Documentation/ Instructions for use of IGBA-AMI-2

This AMI launches the following servers on startup:  (1) Xrdp (2) Postgres  (3) Sshd

In addition you can manually launch:  (1) Rserve (2) Shiny

To connect with ssh:

(1)    Create a security group in your AWS account allowing ssh (port 22) connections.  To connect to the Xrdp remote desktop server, also allow rdp (port 3389) connections in the security group.

(2)    Create if you have not already done so, a “.pem” authentication file based on your AWS credentials and download it to your local machine.

(3)    Change the permissions of the \*pem file to owner-only access (chmod 600).

(4)    Make sure your VPC setup assigns a public IP address to access the instance through your VPC.  The AWS defaults should permit this.  Note the public IP address assigned to the launched AMI instance.

(5)    Connect by “ssh –I <your pem file name> ubuntu@<your instance public IP address> “.

To connect to the remote desktop server:

(6)    Create a new user with “sudo adduser <your user name>” from within the “ubuntu” user account.

(7)    Restart the Xrdp server with “sudo service xrdp restart” ur Xrdp server should now be ready to accept connections through a remote desktop client with the new username and password.  Make sure your security group allows connections through port 3389, the default RDP connection port.  Upon logging into the MATE desktop, make sure to add a “Main Menu” panel for convenient use, or consult the MATE documentation to set up an Xrdp profile in your user directory.

(8)    The Firefox browser is installed and ready for use in this server.

(9) This AMI has a pre-installed miniconda environment. This environment contains the necessary installations of SEQprocess and related tools, an R-based NGS analysis pipeline and customization framework.

(10) The default configurations in this AMI boot into a “base” conda environment. You’re welcome to run analyses in this or modify the environment for your needs.

At this point, download the following example files as follows:

wget <https://ngs-samples.s3.amazonaws.com/SRR4296627_1.fastq.gz>

wget <https://ngs-samples.s3.amazonaws.com/SRR4296627_2.fastq.gz>

gunzip \*gz

sudo chmod a+w /data/output/\*

Then start R, and In the R console:

>library(SEQprocess)

>source(“SEQprocess-GATK.txt”)

This will start the NGS analysis of the downloaded fastq files against hg38. Depending on the type of AMI launched, the analysis will take from a few minutes to several hours.