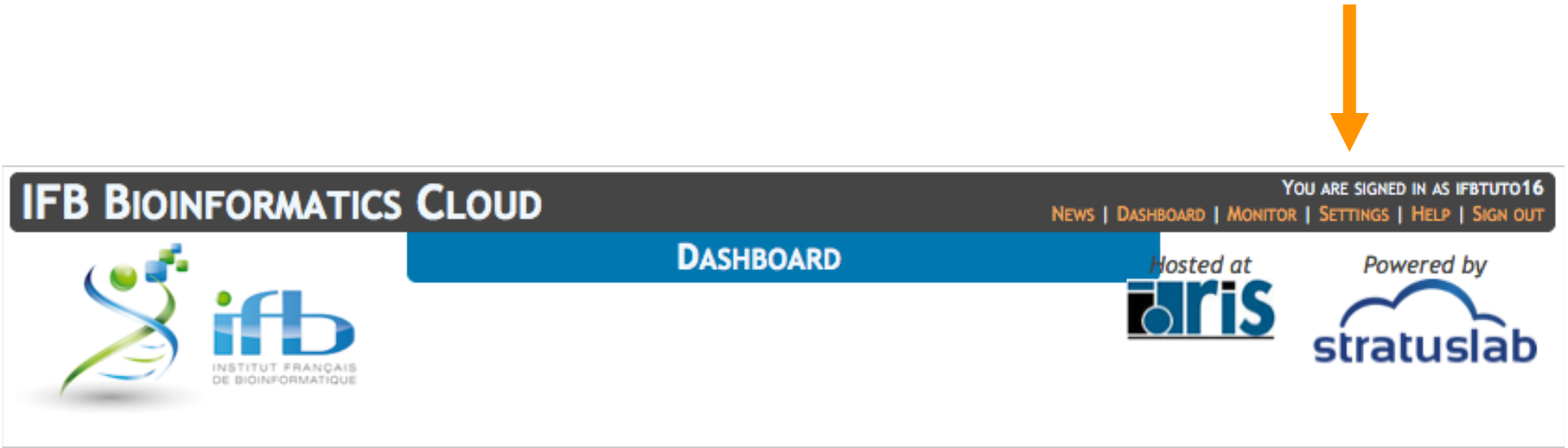
ANR
INVESTISSEMENTS D'AVENIR
cnrs
INRA
SCIENCE & IMPACT
cea
Inserm
Inria
IFB is the French ELIXIR node
elixir

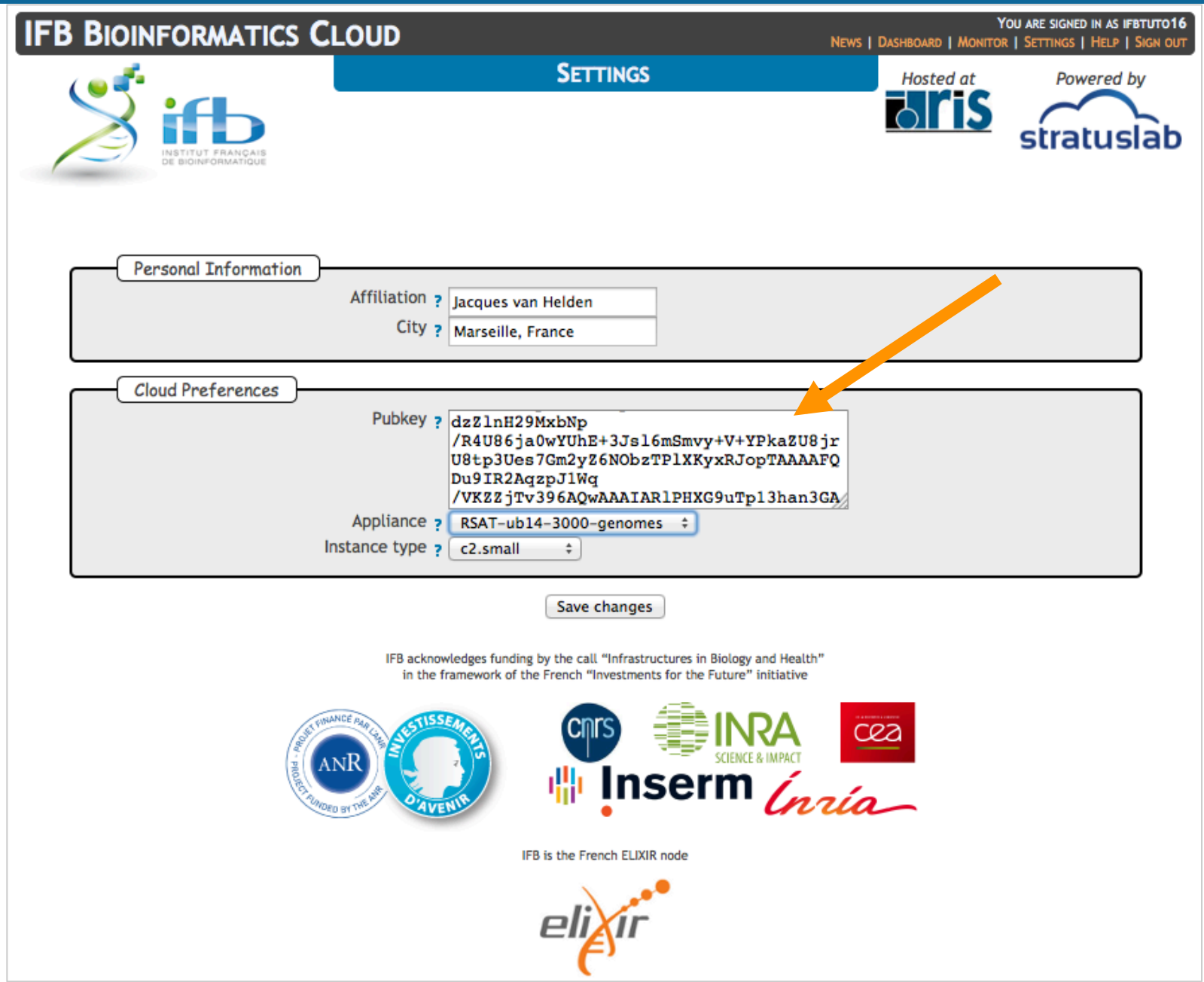
Click “Settings”

- Before starting to use the IFB cloud, it is worth filling the “Settings” form.
- BEWARE: you need a **public ssh key**.

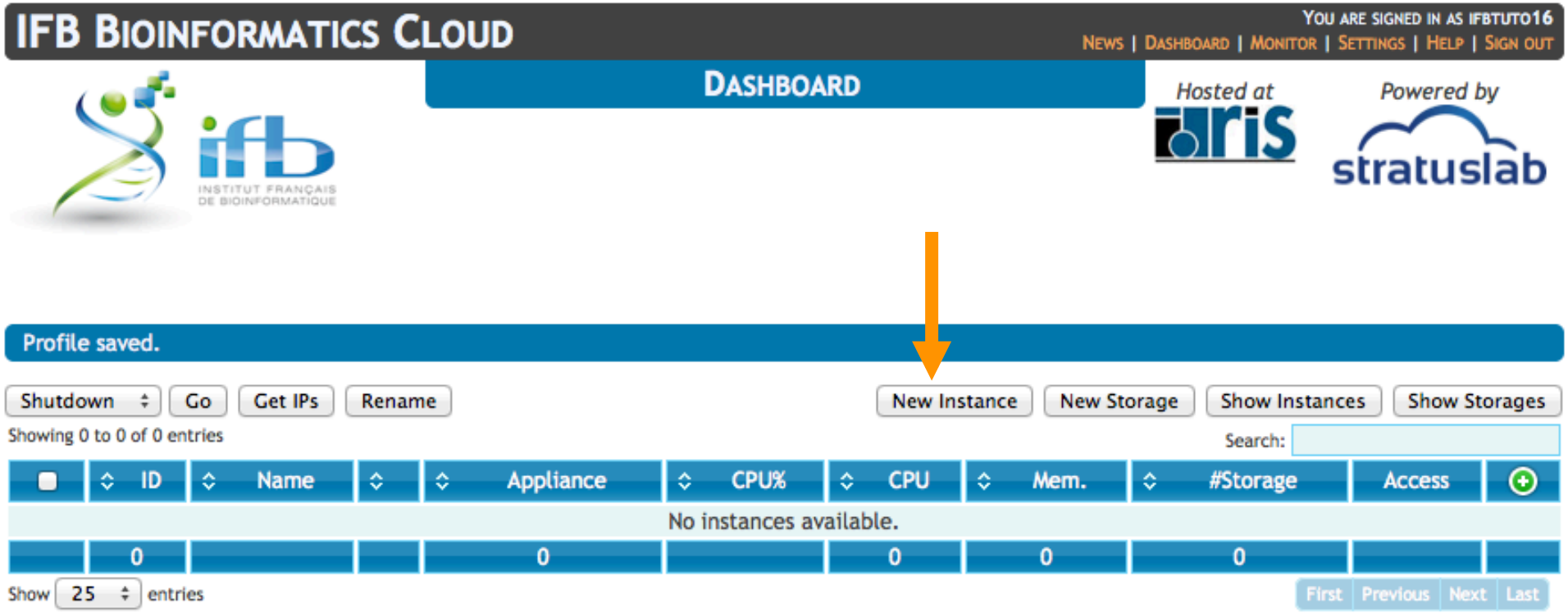
- You can find instructions about ssh keys (for example) here
  https://help.github.com/articles/generating-ssh-keys
- and for Windows users here
  http://wiki.joyent.com/wiki/display/jpc2/Manually+Generating+Your+SSH+Key+in+Windows



Enter your **public** ssh key in "Settings"

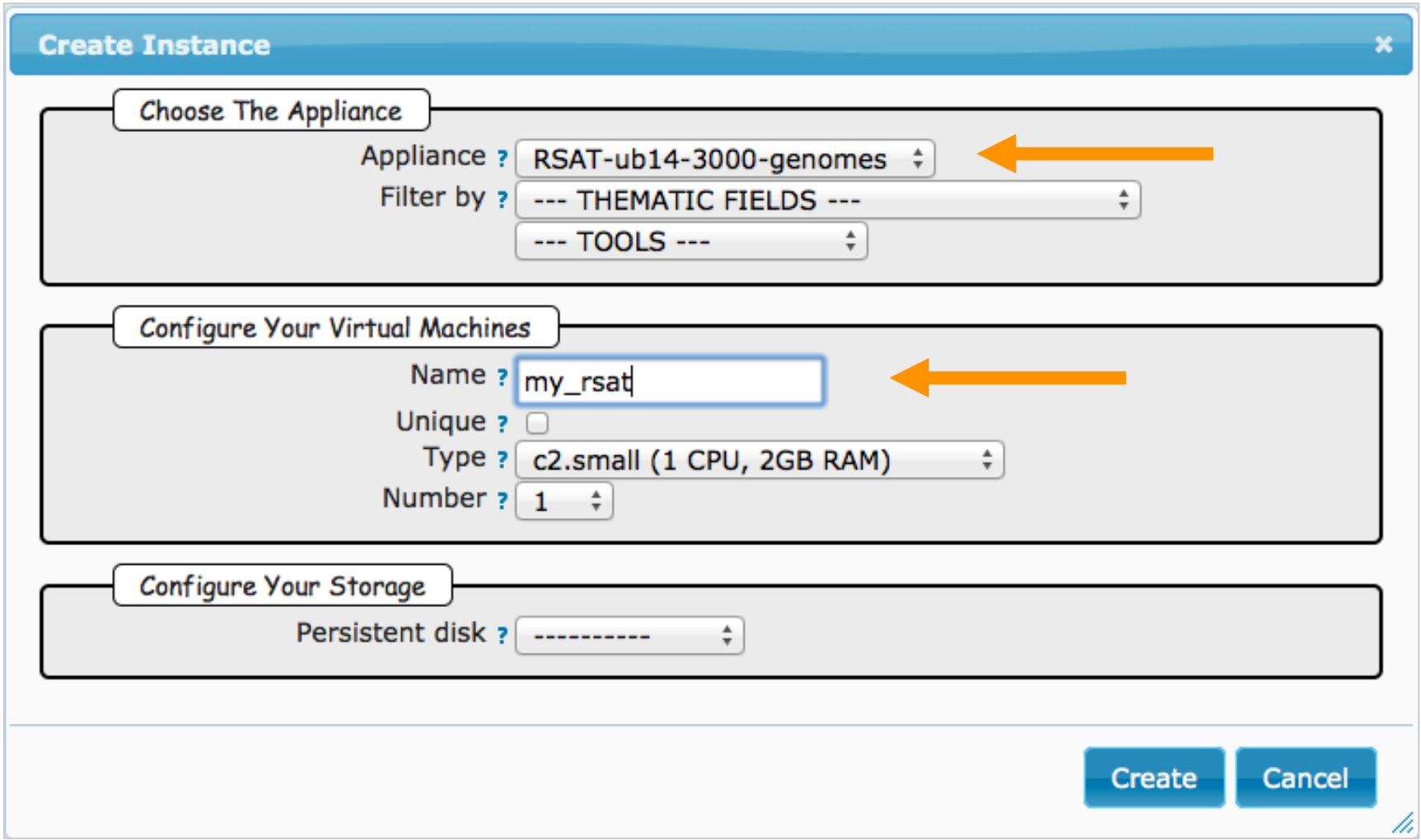


Click “New Instance” to create an instance



Create a new instance

- Note
  - The appliance “RSAT-ub14-3000-genomes” is preloaded with genomes of 3000 species (mostly Bacteria).
  - The appliance “RSAT-mini” has only 2 genomes (*S.cerevisiae* and *E.coli*)



Your instance of the RSAT server

- After having created the instance, wait for a few seconds and refresh the page (the virtual machine takes ~1 minute to boot).
- You can use this instance in three ways
  - As web server (right-click "**http**" under "Access")
  - On the Linux terminal (click "**ssh**" under "Access")