

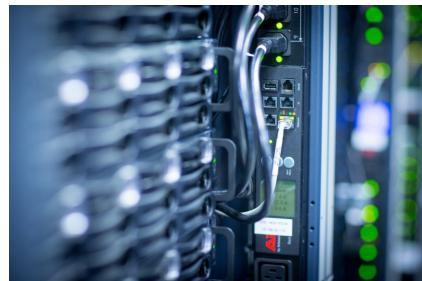


# INTRODUCTION TO RIVANNA

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# Rivanna

Rivanna is the university's primary resource for high-performance computation. It provides a platform for computationally-intensive research across disciplines.



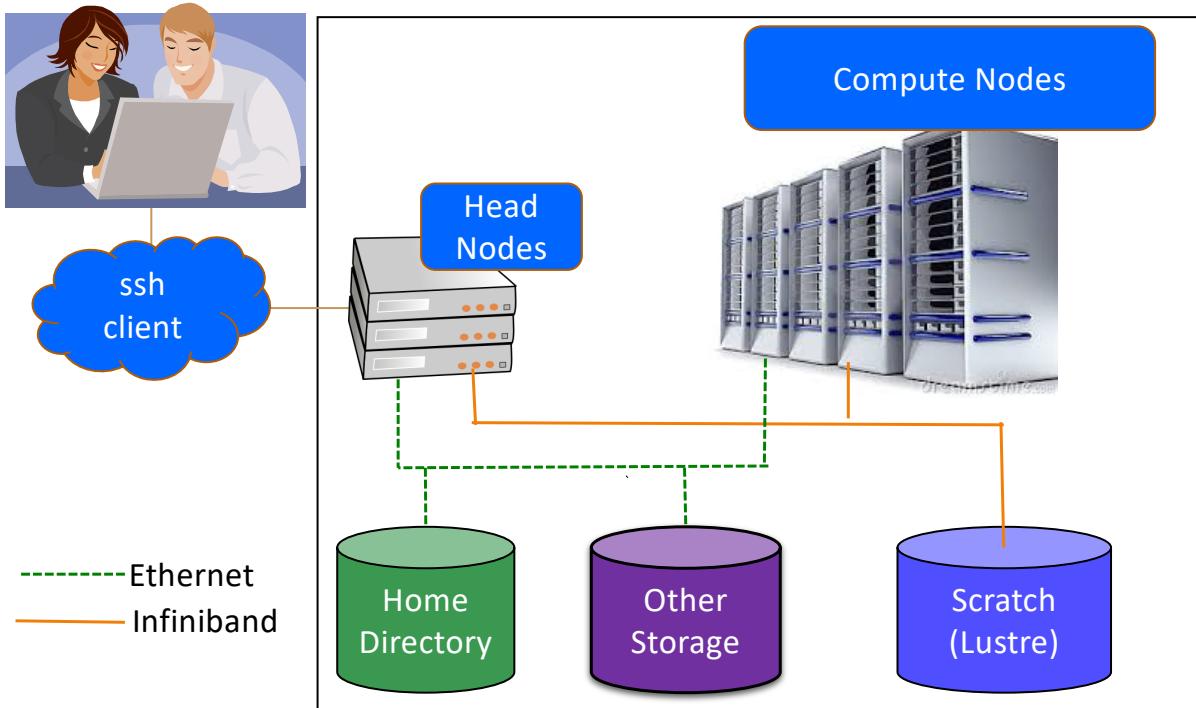
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# Terminology

- Node
  - Basic building block of a cluster
  - Usually a specialized computer
- Two types of nodes:
  - Head Node – computer used for logging on and submitting jobs
  - Compute Node -- computer that does most of the work
- Core – an individual processor on a computer

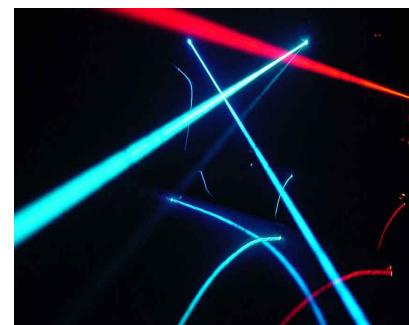


# Rivanna Overview



# Before we can use the Cluster . . .

- We need to know about:
  - [Allocations & Accounts](#)
  - [Connections to the cluster](#)
  - [Cluster environment](#)
  - [Modules & Partitions](#)
  - [SLURM & Job Submissions](#)
- The remaining slides will cover the basics of these topics.





# ALLOCATIONS

---

# Allocations

- Rivanna is allocated:

At the most basic level, an allocation refers to a chunk of CPU time that you can use to run your computations.

Allocations are measured in service units (SUs), where **1 SU = 1 core-hour**

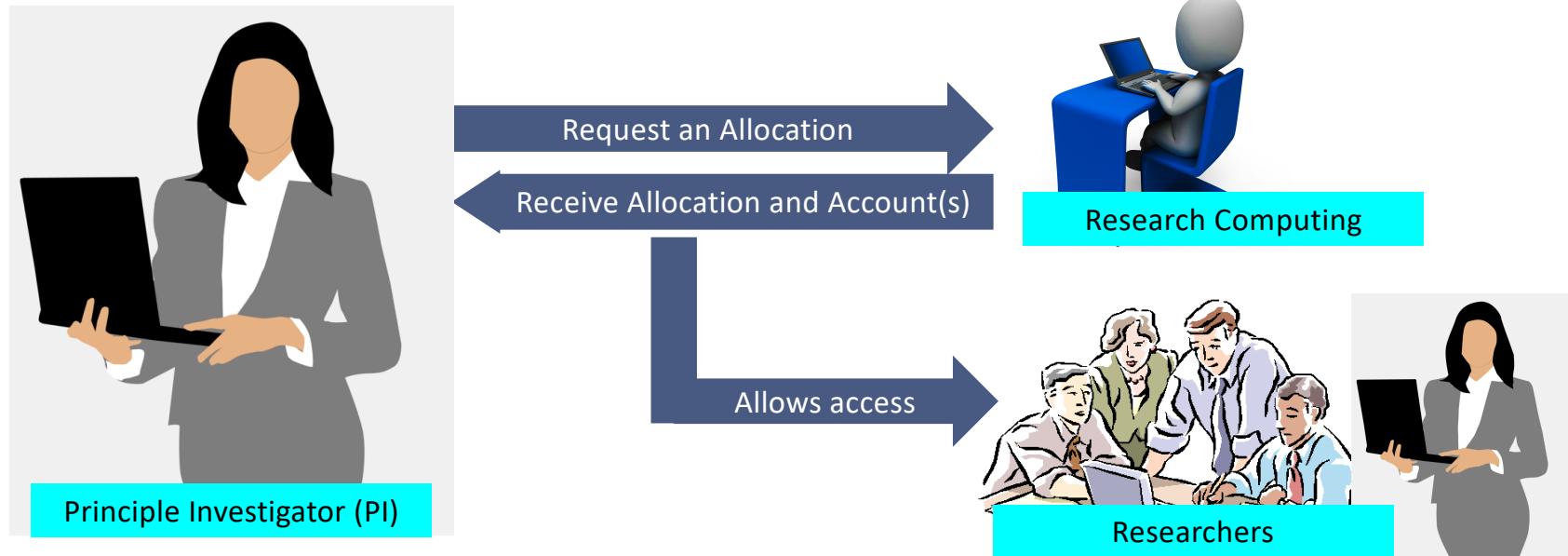
- Only faculty, postdocs, and research staff may request an allocation.
  - Students must be sponsored by a faculty or research staff.
  - All individuals on a given allocation share the service units.
- Allocations may be requested at

<https://www.rc.virginia.edu/userinfo/rivanna/allocations/>



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# Getting an account on Rivanna



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# CONNECTING & LOGGING ONTO RIVANNA

---

# If You are Off-Grounds . . .

- You may need to use the UVa Anywhere VPN when connecting to Rivanna
- To install the VPN on your computer, go to <https://in.virginia.edu/vpn> and follow the instructions.

During the COVID-19 outbreak, we are asking users to connect with the "UVa More Secure" VPN if it is available to them.

Follow the same installation instructions. When launching the VPN, select "More Secure" from the dropdown box.

# How to connect to Rivanna

There are three ways to connect to Rivanna:

1. Open-on-Demand, a graphical user interface through a web browser
  - examine and manipulate files and submit jobs.
  - access applications such as Matlab, Jupyterlab, and R Studio Server.
  - <https://rivanna-portal.hpc.virginia.edu>
2. FastX Web, direct access to a desktop for Rivanna  
<https://rivanna-desktop.hpc.virginia.edu>
3. ssh client, direct access to the command line



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# Connecting to Open onDemand

- To connect to Open OnDemand, open your web browser and type  
<https://rivanna-portal.hpc.virginia.edu>  
You will need to authenticate with Netbadge (i.e., “Netbadge” in).
- After you log in, you will see the Dashboard.



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# Open onDemand Dashboard

UVA OpenOnDemand    Files ▾    Jobs ▾    Clusters ▾    Interactive Apps ▾    My Interactive Sessions    ? Help ▾    Logged in as jmh5ad    Log Out

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OnDemand provides an integrated, single access point for all of your HPC resources.

**Message of the Day**

---

**2019-10-08 Scratch Directory**

RC system engineers will begin actively clearing /scratch files more than 90 days old **beginning 10/14/2019**. /scratch is intended as temporary storage (90 days maximum) for active work. It is not backed up and needs to be purged periodically in order to maintain a stable HPC environment. We encourage users to back up their important data. RC offers several low-cost storage options to researchers. For more information, visit <https://www.rc.virginia.edu/userinfo/rivanna/storage/>

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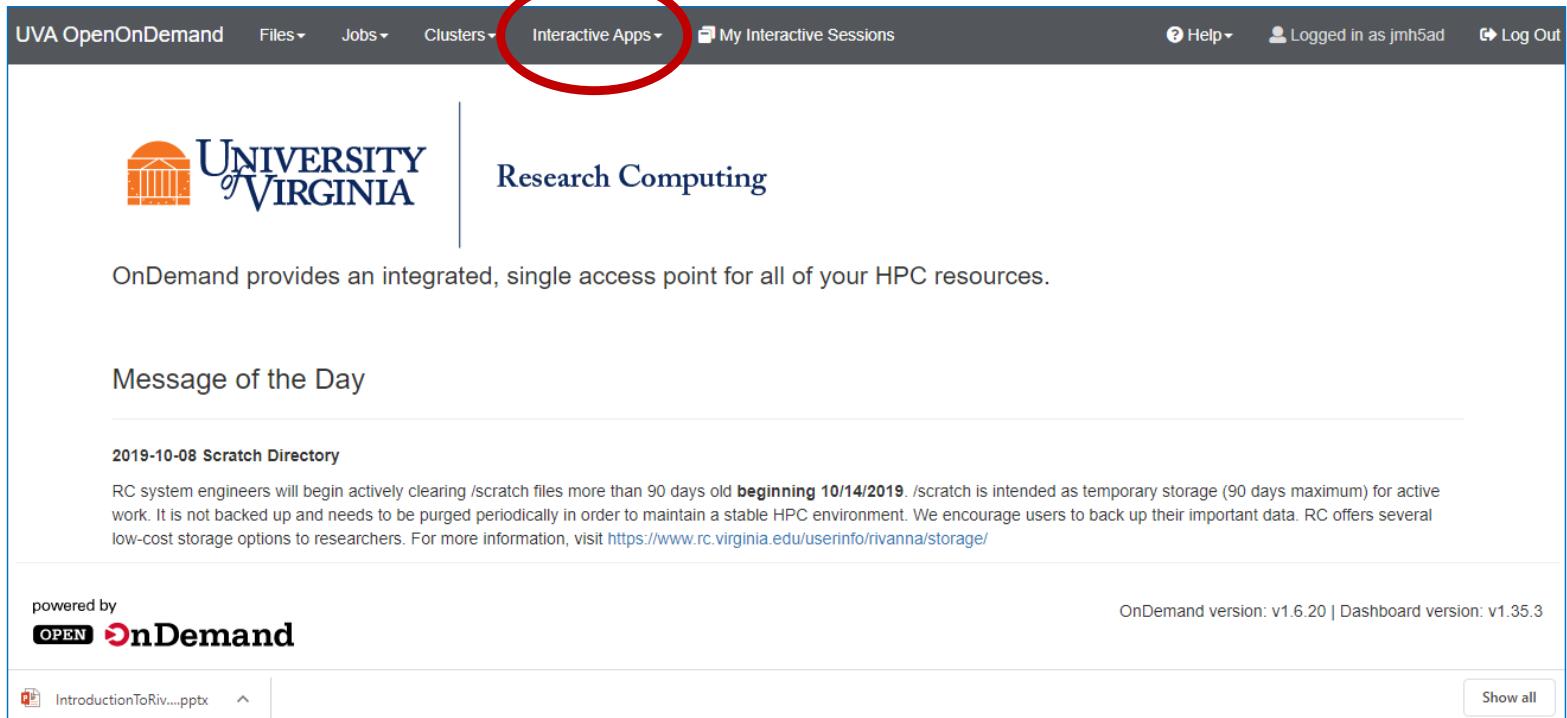
powered by  OnDemand    OnDemand version: v1.6.20 | Dashboard version: v1.35.3

 IntroductionToRiv....pptx    ^    Show all



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# Open onDemand Dashboard



The screenshot shows the UVA OpenOnDemand dashboard. At the top, there is a navigation bar with links for "UVA OpenOnDemand", "Files", "Jobs", "Clusters", "Interactive Apps" (which is highlighted with a red circle), "My Interactive Sessions", "Help", "Logged in as jmh5ad", and "Log Out". Below the navigation bar, the page header features the University of Virginia logo and the text "Research Computing". A message states: "OnDemand provides an integrated, single access point for all of your HPC resources." Under the "Message of the Day" section, there is a heading "2019-10-08 Scratch Directory" followed by a detailed message about the clearing of scratch files. At the bottom of the dashboard, it says "powered by OPEN onDemand" and "OnDemand version: v1.6.20 | Dashboard version: v1.35.3". There is also a "Show all" button and a file preview for "IntroductionToRiv....pptx".



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# Interactive Apps

The screenshot shows the UVA OpenOnDemand dashboard. At the top, there's a navigation bar with links for "UVA OpenOnDemand", "Files", "Jobs", and "Clusters". On the right side of the top bar are "Interactive Apps", "My Interactive Sessions", "Help", "Logged in as jmh5ad", and "Log Out". Below the top bar, the main content area has a sidebar on the left containing the University of Virginia logo, a "Message of the Day" section about a scratch directory cleanup, and a "2019-10-08 Scratch Directory" section. The main content area has a heading "Interactive Apps" and a sub-section "My Interactive Sessions". A yellow callout bubble on the right contains the text "Let's try FastX for now.".

UVA OpenOnDemand

Files ▾ Jobs ▾ Clusters ▾

Interactive Apps ▾ My Interactive Sessions

Help ▾ Logged in as jmh5ad Log Out

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OnDemand provides an integrated, s

Message of the Day

2019-10-08 Scratch Directory

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powered by

OPEN OnDemand

OnDemand version: v1.6.20 | Dashboard version: v1.35.3

Show all

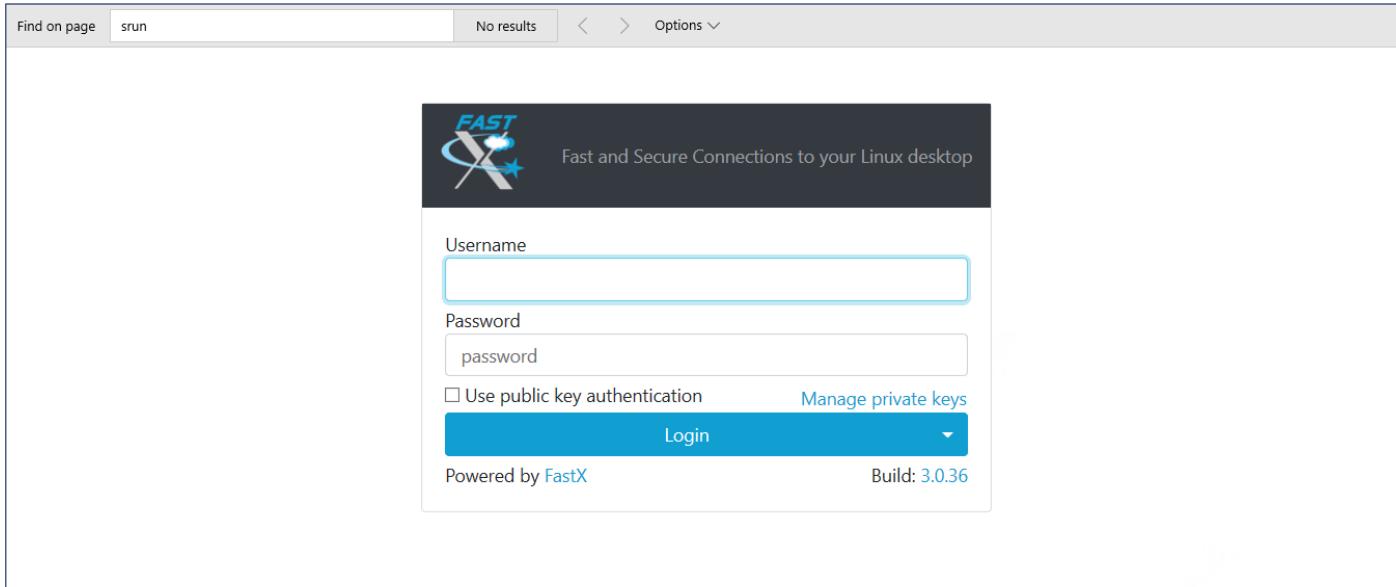
IntroductionToRiv....pptx

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Let's try FastX for now.

# Log in Using Your Netbadge Credential



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# Log in Using Your Netbadge Credentials

Find on page srun No results < > Options ▾

Fast and Secure Connections to your Linux desktop

Username

Password  password

Use public key authentication [Manage private keys](#)

[Login](#)

Powered by [FastX](#) Build: 3.0.36

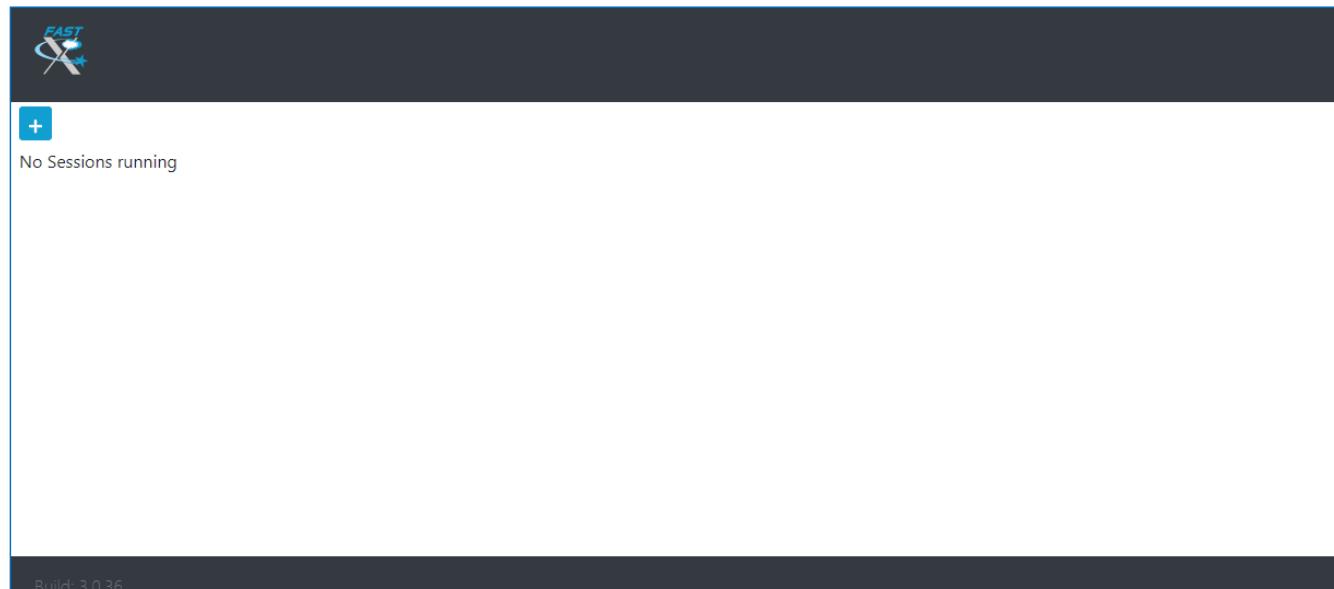
If this page does not appear, make sure that you are connected to the UVa VPN..



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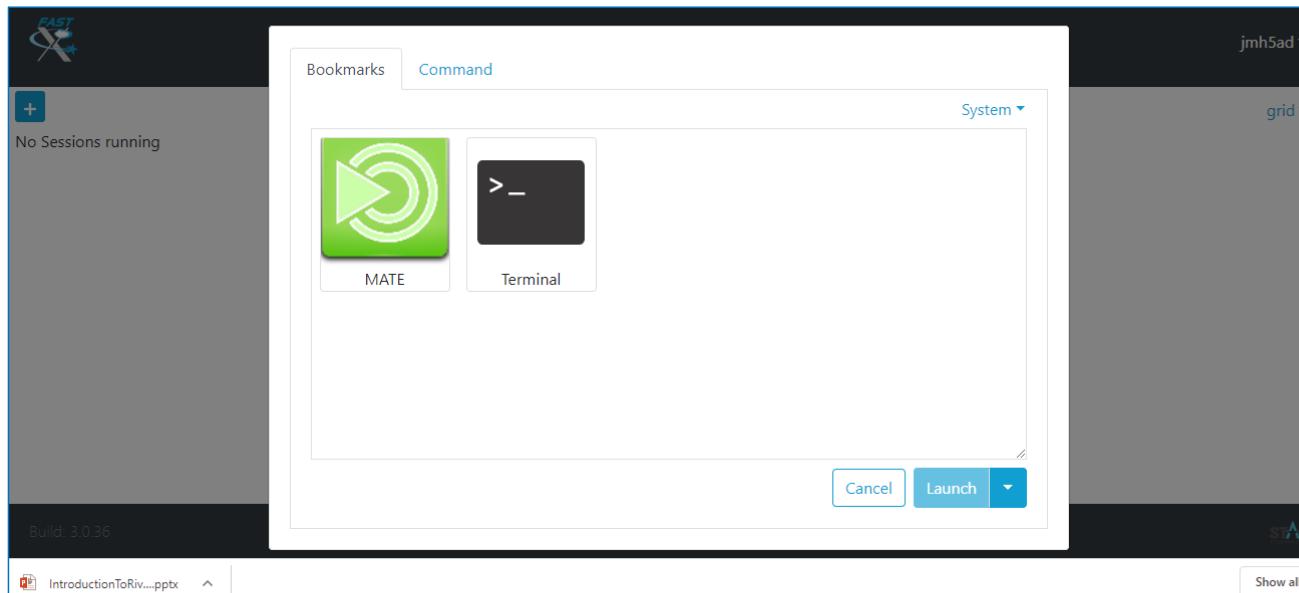
# Starting up FastX

- Click on the plus sign

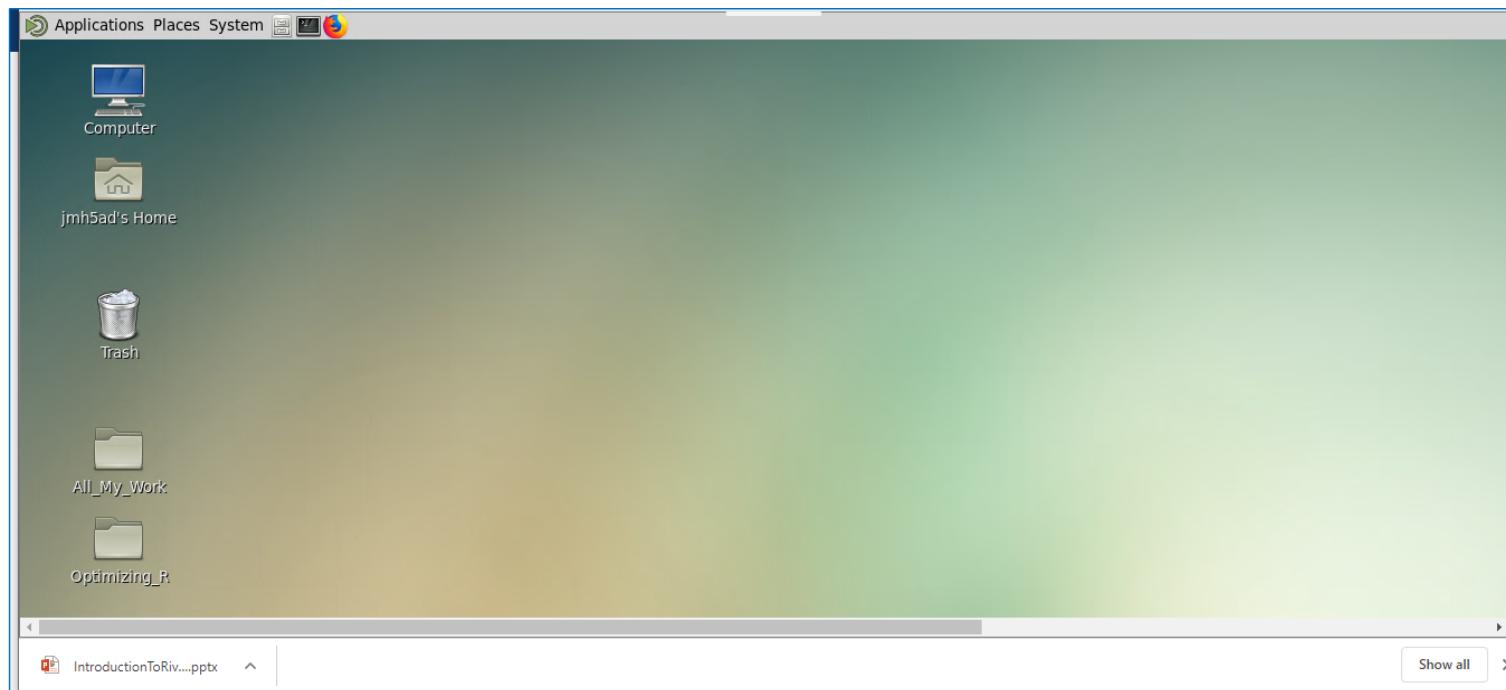


# Starting up FastX

- Select MATE; Click Launch



# FastX Desktop



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Now, let's see how we can connect with an ssh client.

# SSH Clients

- Connecting to Rivanna

- On a Mac or Linux system, simply open a Terminal application and type  
`ssh -Y mst3k@rivanna.hpc.virginia.edu`
- You may also want to install XQuartz on your Mac to use graphical tools on Rivanna.
- On a Windows system, open the Command Prompt app and type  
`ssh -Y mst3k@rivanna.hpc.virginia.edu`

Replace `mst3k`  
with your user  
ID.

You must use the  
UVa VPN when  
off-Grounds.



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# SSH Clients

- SSH clients mostly use instructions typed at the command prompt.
- You will need to become familiar with Linux/Unix commands.
  - See [learning.rc.virginia.edu/tutorials/unix-tutorial/](http://learning.rc.virginia.edu/tutorials/unix-tutorial/)
  - to learn more about Unix/Linux commands.
- Some useful Unix/Linux commands:

```
$ ls  
$ pwd  
$ cd folder_name  
$ cp file_1 file_2  
$ rm file_1  
$ cd ..
```



# Hostnames for Rivanna

- The hostname for the Interactive frontends:  
[rivanna.hpc.virginia.edu](http://rivanna.hpc.virginia.edu)  
(does round-robin among the three front-ends)
- However, you also can log onto a specific front-end:
  - [rivanna1.hpc.virginia.edu](http://rivanna1.hpc.virginia.edu)
  - [rivanna2.hpc.virginia.edu](http://rivanna2.hpc.virginia.edu)
  - [rivanna3.hpc.virginia.edu](http://rivanna3.hpc.virginia.edu)



# EDITING FILES

---

# How to edit a file on Rivanna

You can use:

1. The built-in editor in Open-on-Demand. Just click on Files on the Dashboard, highlight the file that you want to edit and click on the edit button.
2. When in a Terminal Window, use vi or nano.
  - vi uses all keyboard shortcuts and may take a while to learn.
  - nano is a very basic editor. To launch, type: nano myfile.txt
3. In FastX, you can use gedit or any of your IDEs, like Spyder or Rstudio.



# CLUSTER ENVIRONMENT

---

# After you have logged in . . .

- You will be in your home directory.
- The home directory on Rivanna has 50GB of storage capacity.
- The home directory is for personal use and is not shareable with other users.



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# Checking your Allocation

- To see how many SUs you have available for running jobs, type **allocations** at the command-line prompt:

```
$ allocations
```

Account	Balance	Reserved	Available
robot_build	25000	0	25000
gizmonic-testing	921.952	0	921.952
crow-lab	928826	6236	922590
gypsy	0	0	0

for more information about a specific allocation, run:

'allocations -a <allocation name>'

allocations -a crow-lab

# Your /scratch Directory

- Each user will have access to 10 TB of **temporary** storage.
  - It is located in a subdirectory under /scratch, and named with your userID
  - e.g., `cd /scratch/mst3k`
  - You are limited to 350,000 files in your scratch directory.
  - The /scratch directory is for personal use and is not shareable with other users.

**Important:**

/scratch is **NOT permanent** storage and files that have not been accessed for more than **90 days** will be marked for deletion.



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# Running Jobs from Scratch

- We recommend that you run your jobs out of your /scratch directory for two reasons:
  - /scratch is on a Lustre filesystem (a storage system designed specifically for parallel access).
  - /scratch is connected to the compute nodes with Infiniband (a very fast network connection).

## We also recommend that

- You keep copies of your programs and data in more permanent locations (e.g., your home directory or leased storage).
- After your jobs finish, you copy the results to more permanent storage).



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# Checking your Storage

- To see how much disk space you have used in your home and scratch directories, open a Terminal window and type **hdquota** at the command-line prompt:

```
$ hdquota

Type      Location     Name      Size  Used  Avail  Use%
=====
home      /home        mst3k    50G  472M  50G  1%
                                               
Location   Age_Limit(Days)  Disk_Limit(GB)  Use(GB)  File_Limit  Use
=====
/scratch/mst3k  90          10240          0         350000      3
```



# Moving data onto Rivanna

You have several options for transferring data onto your home or /scratch directories.

1. Use the scp command in a terminal window.
2. Use a drag-and-drop option with MobaXterm (Windows) or Cyberduck (Mac OS).
3. For small files, use the Upload and Download buttons in the Open onDemand Files App
4. Use the web browser in the FastX desktop to download data from UVA Box.
5. Use the git clone command to copy git repositories
6. Set up a Globus endpoint on your laptop and use the Globus web interface to transfer files.

(See <https://www.rc.virginia.edu/userinfo/globus/> for details)



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# MODULES

---

# Modules

- Any application software that you want to use will need to be loaded with the **module load** command.
- For example:
  - module load matlab
  - module load anaconda/2019.10-py3.7
  - module load goolf/7.1.0\_3.1.4 R/4.0.0
- You will need to load the module any time that you create a new shell
  - Every time that you log out and back in
  - Every time that you run a batch job on a compute node



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# Module Details

- `module avail` – Lists all available modules and versions.
- `module spider` – Shows all available modules
- `module key keyword` – Shows modules with the keyword in the description
- `module list` – Lists modules loaded in your environment.
- `module load mymod` – Loads the default module to set up the environment for some software.
  - `module load mymod/N.M` – Loads a specific version N.M of software mymod.
  - `module load compiler mpi mymod` – For compiler- and MPI- specific modules, loads the modules in the appropriate order and, optionally, the version.
- `module purge` – Clears all modules.

# Learning more about a Module

- To locate a python module, try the following:

```
$ module avail python  
  
$ module spider python  
  
$ module key python
```

- To find bioinformatics software packages, try this:

```
$ module key bio
```

- The available software is also listed on our website:

<https://www.rc.virginia.edu/userinfo/rivanna/software/complete-list/>



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# PARTITIONS (QUEUES)

---

# Partitions (Queues)

- Rivanna has several partitions (or queues) for job submissions.
  - You will need to specify a partition when you submit a job.
  - To see the partitions that are available to you, type `qlist` at the command-line prompt.

```
$ qlist
```

Queue (partition)	Total Cores	Free Cores	Jobs Running	Jobs Pending	Time Limit	SU Charge
<hr/>						
bii	200	180	0	0	7:00:00:00	1
standard	200	180	0	0	7:00:00:00	1
dev	200	180	0	0	1:00:00	0
parallel	200	180	0	0	3:00:00:00	1
largemem	200	180	0	0	4:00:00:00	1
gpu	28	28	0	0	3:00:00:00	3
knl	200	180	0	0	3:00:00:00	1



# Compute Node Partitions (aka Queues)

Queue Name	Purpose	Job Time Limit	Memory / Node	Cores / Node
standard	For jobs on a single compute node	7 days	256 GB 384 GB	28 40
gpu	For jobs that can use general purpose graphical processing units (GP GPUs) (K80 or P100)	3 days	256 GB	16
parallel	For large parallel jobs on up to 120 nodes (<= 2400 CPU cores)	3 days	128 GB	40
largemem	For memory intensive jobs (<= 16 cores/node)	4 days	1 TB	16
dev	To run jobs that are quick tests of code	1 hour	128 GB	4





# SLURM SCRIPTS

---

# SLURM

- SLURM is the Simple Linux Utility for Resource Management.
  - It manages the hardware resources on the cluster (e.g. compute nodes/cpu cores, compute memory, etc.).
- SLURM allows you to request resources within the cluster to run your code.
  - It is used for submitting jobs to compute nodes from an access point (generally called a *frontend*).
  - Frontends are intended for editing, compiling, and very short test runs.
  - Production jobs go to the compute nodes through the resources manager.
- SLURM documentation:

<https://www.rc.virginia.edu/userinfo/rivanna/slurm/>

<http://slurm.schedmd.com/documentation.html>



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# SLURM Script Example for R

- A SLURM script is a bash script with SLURM directives (#SBATCH) and command-line instructions for running your program.

```
#!/bin/bash
#SBATCH --nodes=1          #total number of nodes for the job
#SBATCH --ntasks=1          #how many copies of code to run
#SBATCH --time=1-12:00:00    #amount of time for the whole job
#SBATCH --partition=standard #the queue/partition to run on
#SBATCH --account=myGroupName #the account/allocation to use

module purge
module load goolf/7.1.0_3.1.4 R  #load modules that my job needs
Rscript myProg.R                #command-line execution of my job
```



# SLURM Script Example for Python

- A SLURM script is a bash script with SLURM directives (#SBATCH) and command-line instructions for running your program.

```
#!/bin/bash
#SBATCH --nodes=1          #total number of nodes for the job
#SBATCH --ntasks=1          #how many copies of code to run
#SBATCH --time=1-12:00:00    #amount of time for the whole job
#SBATCH --partition=standard #the queue/partition to run on
#SBATCH --account=myGroupName #the account/allocation to use

module purge
module load anaconda/2019.10-py3.7 #load modules my job needs
python myProg.py                 #command-line execution of my job
```



# Submitting a SLURM Job

- To submit the SLURM command file to the queue, use the **sbatch** command at the command line prompt.
- For example, if the script on the previous slide is in a file named `job_script.slurm`, we can submit it as follows:

```
-bash-4.1$ sbatch job_script.slurm
Submitted batch job 18316
```



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# Checking Job Status

- To display the status of only your *active* jobs, type:

```
squeue -u <your_user_id>
```

```
-bash-4.2$ squeue -u mst3k

JOBID      PARTITION      NAME      USER      ST      TIME      NODES      NODELIST (REASON)
18316      standard      job_sci    mst3k     R       1:45      1          udc-aw38-34-1
```

- The `squeue` command will show pending jobs and running jobs, but not failed, canceled or completed job.



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# Checking Job Status

- To display the status of all jobs, type:

```
sacct -S <start_date>
```

```
-bash-4.2$ sacct -S 2019-01-29

3104009      RAXML_NoC+    standard  hpc_build          20  COMPLETED   0:0
3104009.bat+    batch      hpc_build          20  COMPLETED   0:0
3104009.0     raxmlHPC-+    hpc_build          20  COMPLETED   0:0
3108537      sys/dashb+    gpu       hpc_build          1  CANCELLED+ 0:0
3108537.bat+    batch      hpc_build          1  CANCELLED  0:15
3108562      sys/dashb+    gpu       hpc_build          1  TIMEOUT     0:0
3108562.bat+    batch      hpc_build          1  CANCELLED  0:15
3109392      sys/dashb+    gpu       hpc_build          1  TIMEOUT     0:0
3109392.bat+    batch      hpc_build          1  CANCELLED  0:15
3112064        srun       gpu       hpc_build          1  FAILED      1:0
3112064.0     bash       hpc_build          1  FAILED      1:0
```

- The `sacct` command lists all jobs (pending, running, completed, canceled, failed, etc.) since the specified date.



# Cancelling a Job

- To delete a job from the queue, use the **scancel** command with the job ID number at the command line prompt:

```
-bash-4.2$ scancel 18316
```

- To cancel all your jobs, run this command:

```
-bash-4.2$ scancel -u $USER
```



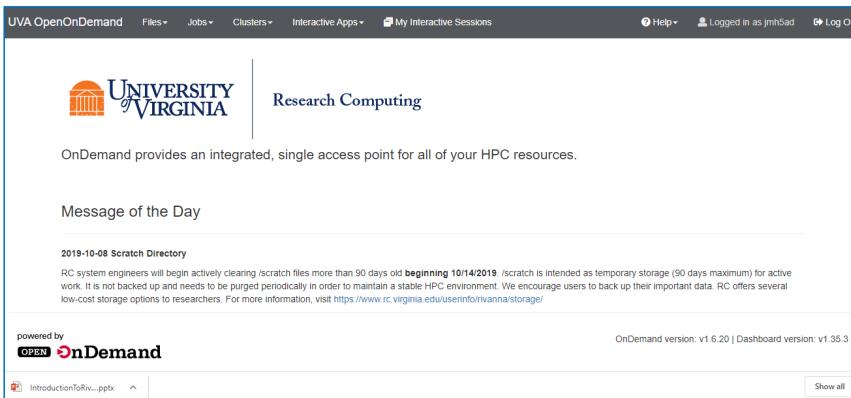
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# JUPYTERLAB

# Open onDemand Dashboard

- Open onDemand is the software that we use to create our web portal to Rivanna.
- As soon as you see the Dashboard (shown below), you are connected to Rivanna.



The screenshot shows the UVA OpenOnDemand dashboard. At the top, there's a navigation bar with links for 'UVA OpenOnDemand', 'Files', 'Jobs', 'Clusters', 'Interactive Apps', 'My Interactive Sessions', 'Help', 'Logged in as jmlisicki', and 'Log Out'. Below the navigation bar, the University of Virginia logo is displayed next to the text 'Research Computing'. A message states: 'OnDemand provides an integrated, single access point for all of your HPC resources.' Underneath, there's a 'Message of the Day' section with the date '2019-10-08' and a link to the 'Scratch Directory'. A note about scratch storage is present. At the bottom, it says 'powered by OPEN OnDemand' and shows a file named 'IntroductionToRivanna.pptx' with a preview icon. Version information 'OnDemand version: v1.6.20 | Dashboard version: v1.35.3' is also at the bottom.

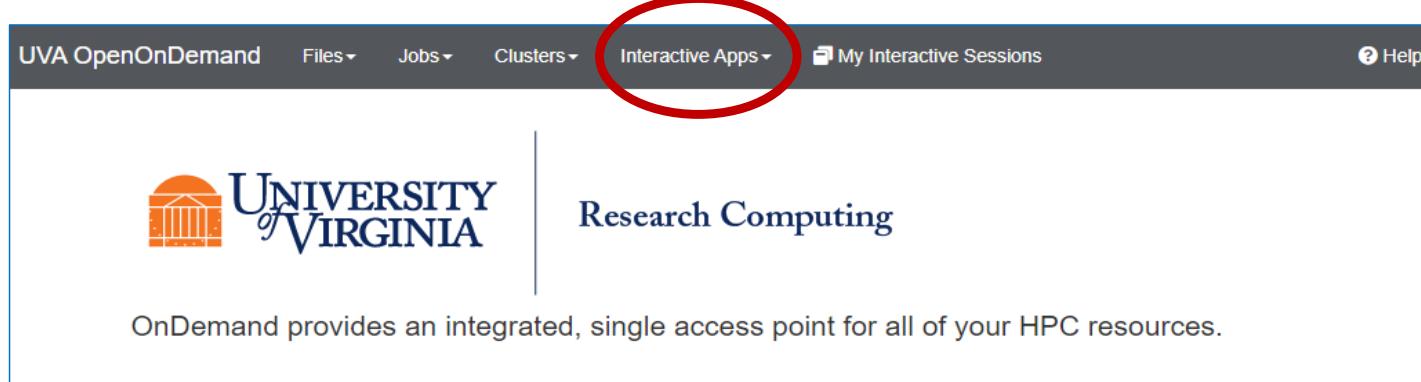


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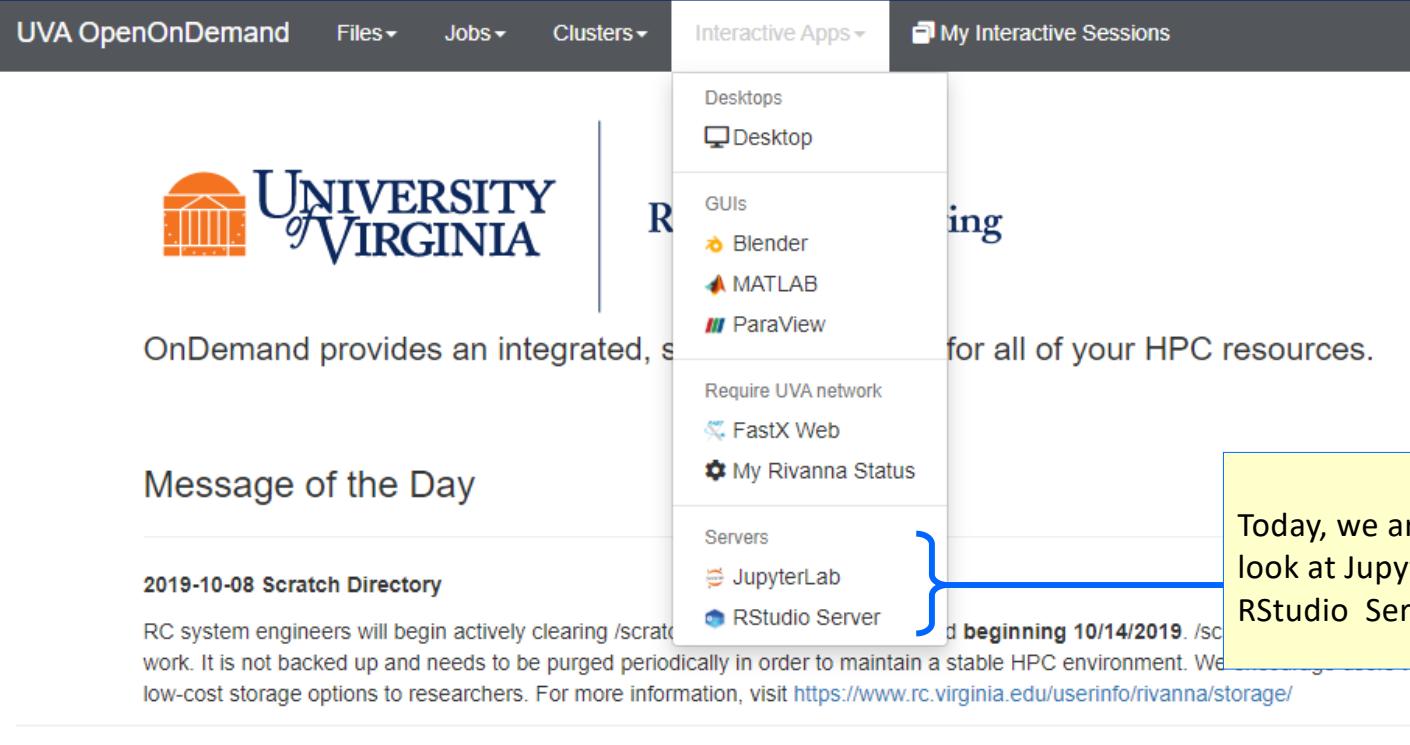
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# Open onDemand Dashboard

- The Dashboard gives you links to various applications.
- To see the links, click on “Interactive Apps” on the menu bar.



# Links to Applications



The screenshot shows the UVA OpenOnDemand web interface. At the top, there is a navigation bar with links for "UVA OpenOnDemand", "Files", "Jobs", "Clusters", "Interactive Apps", and "My Interactive Sessions". The "Interactive Apps" dropdown is open, showing a list of applications: "Desktops" (with "Desktop" option), "GUIs" (with "Blender", "MATLAB", and "ParaView" options), and "Servers" (with "FastX Web", "My Rivanna Status", "JupyterLab", and "RStudio Server" options). A yellow callout box with a blue border is positioned over the "RStudio Server" item, containing the text: "Today, we are going to look at JupyterLab and RStudio Server." A blue bracket is drawn from the right side of the "RStudio Server" entry to the start of the callout box.

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OnDemand provides an integrated, s

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for all of your HPC resources.

Message of the Day

2019-10-08 Scratch Directory

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d beginning 10/14/2019. /sc

Today, we are going to look at JupyterLab and RStudio Server.



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# JupyterLab

The screenshot shows the UVA OpenOnDemand web interface. At the top, there is a navigation bar with links for "UVA OpenOnDemand", "Files", "Jobs", "Clusters", "Interactive Apps", and "My Interactive Sessions". The "Interactive Apps" menu is open, showing a list of options: "Desktops" (with "Desktop" listed), "GUIs" (with "Blender", "MATLAB", and "ParaView" listed), "Require UVA network" (with "FastX Web" and "My Rivanna Status" listed), and "Servers" (with "JupyterLab" and "RStudio Server" listed). The "JupyterLab" option is circled in red. To the right of the interface, a yellow callout box contains the text "Click on JupyterLab.". At the bottom of the interface, there is a message about the scratch directory being purged starting on 10/14/2019. The University of Virginia logo is visible on the left side of the interface.

UVA OpenOnDemand

Files ▾ Jobs ▾ Clusters ▾

Interactive Apps ▾ My Interactive Sessions

Desktops

Desktop

GUIs

Blender

MATLAB

ParaView

Require UVA network

FastX Web

My Rivanna Status

Servers

JupyterLab

RStudio Server

OnDemand provides an integrated, s

Message of the Day

2019-10-08 Scratch Directory

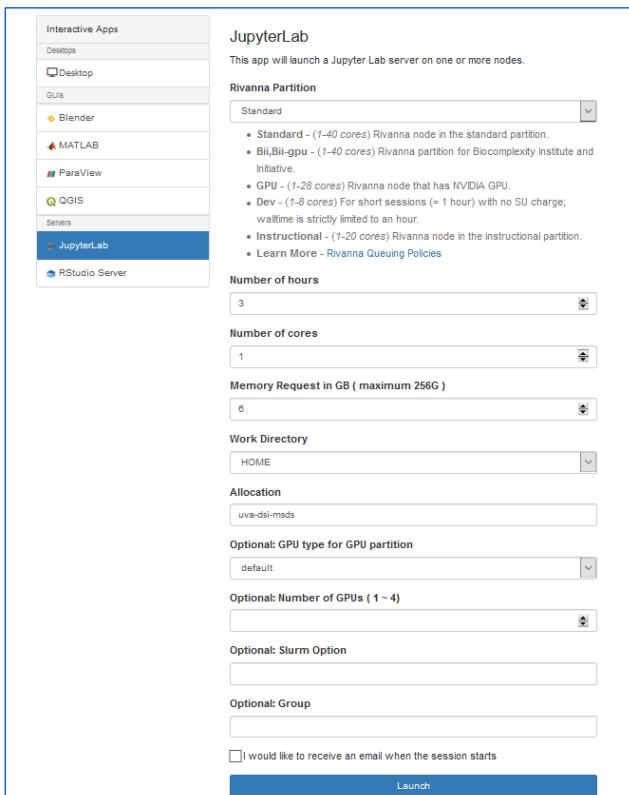
RC system engineers will begin actively clearing /scratch beginning 10/14/2019. /sc work. It is not backed up and needs to be purged periodically in order to maintain a stable HPC environment. We low-cost storage options to researchers. For more information, visit <https://www.rc.virginia.edu/userinfo/rivanna/storage/>

Click on JupyterLab.

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# JupyterLab Web Form



The screenshot shows a web-based application for launching a Jupyter Lab server. On the left, there's a sidebar titled "Interactive Apps" with categories like Desktops, Desktops, GUIs, and Servers. Under Servers, "JupyterLab" is selected and highlighted in blue. The main panel has a title "JupyterLab" and a sub-instruction: "This app will launch a Jupyter Lab server on one or more nodes." Below this is a section titled "Rivanna Partition" with a dropdown menu set to "Standard". A list of options follows: Standard - (1-40 cores) Rivanna node in the standard partition; BiBiLi-gpu - (1-40 cores) Rivanna partition for Biocomplexity Institute and Initiative; GPU - (1-28 cores) Rivanna node that has NVIDIA GPU; Dev - (1-8 cores) For short sessions (~ 1 hour) with no SU charge; walltime is strictly limited to an hour; Instructional - (1-20 cores) Rivanna node in the instructional partition; and a link to "Learn More - Rivanna Queuing Policies". There are several input fields: "Number of hours" (set to 3), "Number of cores" (set to 1), "Memory Request in GB (maximum 256G)" (set to 6), "Work Directory" (set to HOME), "Allocation" (set to uva-dsi-msds), "Optional: GPU type for GPU partition" (dropdown menu showing "default"), "Optional: Number of GPUs (1 ~ 4)" (empty input field), "Optional: Slurm Option" (empty input field), and "Optional: Group" (empty input field). At the bottom is a checkbox "I would like to receive an email when the session starts" and a blue "Launch" button.

- The Jupyter Web Form gathers information about the computing resources that you need for your Jupyter Notebook.
- After you fill in the form, it will re-populate with the same settings the next time that you connect to it.
- Let's look at how you would fill it in!

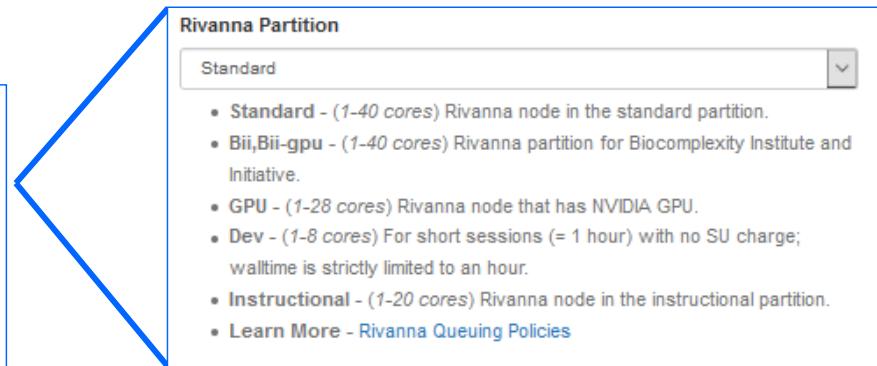


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# Rivanna Partition

The screenshot shows the JupyterLab interface. On the left, there's a sidebar titled "Interactive Apps" with categories like Desktops, Desktop, GUIs, and Servers. Under Servers, "JupyterLab" is selected. The main panel is titled "JupyterLab" and contains the following configuration:

- Rivanna Partition:** A dropdown menu set to "Standard".
- Number of hours:** A dropdown menu set to "3".
- Number of cores:** A dropdown menu set to "1".
- Memory Request in GB (maximum 256G):** A dropdown menu set to "8".
- Work Directory:** A dropdown menu set to "HOME".
- Allocation:** A dropdown menu set to "uva-dsi-msds".
- Optional: GPU type for GPU partition:** A dropdown menu set to "default".
- Optional: Number of GPUs (1 ~ 4):** An input field containing "1".
- Optional: Slurm Option:** An empty input field.
- Optional: Group:** An empty input field.
- I would like to receive an email when the session starts:** A checkbox.
- Launch:** A blue button at the bottom.



- Recall that Rivanna has lots of Compute Nodes.
- The nodes are partitioned (i.e., organized) by the type of processing that they can do.
- Most of the time, you will select the **Standard** partition.
- If you are running a deep learning model, you will want to choose a **GPU** Partition.

# Number of Hours

JupyterLab  
This app will launch a Jupyter Lab server on one or more nodes.

Rivanna Partition  
Standard

- Standard - (1-40 cores) Rivanna node in the standard partition.
- BiBiLi-gpu - (1-40 cores) Rivanna partition for Biocomplexity Institute and Initiative.
- GPU - (1-28 cores) Rivanna node that has NVIDIA GPU.
- Dev - (1-8 cores) For short sessions ( $\approx$  1 hour) with no SU charge; walltime is strictly limited to an hour.
- Instructional - (1-20 cores) Rivanna node in the instructional partition.
- Learn More - Rivanna Queuing Policies

Number of hours  
3

Number of cores  
1

Memory Request in GB ( maximum 256G )  
6

Work Directory  
HOME

Allocation  
uva-dsi-msds

Optional: GPU type for GPU partition  
default

Optional: Number of GPUs ( 1 ~ 4 )

Optional: Slurm Option

Optional: Group

I would like to receive an email when the session starts

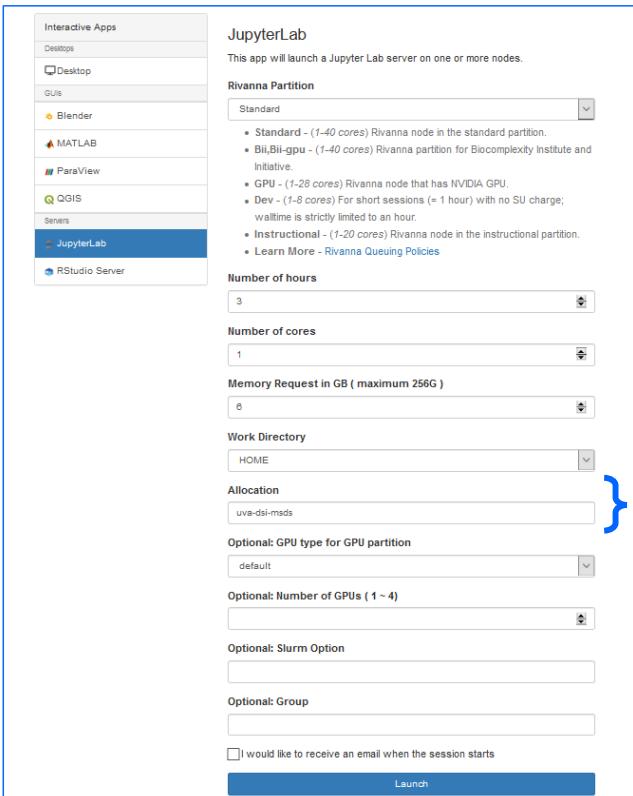
Launch

- The “Number of hours” is the amount of time that your session will be active.

Number of hours  
3

- Beware! When time runs out the session will end without warning!

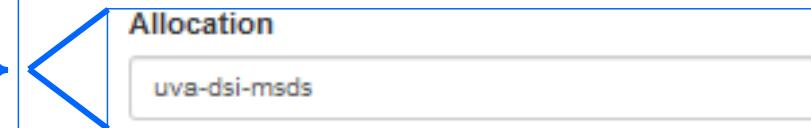
# Allocation



The screenshot shows a web-based form for launching a JupyterLab session. On the left, there's a sidebar titled "Interactive Apps" with categories: Desktops, Desktop, GUIs, and Servers. Under Servers, "JupyterLab" is selected. The main area is titled "JupyterLab" and contains the following fields:

- Rivanna Partition:** Standard (dropdown menu)
- Number of hours:** 3 (input field)
- Number of cores:** 1 (input field)
- Memory Request in GB (maximum 256G):** 6 (input field)
- Work Directory:** HOME (dropdown menu)
- Allocation:** uva-dsi-msds (input field)
- Optional: GPU type for GPU partition:** default (dropdown menu)
- Optional: Number of GPUs (1 ~ 4):** (input field)
- Optional: Slurm Option:** (input field)
- Optional: Group:** (input field)
- I would like to receive an email when the session starts:** (checkbox)
- Launch:** (blue button)

- The allocation is a special MyGroups group that allows you to have access to Rivanna.
- You must be a member of a Rivanna-enabled MyGroup to have an active account.
- In general, your professor or research advisor will add you as a member to an allocation.



- You can have membership in more than one allocation.

# Launch

The screenshot shows a web-based interface for launching a JupyterLab session. On the left, a sidebar lists "Interactive Apps" including Desktops, Desktop, GUIs (Blender, MATLAB, ParaView, QGIS), Servers (JupyterLab, RStudio Server), and a "Launch" button. The main area is titled "JupyterLab" and describes the app as launching a Jupyter Lab server. It includes a dropdown for "Rivanna Partition" set to "Standard", a "Number of hours" input field containing "3", a "Number of cores" input field containing "1", a "Memory Request in GB (maximum 256G)" input field containing "6", a "Work Directory" dropdown set to "HOME", and several optional fields: "Allocation" (uva-dsi-msds), "Optional: GPU type for GPU partition" (default), "Optional: Number of GPUs (1 ~ 4)", "Optional: Slurm Option", "Optional: Group", and a checkbox for "I would like to receive an email when the session starts". A large blue "Launch" button is at the bottom.

- Clicking on the “Launch” button will submit a request for the resources that you want.

- There will be a slight delay before the resources are available.



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# Waiting for the Session to Start

JupyterLab (12492035)

Created at: 2020-05-29 00:18:04 EDT

Time Requested: 3 hours

Session ID: [5763459f-60b3-4af3-a4f4-379d56a61354](#)

Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested.

Queued

Delete

JupyterLab (12492035)

Host: [jude-ba25-23](#)

Created at: 2020-05-29 00:18:04 EDT

Time Remaining: 2 hours and 59 minutes

Session ID: [5763459f-60b3-4af3-a4f4-379d56a61354](#)

1 node | 1 core | Running

Delete

Connect to Jupyter

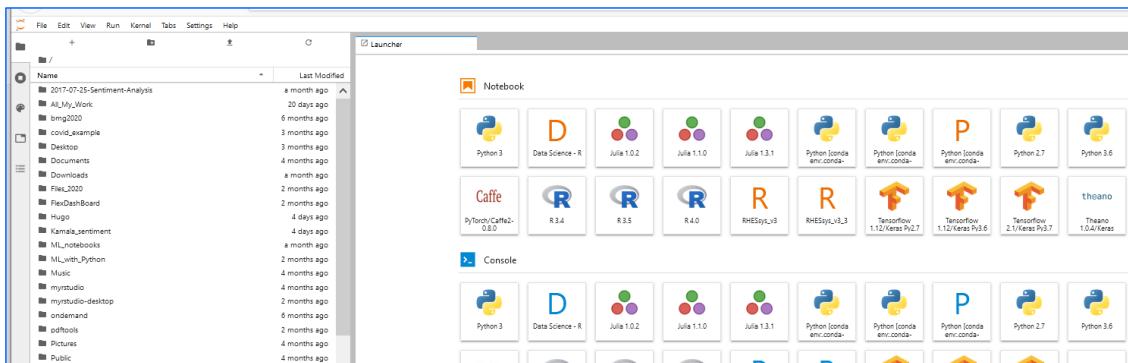


The screen will transition from a “Please be patient” statement to a “Connect to Jupyter” button.

Click on the “Connect to Jupyter” button.

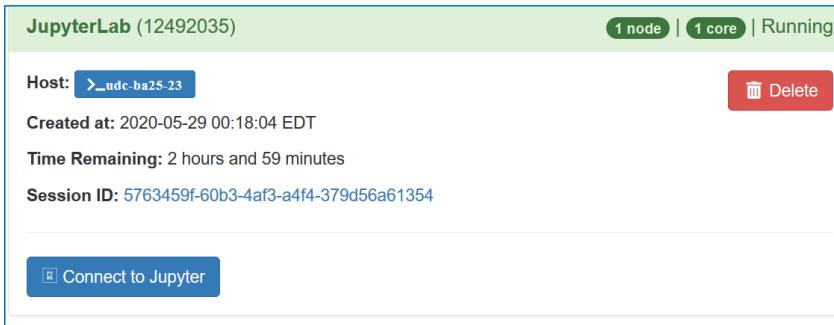
# Hands-on Activity

- Connect to Open onDemand and start a JupyterLab session.
  - When it comes up, you will see a list of files (if any) in your home directory and a set of tiles for underlying applications (e.g., Python, R, Tensorflow).
  - You may see a slightly different set of tiles in your account – there are some customized tiles in this account.



# Deleting Your Session

- When you are done with your Jupyter Notebook, it is very important to delete the session.
- Go back to the browser tab labeled “Interactive Sessions” and click on the red “Delete” button.



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# RSTUDIO SERVER

# RStudio Server

The screenshot shows the UVA OpenOnDemand web interface. At the top, there is a navigation bar with links for "UVA OpenOnDemand", "Files", "Jobs", "Clusters", "Interactive Apps", and "My Interactive Sessions". The "Interactive Apps" menu is open, showing categories like "Desktops", "GUIs", and "Servers". In the "Servers" category, the "RStudio Server" option is circled in red. A yellow callout box with a blue border is positioned to the right of the circled link, containing the text: "Return to the Dashboard tab and click on RStudio Server." Below the navigation bar, the main content area features the University of Virginia logo and a message about OnDemand providing an integrated service for HPC resources. A "Message of the Day" section is present, along with a "2019-10-08 Scratch Directory" update.

OnDemand provides an integrated, s

ing

for all of your HPC resources.

Message of the Day

2019-10-08 Scratch Directory

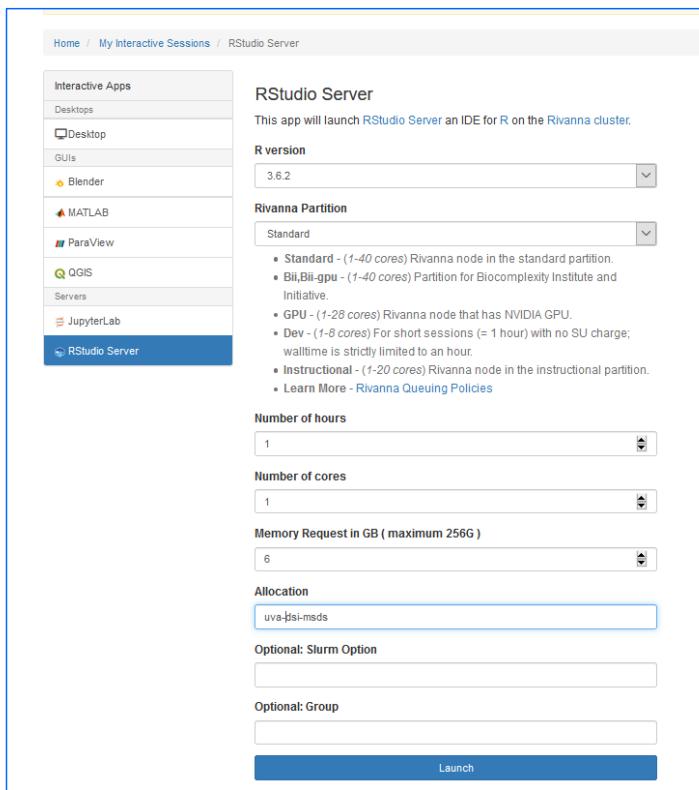
RC system engineers will begin actively clearing /scratch and beginning 10/14/2019. /sc work. It is not backed up and needs to be purged periodically in order to maintain a stable HPC environment. We low-cost storage options to researchers. For more information, visit <https://www.rc.virginia.edu/userinfo/rivanna/storage/>

Return to the Dashboard tab and click on RStudio Server.



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# RStudio Web Form



The screenshot shows the RStudio Server web form. On the left, there's a sidebar with a navigation menu under 'Interactive Apps' containing options like Desktops, GUIs (Blender, MATLAB, ParaView, QGIS), Servers (JupyterLab), and RStudio Server (which is highlighted). The main content area has a title 'RStudio Server' and a subtitle: 'This app will launch RStudio Server an IDE for R on the Rivanna cluster.' It includes fields for 'R version' (set to 3.6.2), 'Rivanna Partition' (set to Standard), 'Number of hours' (set to 1), 'Number of cores' (set to 1), 'Memory Request in GB (maximum 256G)' (set to 6), and an 'Allocation' field containing 'uva-hsi-msds'. There are also optional fields for 'Slurm Option' and 'Group'. At the bottom is a large blue 'Launch' button.

- The RStudio Web Form is similar to what you saw with the Jupyter Web Form.
- Let's take a quick look at some of the fields.



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# R Version

The screenshot shows the RStudio Server configuration interface. The left sidebar lists "Interactive Apps" including Desktops, GUIs (Blender, MATLAB, ParaView, QGIS), Servers (JupyterLab), and RStudio Server (which is selected). The main panel is titled "RStudio Server" and describes launching RStudio Server on the Rivanna cluster. It includes fields for "R version" (set to 3.6.2), "Rivanna Partition" (set to Standard), "Number of hours" (1), "Number of cores" (1), "Memory Request in GB (maximum 256G)" (6), and an "Allocation" field containing "uva-bisi-msds". There are also optional fields for "Slurm Option" and "Group". A large blue bracket on the right side of the slide points to the "R version" field in the screenshot.

## R version

3.6.2

- We have three versions of R available.
- R/3.6.2 is the most stable at this time.



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# Rivanna Partition

The screenshot shows the JupyterLab web form for launching an RStudio Server session on the Rivanna cluster. The 'Rivanna Partition' dropdown is set to 'Standard'. The description below it lists several partition options:

- Standard - (1-40 cores) Rivanna node in the standard partition.
- Bii,Bii-gpu - (1-40 cores) Partition for Biocomplexity Institute and Initiative.
- GPU - (1-28 cores) Rivanna node that has NVIDIA GPU.
- Dev - (1-8 cores) For short sessions (= 1 hour) with no SU charge; walltime is strictly limited to an hour.
- Instructional - (1-20 cores) Rivanna node in the instructional partition.
- Learn More - Rivanna Queuing Policies

Other configuration fields visible include R version (3.6.2), Number of hours (1), Number of cores (1), Memory Request in GB (maximum 256G) (6), Allocation (uva-bisi-msds), Optional: Slurm Option, and Optional: Group. A 'Launch' button is at the bottom.

- The partitions are the same as in the JupyterLab Web Form, but we recommend mostly **Standard**, **Dev**, or **Instructional** for RStudio Server.

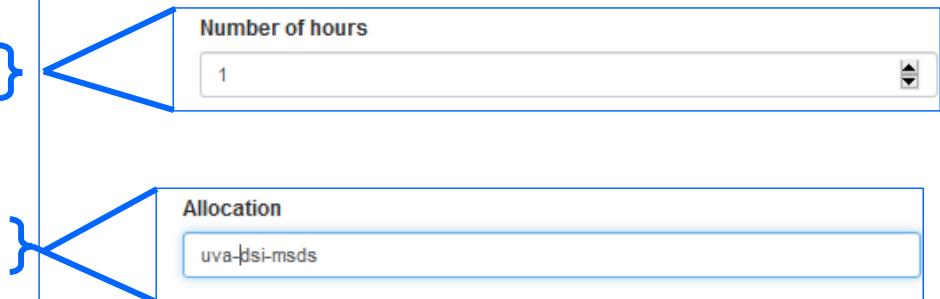


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# Number of hours & Allocation

The screenshot shows the RStudio Server configuration page. On the left, a sidebar lists various interactive apps: Desktops, Desktop, GUIs, Blender, MATLAB, ParaView, QGIS, Servers, JupyterLab, and RStudio Server. The RStudio Server option is selected and highlighted in blue. The main panel displays the RStudio Server configuration. It includes fields for R version (set to 3.6.2), Rivanna Partition (set to Standard), Number of hours (set to 1), Number of cores (set to 1), Memory Request in GB (maximum 256G) (set to 6), Allocation (set to uva-hsi-msds), and optional fields for Slurm Option and Group. A large blue bracket on the right side of the slide groups the 'Number of hours' and 'Allocation' fields.

- The Number of hours and the Allocation are the same as in the JupyterLab Web Form.



# Launch

The screenshot shows the "Interactive Apps" section of a web-based resource management interface. The "RStudio Server" app is selected. The form includes:

- R version:** 3.6.2
- Rivanna Partition:** Standard (dropdown menu listing: Standard, BiIBI-gpu, GPU, Dev, Instructional, Learn More - Rivanna Queuing Policies)
- Number of hours:** 1
- Number of cores:** 1
- Memory Request in GB (maximum 256G):** 6
- Allocation:** uva-bsi-msds
- Optional: Slurm Option:** (empty input field)
- Optional: Group:** (empty input field)

A large blue "Launch" button is at the bottom.

- Clicking on the “Launch” button will submit a request for the resources that you want.
- Again, there will be a slight delay before the resources are available.



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# Waiting for the Session to Start

RStudio Server (15654717)

Queued

Created at: 2020-09-22 23:44:55 EDT

Time Requested: 1 hour

Session ID: b5be6480-4df8-4045-92d4-5adf97d6cbae

Delete

Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested.

RStudio Server (15654717)

1 node | 1 core | Running

Host: >\_adc-ba25-34c0

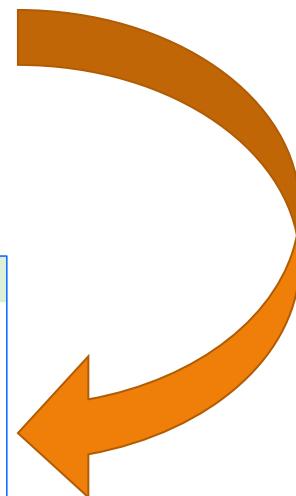
Created at: 2020-09-22 23:44:55 EDT

Time Remaining: 59 minutes

Session ID: b5be6480-4df8-4045-92d4-5adf97d6cbae

Delete

[@ Connect to RStudio Server](#)

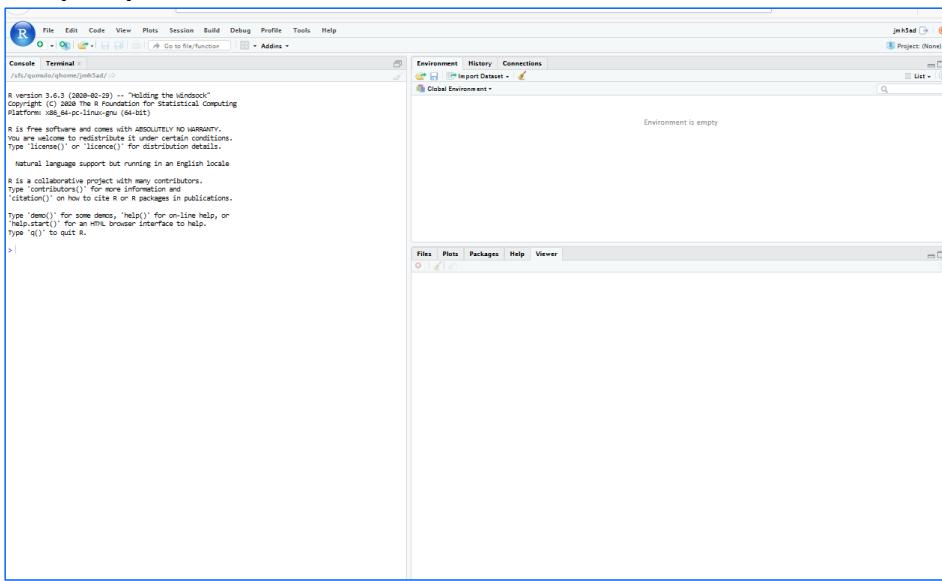


The screen will transition from a “Please be patient” statement to a “Connect to RStudio Server” button.

Click on the “Connect to RStudio Server” button.

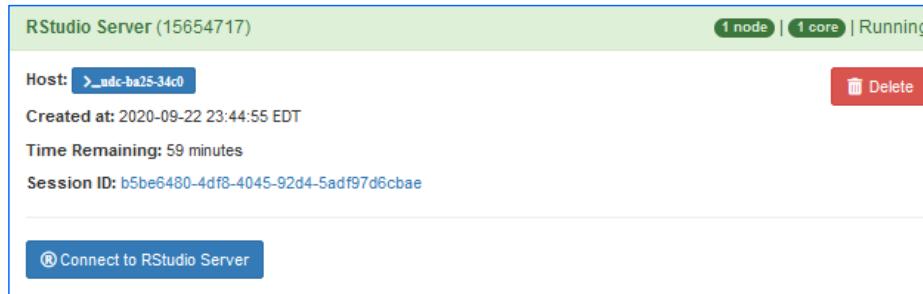
# Hands-on Activity

- Connect to Open onDemand and start an RStudio Server session.
  - When it comes up, you will see an RStudio interface – just like you would see on your laptop.



# Deleting Your Session

- Again, when you are done with RStudio Server, it is very important to delete the session.
- Go back to the browser tab labeled “Interactive Sessions” and click on the red “Delete” button.



# What about the other fields?

Field	Description
Number of cores	Used in parallel processing. Your code must be modified to take advantage of using multiple cores.
Memory Request in GB	When dealing with Big Data, you will need to increase the amount of memory. My rule-of-thumb: request 2 to 3 times the size of data that you are reading in or generating.
Work Directory	Allows you to change the working directory of a Jupyter Notebook to your /scratch folder.
Optional: Slurm Option	Allows you to provide advanced features, like requesting specific nodes or providing a reservation
Optional Group	Only needed if you are in more than 16 allocations. You may need to force Rivanna to see your allocation.
Optional: GPU type for GPU partition & Optional: Number of GPUs	Only needed if you are running on a GPU node. The “default” for GPU type will put you on the first available GPU node. For now, the number of GPUs should be 1.

# NEED HELP?

## Research Computing Zoom Office Hours

Tuesdays: 3 pm – 5 pm

Thursdays: 10 am – noon

Or, contact us through the forms at:

<https://www.rc.virginia.edu/support/>

To connect to the Zoom sessions,  
go to  
<https://www.rc.virginia.edu/support/#office-hours> and click on the  
“Join us via Zoom” button



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