OPEN ONDEMAND 101

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OOD 101

Outline



What to Expect from Open OnDemand 101?

Objectives

- Understand how science gateways like Open OnDemand address the challenges faced in typical high-performance computing (HPC) work
- Ensure you know how to login to Open OnDemand with your ACCESS account associated with your allocation here on Anvil
- Become comfortable with the purpose and location of different features in Open OnDemand
- Feel confident running your own workflows in Open OnDemand



00D 101

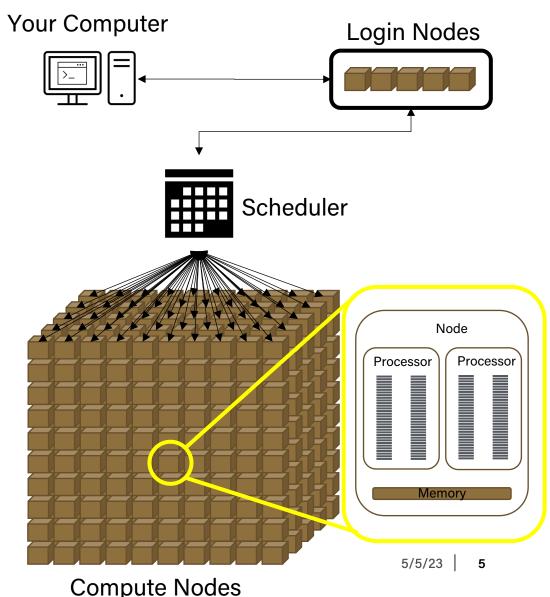
Lowering the Barrier to HPC



Lowering the Barrier to HPC

Layout of a Cluster

- HPC systems are often organized into clusters
 - We call them clusters because they are a multitude of independent nodes that can communicate with one another
 - Because each node is independent, we can have different types of nodes with specialized hardware
- When you login to a cluster, typically you will land on login node along with all the other users on the cluster
 - In order to carve out dedicated resources for your work, you need to ask the scheduler to allocate you resources on the compute nodes

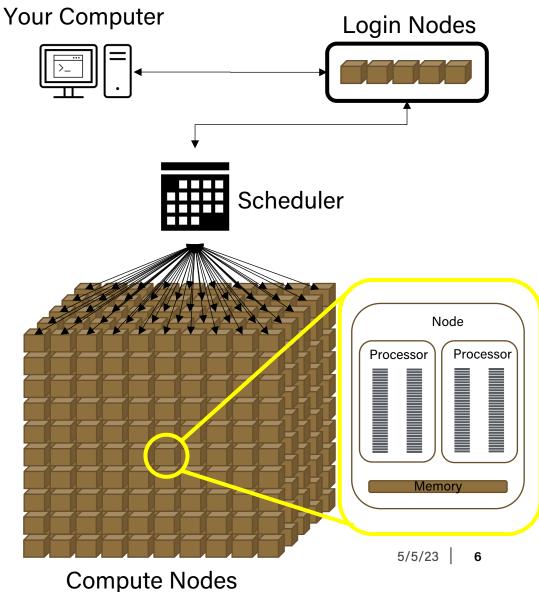




Lowering the Barrier to HPC

HPC Presents a Steep Learning Curve

- Working within HPC in this traditional manner presents many challenges to new users
 - Typically use an SSH client/Linux terminal
 - Learning new commands for interacting with the scheduler
 - Software runs without a graphical user interface (GUI)
- This can lead to new domain scientists spending most of their time learning how to use the system as opposed to doing science

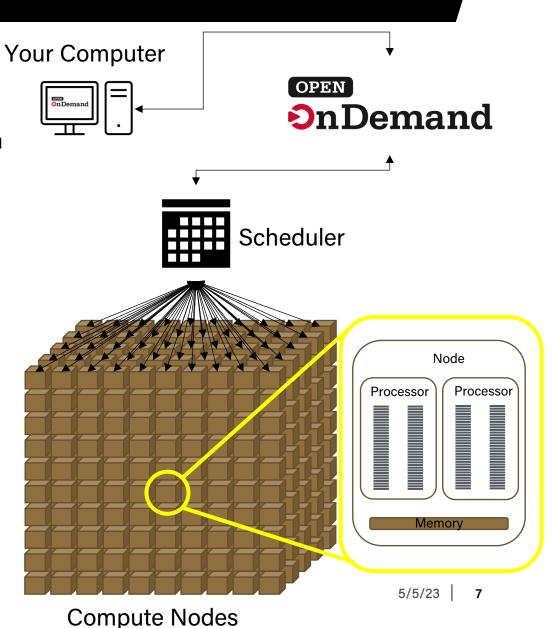




Lowering the Barrier to HPC

Science Gateways

- To make these resources easier to use, there has been a push for the creation of "science gateways"
- Science Gateways are typically web based interfaces that allow users to run science/engineering applications on HPC resources from their web browser
- Open OnDemand is an example of such a science gateway





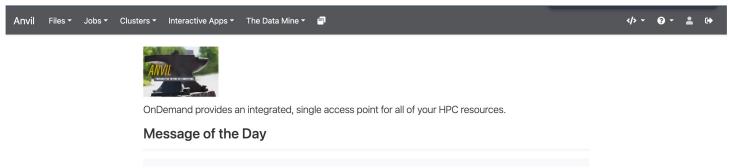
00D 101

Using Open OnDemand: Dashboard



Logging into Open OnDemand

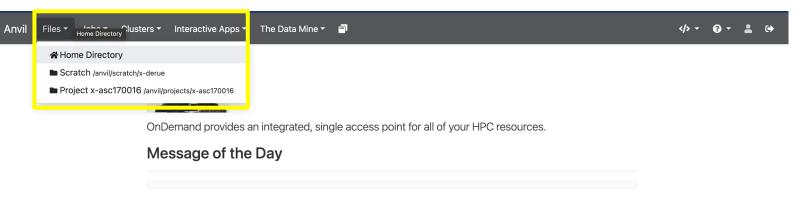
- We offer Open OnDemand on Anvil here at Purdue which can be found by navigating to:
 - ondemand.anvil.rcac.purdue.edu
- Upon navigating to this URL, you will need to login with your ACCESS username and password as well as use 2FA
- Once you are logged in, you will land on your dashboard page
 - My dashboard for can be seen on the right





Getting Familiar with The Dashboard

- 1. Directory Shortcuts
 - Allows you to quickly navigate between your important directories
 - Clicking these will open a file navigator allowing you to view your files or upload/download files to/from the cluster

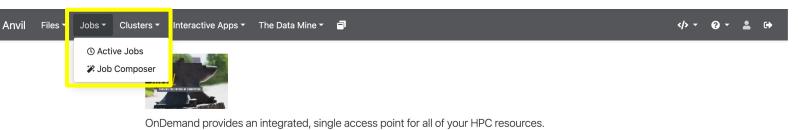




Getting Familiar with The Dashboard

2. Jobs Menu

 Provides shortcuts to widgets for creating new Slurm jobs as well as viewing the status of your current ones



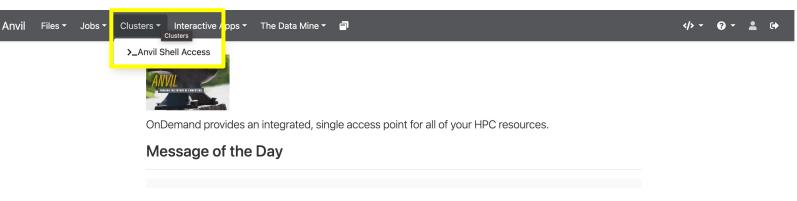
Message of the Day



Getting Familiar with The Dashboard

3. Cluster

- Provides options for interacting with the cluster directly
- Anvil Shell Access will provide you with a Unix shell on one of the login nodes





Getting Familiar with The Dashboard

- 4. Interactive Application Menu
 - This dropdown lists all the applications we support on Open OnDemand
 - Clicking one of the applications will take you to a form through which you can request the resources you want to use

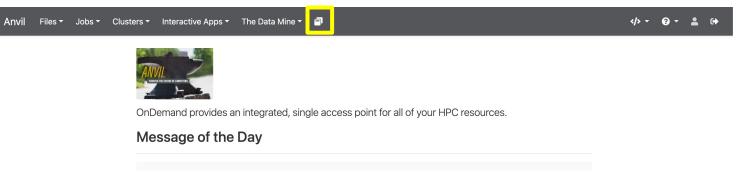
| Anvil | Files 🕶 | Jobs 🕶 | Clusters - | Interactive Apps 🔻 | The Data Mine | - P | > - | •• | 2 | • |
|---------|---------|--------|------------|-----------------------------|---------------|--|---------|-----------|---------|-----|
| | | | OnE | TassalF | omics Viewer | ngle access point for all of your HPC resources. | | | | |
| | | | | A MATLAB | | | | | | |
| powered | | emar | hd | Servers ⊜ Jupyter Notebo | ok | | OnDeman | d versior | n: v2.0 | .20 |



Getting Familiar with The Dashboard

5. My Interactive Sessions

• This will take you to a page wherein you can access all your currently running application sessions





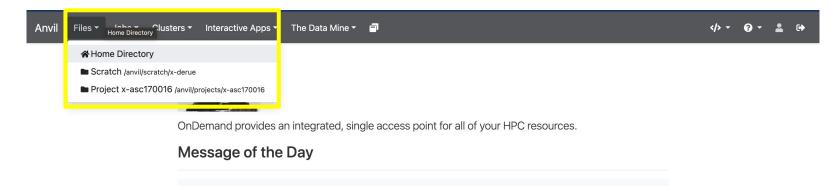
00D 101

Using Open OnDemand: Files



A Web-Based File Explorer

- 1. To access the File Explorer, click on one of the mounted locations listed in the Files dropdown
 - This will open a new tab containing the File Explorer





A Web-Based File Explorer

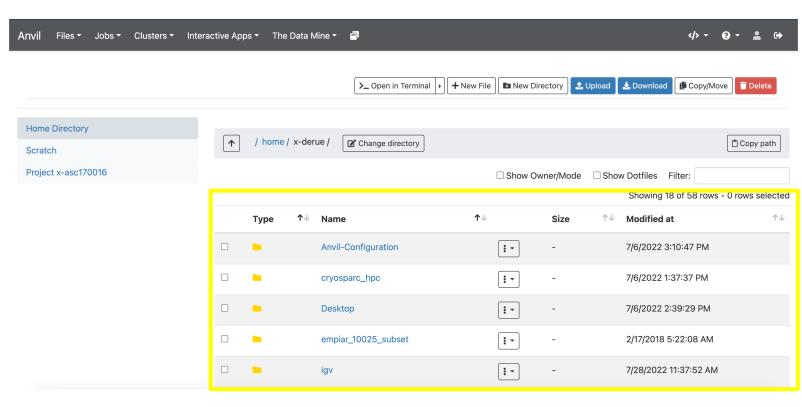
- 2. The menu along the left-hand side of the screen is for navigating to the top-level directories for your home, project, and scratch spaces
 - Even if you change the directory you are currently examining, this menu will continue to display the same shortcuts

| ractive Apps 👻 The Data | a Mine 👻 🗐 | | |
|-------------------------|---|-------------------|---|
| | >_ Open in Terminal +) | + New File | Upload 🕹 Download 🕒 Copy/Move 🔋 🗑 Delete |
| ↑ / home / x-de | lerue / 🕜 Change directory | | Copy path |
| | | □ Show Owner/Mode | Show Dotfiles Filter: Showing 18 of 58 rows - 0 rows selected |
| Type ↑↓ | ↓ Name | ↑ ↓ Size | $\uparrow \downarrow$ Modified at $\uparrow \downarrow$ |
| | Anvil-Configuration | - | 7/6/2022 3:10:47 PM |
| | cryosparc_hpc | - | 7/6/2022 1:37:37 PM |
| | Desktop | - | 7/6/2022 2:39:29 PM |
| | empiar_10025_subset | - | 2/17/2018 5:22:08 AM |
| | igv | - | 7/28/2022 11:37:52 AM |
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A Web-Based File Explorer

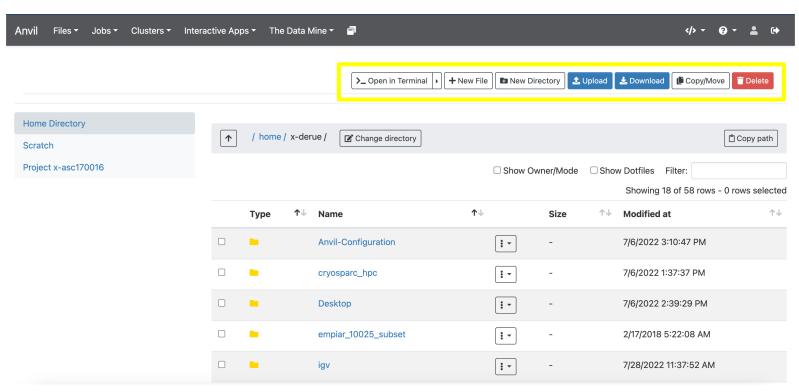
- 3. The central part of this webpage displays the contents of your present working directory as well along with some metadata like the last modified timestamps
 - The result of selecting a file depends on the type of file you select:
 - Selecting a text file will open that file in a viewer whereas selecting a binary file like an executable will download it





A Web-Based File Explorer

4. The toolbar in the upper right corner provides tools for changing your current directory, opening your current directory in a terminal to apply shell commands to the files, and creating new files/directories that are either empty or uploaded from your local workstation.





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Using Open OnDemand: Applications



Application Forms

- To access the App Form for "Desktop", select it from the Interactive Apps dropdown on the Dashboard
 - The form will be opened in your current tab
 - You can return to the Dashboard by clicking on "Anvil" in the top left corner

| Anvil | Files 🕶 | Jobs 🕶 | Clusters - | Interactive Apps - | The Data Mine - | - | | | | | - | •• | 2 | ۥ |
|-----------------|-----------|--------|------------|---|----------------------------|------------|-------------------|----------------|-----------|----|--------|-----------|---------|-----|
| | | | OnD | Bioinformatics Apps Integrative Genor MEGAN MaxQuant QualiMap | | ngle acces | s point for all c | of your HPC re | esources. | | | | | |
| า | | | Ме | Tassel5 💿 scRNAseq RStudi | | | | | | | | | | |
| ٢ | | | | Cryo-EM Apps CryoSPARC RELION | | | | | | | | | | |
| rd | | | | Desktops | | | | | | | | | | |
| | | | | GUIs MATLAB Servers | | | | | | | | | | |
| powered OPEN | ەر DnD | emai | nd | Servers | < | | | | | Or | Demano | l versior | n: v2.0 | .20 |



Application Forms

2. You can navigate to other Interactive Apps by selecting them from the left-hand menu

| Interactive Apps | Desktop |
|-----------------------------|--|
| Bioinformatics Apps | This app will launch an interactive desktop on one or more |
| Integrative Genomics Viewer | compute nodes. Allocation |
| MEGAN | asc170016-gpu (4889.4 SUs remaining) |
| 🜇 MaxQuant | Queue (partition) |
| 🛶 QualiMap | gpuGPU-only allocations MUST use the 'gpu' queue |
| 🚡 Tassel5 | CPU-only allocations MAY NOT use the 'gpu' queue |
| ® scRNAseq RStudio | Wall Time in Hours |
| Cryo-EM Apps | 1 |
| & CryoSPARC | Number of hours you are requesting for your job. |
| | Cores |
| Desktops | 1 |
| - Desktop | Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores per node requested |
| GUIs | |

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Home / My Interactive Sessions / Desktop



Application Forms

3. In order to request access to dedicated resources, you must select the allocation to charge your resource usage to. You may have more than one type of allocation (CPU vs. GPU). Ensure that you're selecting the correct one

Home / My Interactive Sessions / Desktop

| Interactive Apps | Desktop | | | | | |
|-----------------------------|---|--|--|--|--|--|
| Bioinformatics Apps | This app will launch an interactive desktop on one or more compute nodes. | | | | | |
| Integrative Genomics Viewer | Allocation | | | | | |
| MEGAN | asc170016 (75102.6 SUs remaining) ~ | | | | | |
| 🜇 MaxQuant | Queue (partition) | | | | | |
| 🗤 QualiMap | • GPU-only allocations MUST use the 'gpu' queue | | | | | |
| 🚡 Tassel5 | CPU-only allocations MAY NOT use the 'gpu' queue | | | | | |
| ® scRNAseq RStudio | Wall Time in Hours | | | | | |
| Cryo-EM Apps | 1 | | | | | |
| % CryoSPARC | Number of hours you are requesting for your job. | | | | | |
| ∞ RELION | Cores | | | | | |
| Desktops | Number of some (up to 100) for a shared isk. Northern t | | | | | |
| ₽Desktop | Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores | | | | | |
| GUIs | per node requested | | | | | |



Application Forms

In addition to your allocation, 4. you must specify the partition to which you want to submit your job. Each of the partitions has a specialized use case, and submitting to the wrong partition can cause you to use more SUs than you intend. Refer to our knowledge guide for more information.

Home / My Interactive Sessions / Desktop

| Interactive Apps | Desktop | | | | |
|-----------------------------------|---|--|--|--|--|
| Bioinformatics Apps | This app will launch an interactive desktop on one or more | | | | |
| i≓ Integrative Genomics Viewer | compute nodes. Allocation | | | | |
| MEGAN | asc170016 (75102.6 SUs remaining) | | | | |
| 🜇 MaxQuant | Queue (partition) | | | | |
| 🗤 QualiMap | shared GPU-only allocations MUST use the 'gpu' queue | | | | |
| Tassel5 | CPU-only allocations MAY NOT use the 'gpu' queue | | | | |
| ® scRNAseq RStudio | Wall Time in Hours | | | | |
| Cryo-EM Apps | • | | | | |
| * CryoSPARC | Number of hours you are requesting for your job. | | | | |
| ·• RELION | Cores | | | | |
| Desktops | Number of cores (up to 100) for a shared ish. New shared | | | | |
| ₽Desktop | Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores | | | | |
| GUIs | per node requested | | | | |

https://www.rcac.purdue.edu/knowledge/anvil/run/partitions



Application Forms

- 5. You must also specify the number/type of resources you wish to have allocated and for how long you intend to use them
 - You will be given memory proportional to the number of CPUs requested on the node type in the partition you select
 - Shared/Wholenode: ~2 GB/CPU
 - GPU: ~3.5GB/CPU
 - Highmem: 8GB/CPU

| 🜇 MaxQuant | Queue (partition) |
|--------------------|---|
| 🗤 QualiMap | gpu ~ GPU-only allocations MUST use the 'gpu' queue |
| Tassel5 | CPU-only allocations MAY NOT use the 'gpu' queue |
| ® scRNAseq RStudio | Wall Time in Hours |
| Cryo-EM Apps | |
| & CryoSPARC | Number of hours you are requesting for your job. |
| RELION | Cores |
| Desktops | |
| ☐ Desktop | Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores |
| GUIs | per node requested |
| 📣 MATLAB | Number of GPUs |
| Servers | 1 ~ |
| 😇 Jupyter Notebook | Number of Nvidia A100 GPUs you are requesting. |
| 🗢 RStudio Server | Launch |



Application Forms

6. After selecting the options you would like for your session, click launch to send your request to the scheduler

| Image: Second | 🜇 MaxQuant | Queue (partition) |
|---|--------------------|--|
| GPU-only allocations MUST use the 'gpu' queue CPU-only allocations MAY NOT use the 'gpu' queue CPU-only allocations MAY NOT use the 'gpu' queue CPU-only allocations MAY NOT use the 'gpu' queue Wall Time in Hours 1 Number of hours you are requesting for your job. Cores RELION 1 Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores per node requested Number of GPUs 1 Number of GPUs 1 Number of Nvidia A100 GPUs you are requesting. | | gpu |
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| scRNAseq RStudio Cryo-EM Apps CryoSPARC RELION Desktops Unmber of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores per node requested Number of GPUs Servers Jupyter Notebook | Tassel5 | CPU-only allocations MAY NOT use the 'gpu' queue |
| Cryo-EM Apps & CryoSPARC & CryoSPARC RELION Desktops Desktop GUIs MATLAB Servers Jupyter Notebook 1 Number of CPUs Number of Nvidia A100 GPUs you are requesting. | scRNAseg RStudio | Wall Time in Hours |
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| ↓ Desktop Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores per node requested GUIs Number of GPUs ▲ MATLAB 1 Servers 1 → Jupyter Notebook Number of Nvidia A100 GPUs you are requesting. | RELION | 1 |
| □ Desktop □ GUIs ▲ MATLAB Servers □ Jupyter Notebook Instant of Servers Instan | Desktops | Number of cores (up to 128) for a shared job. Non-shared |
| GUIs Number of GPUs ▲ MATLAB 1 Servers 1 ☑ Jupyter Notebook Number of Nvidia A100 GPUs you are requesting. | ⊈ Desktop | jobs will have exclusive nodes and be charged at 128 cores |
| ▲ MATLAB Servers | GUIs | per node requested |
| Jupyter Notebook | 📣 MATLAB | Number of GPUs |
| | Servers | 1 |
| RStudio Server | 🚎 Jupyter Notebook | Number of Nvidia A100 GPUs you are requesting. |
| | 🗢 RStudio Server | Launch |



Application Forms

- 7. This will create a "card" for this session which will assign it two IDs
 - The first ID is the Slurm scheduler's • job ID and is parenthesized next to the application name
 - The second ID is the Session ID and • is the name of the directory where Open OnDemand will track information about the session
 - Clicking this session ID will open this directory in the File Explorer •
 - When the scheduler finds resources • for your job, the card will transform into the second image, and you can access the application by clicking the blue button labelled "Launch..."



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| iteractive Apps | Desktop (1677891) | 1 node 1 core Running |
|------------------|------------------------------------|-----------------------------|
| informatics Apps | | |
| Integrative | Host: >_a240.anvil.rcac.purdue.edu | 🛅 Delete |
| nomics Viewer | Created at: 2023-05-05 10:57:4 | 14 EDT |
| MEGAN | Time Remaining: 59 minutes | |
| MaxQuant | Session ID: c6f0c9a0-af73-49c | 2-b8b6-26369d037cb3 |
| QualiMap | Compression | Image Quality |
| Quantap | 0 | 0 |
| Tassel5 | 0 (low) to 9 (high) | 0 (low) to 9 (high) |
| scRNAseq RStudio | Launch Desktop | View Only (Share-able Link) |
| ryo-EM Apps | | |

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Home / My Interactive Sessions

Home / My Interactive Sessions

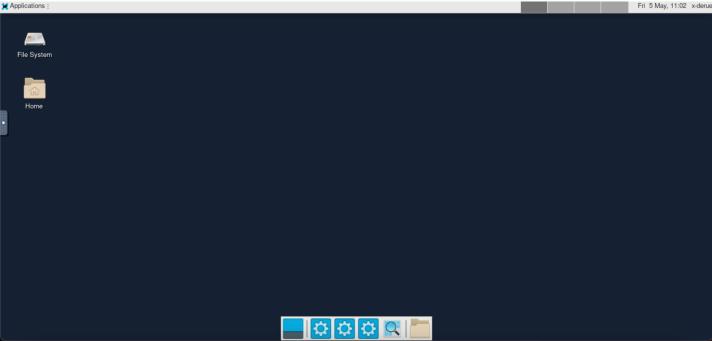
Specific Applications: Compute Desktop

The Desktop application is an extremely useful application for interfacing with Anvil

- This application will launch a lightweight graphical desktop that you can use to interact with the HPC cluster as you would your own local workstation
- It includes a native file explorer, Firefox as an internet browser, a terminal, and a typical Desktop that you can save files to
- This application can be used to launch software that requires a GUI
 - This can be used on system-wide installations by RCAC as well as with software you personally install



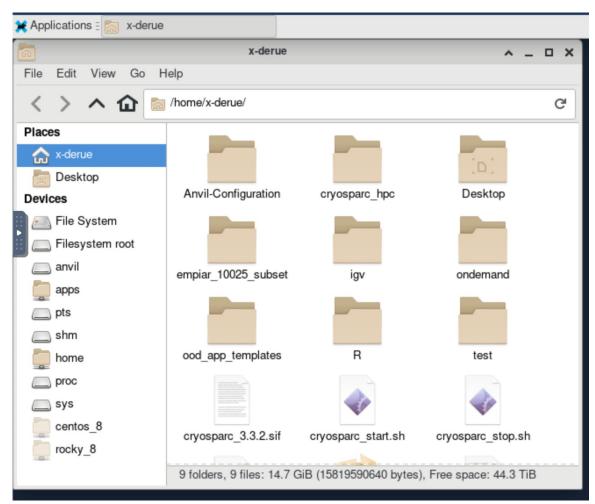
- 1. When you first launch the Compute Desktop, you will be presented with a desktop that appears as the one on the right
 - You can access your files by selecting the folder icon in the taskbar along the bottom, or by selecting the directory icon labelled "Home".





Specific Applications: Compute Desktop

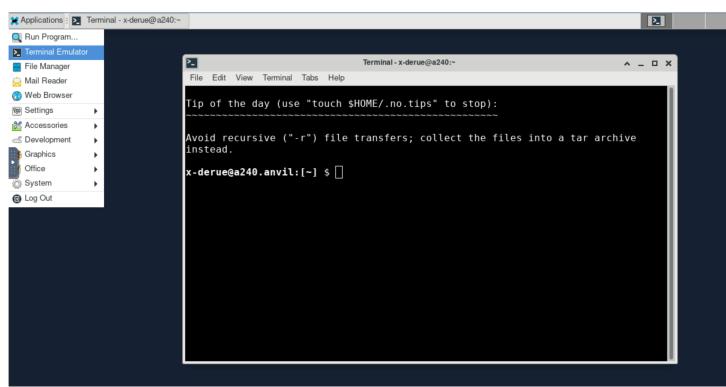
- 2. From this file menu, you can access any file on the cluster, but by default it will open to your home directory
 - You can change the directory you are viewing by clicking on other directories or by typing the absolute path into the search bar at the top





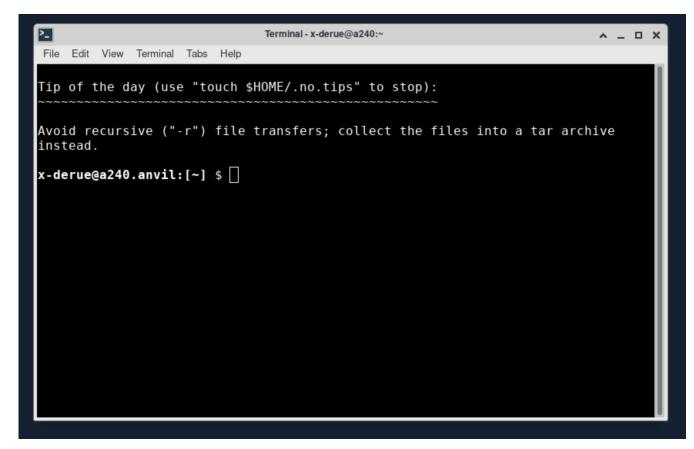
Rosen Center for Advanced Computing

- 3. You can launch a terminal on the desktop by selecting Applications menu in the top right, and then selecting "Terminal Emulator" from the sub-menu.
 - This is extremely useful for launching GUI applications from the command-line



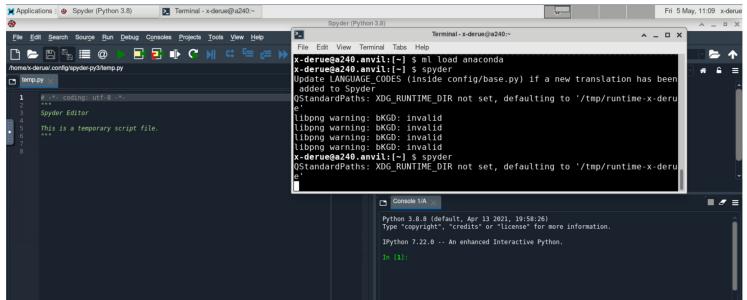


- 4. Notice that the prompt says that host is a240.anvil. This is the name of the compute node that we are on
 - If we were to try to do the same thing through ThinLinc (desktop.anvil.rcac.purdue.edu), which provides a similar interface, the terminal would indicate that we are on a login node (not a compute node) with a label of loginXX.anvil.





- 5. By loading a module (anaconda) for software that I know provides a GUI, I can launch that GUI by typing the name of the command to do so.
 - Usually, you can find such commands in the user manual for software you personally install
 - This allows me to run scientific software the same way many users do on ThinLinc, but I get all the resources dedicated to my application which improves performance!





Specific Applications: Jupyter

- 1. Jupyter is by far the most popular application for Open OnDemand on Anvil
 - Very useful application for interactive work with languages like Python, R, Julia, etc.
 - App form is very similar to the previous one, but it does have an option to select whether you want to run "Jupyter Lab" or "Jupyter Notebook".
 - Notebook is the original Jupyter application and is a more barebones method of using Jupyter

Jupyter Notebook

This app will launch a Jupyter Notebook server on a node.

Allocation

asc170016 (75102.6 SUs remaining)

Queue (partition)

shared

- GPU-only allocations MUST use the 'gpu' queue
- CPU-only allocations MAY NOT use the 'gpu' queue

Wall Time in Hours

| | | | iele | |
|---|--|--|------|--|
| 1 | | | | |
| | | | | |

Number of hours you are requesting for your job.

Cores

1

Number of cores (up to 128) for a shared job. Non-shared jobs will have exclusive nodes and be charged at 128 cores per node requested

✓ Use Jupyter Lab instead of Jupyter Notebook

 $\hfill\square$ I would like to receive an email when the session starts



Specific Applications: Jupyter

- 2. We have installed a few system wide Jupyter kernels for Python as well as R.
 - You cannot install additional packages into these kernels, but you can create your own anaconda environment containing the packages you want
 - For more information about how to expose your anaconda environments to Jupyter see our knowledge guide article on the topic.

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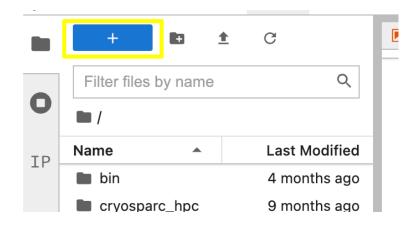
https://www.rcac.purdue.edu/knowledge/anvil/run/examples/apps/python/packages



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Specific Applications: Jupyter

- 3. Regardless of whether you choose to use Jupyter Notebook or Jupyter Lab, it will open to your home directory.
 - To create a new notebook in Jupyter Lab click the blue "+" button in the top left corner (Shown in the top-most picture)
 - To create a new notebook in Jupyter Notebook, select the "New" button in the top right corner. (Shown in the bottommost picture)



| Upload | New 🗸 🕄 |
|------------------------|-----------|
| Name 🕁 🛛 Last Modified | File size |
| 4 months ago | |
| 9 months ago | |
| a year ago | |
| 8 months ago | |
| a year ago | |
| a year ago | |
| a year ago | |
| a year ago | |
| a year ago | |
| 9 months ago | |
| 7 months ago | |
| . | |

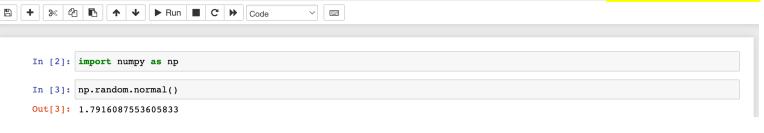


Using Open OnDemand: Applications

Specific Applications: Jupyter

- 4. After we have created a new notebook, we will be presented with our new notebook in an interface shown to the right
 - Jupyter Lab is shown in top-most picture and Jupyter Notebook shown below that
 - To select the kernel you wish to use, click on the name of the kernel shown to the right in a yellow box, and an option to select a new kernel will appear







OOD 101

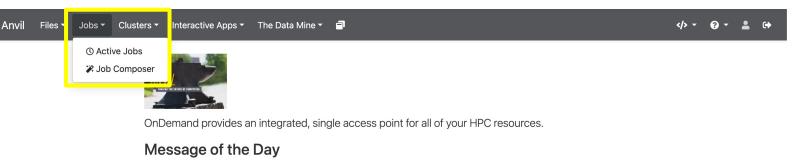
Using Open OnDemand: Job Composer



A Widget For Talking to the Scheduler

Often, we may also want to run non-interactive jobs. In such cases Open OnDemand provides an interface for creating such jobs as well as monitoring your interactive and non-interactive jobs.

We can access these tools using the Jobs menu



OnDemand version: v2.0.20



A Widget For Talking to the Scheduler

- 1. The Active Jobs widget will allow you to query certain usage statistics from the scheduler that you would otherwise need to do through the command line interface (CLI)
 - When a job fails due to an error, this is a useful tool to discover what may have happened
 - You can look at the amount of memory that was requested to see if perhaps there was an out of memory error
 - You can also use the "Open in File Manager" button to view the output.log file that may contain information about the error that occurred

| Active Jobs Show 50 + entries | | | | | | Filter: | |
|----------------------------------|------------|-------------------------------|---------------------------------|---------|-------------|-----------|---|
| ID ↑↓ Name | ↑↓ User ↑↓ | Account $\uparrow \downarrow$ | Time Used $\uparrow \downarrow$ | Queue 1 | ∕ Status ↑↓ | Cluster 1 | \downarrow Actions $\uparrow\downarrow$ |
| > 1677958 OnDemand/Jupyter | x-derue | asc170016 | 00:07:09 | shared | Running | Anvil | â |
| ✓ 1677957 OnDemand/Jupyter | x-derue | asc170016 | 00:07:16 | shared | Running | Anvil | â |

| Running OnDemand/Jupyter 1677957 | |
|----------------------------------|------------------|
| Cluster | Anvil |
| Job Id | 1677957 |
| Job Name | OnDemand/Jupyter |
| User | x-derue |
| Account | asc170016 |
| Partition | shared |
| State | RUNNING |
| Reason | None |
| Total Nodes | 1 |
| Node List | a240 |
| Total CPUs | 1 |
| Time Limit | 1:00:00 |
| Time Used | 7:31 |
| Memory | 1918M |
| | |

Output Location:

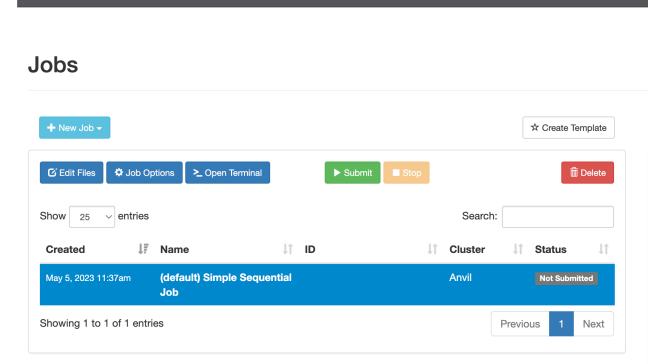
Den in File Manager

 $/home/x-derue/ondemand/data/sys/dashboard/batch_connect/sys/jupyter/output/d86cc533-1e77-4480-b17f-aeded1f525b1$



A Widget For Talking to the Scheduler

- 2. The Job Composer widget is used for submitting non-interactive jobs to the scheduler. This is very useful when you have some work to accomplish as part of your workflow that doesn't need to be done interactively.
 - An example of this might be post processing the output of some work that was generated interactively
 - This tool provides a simple default template for submitting a "Hello World" job script, but allows you to save template job scripts for workflows you may regularly repeat



Anvil / Job Composer

Jobs

Templates



A Widget For Talking to the Scheduler

- 3. Selecting the "+ New Job" button will allow you to begin working on creating a new job either from one of your existing templates, or from the default hello world template.
 - This will create a new entry in your table of jobs with a status of "Not Submitted"

Anvil / Job Composer Jobs Templates

Jobs

| Create a new job from th template | e defaul | t | | | | | | ☆ Create 1 | emplate |
|---------------------------------------|----------|----------------------|-------|----------|-----|------------------|-----------------------|--------------------|---------|
| From Default Tem | plate | | | | | | | | |
| From Specified Pa | ath | >_ Open Terminal | | ► Submit | top | | | đ | Delete |
| From Selected Jol | b | | | | | Search | : | | |
| | | | | | | | | | |
| Created | ↓≣ Na | ame | J† ID | | 11 | Cluster | $\downarrow \uparrow$ | Status | 11 |
| Created May 5, 2023 11:37am | • | efault) Simple Seque | | | ţţ. | Cluster Anvil | ţţ | Status Not Subm | |



A Widget For Talking to the Scheduler

- 4. If we select the newly created job in the table, we can then click on the "Job Options" button to bring up configurable options for that job.
 - The most important fields here are the job name, which is for your own reference, and the "Account"
 - "Account" is the name of your allocation. You can enter the name of one of the queues which you are able to select from the Allocation dropdown on any of the app forms

Anvil / Job Composer Jobs Templates

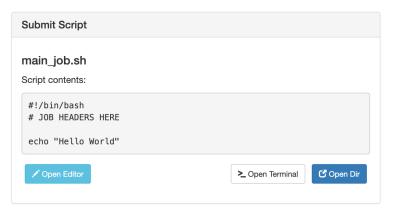
| Job Options | |
|---|---|
| Name | |
| (default) Simple Sequential Job | |
| Cluster | |
| Anvil | ~ |
| Specify job script | |
| main_job.sh | ~ |
| Files larger than 65KB are omitted for the job script field | |
| Account | |
| | |
| Account is an optional field. If not set, the account may be auto-set by the submit filter. | |
| Job array specification | |
| 1-10 | |
| Job arrays are optional. e.g. 1-10 | |
| Save Reset Back | |



A Widget For Talking to the Scheduler

- 5. After saving the job options, we can scroll along the boxes on the right side of the table to do two things
 - We can see some details about the job
 - We can edit the job script that this job will run
 - This is the most important part of this workflow because this is defining what we want our non-interactive job to do
 - Select "Open Editor" to change the contents of this script

| Submit to: | |
|--------------|---|
| Submit to: | |
| Anvil | |
| Account: | |
| asc170016 | |
| | ondemand/data/sys/myjobs/projects/default/1 |
| Script name: | |
| main_job.sh | |
| | |
| | |





A Widget For Talking to the Scheduler

- 6. Within your job script, you will want to put all the commands which you want to be ran as part of the job, as well as any options to Slurm, and then hit "Save"
 - For more information about how to do this, see the user guide page for example Slurm job scripts

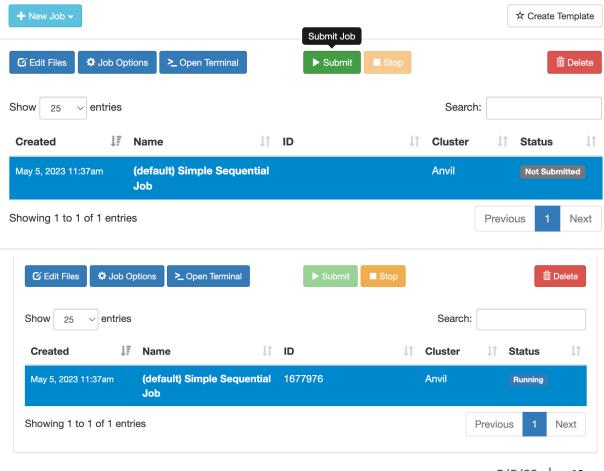
| | Save /home/x-derue/ondemand/data/sys/myjobs/projects/default/1/main_job.sh |
|---|--|
| 1 | #!/bin/bash |
| 2 | # JOB HEADERS HERE |
| 3 | |
| 4 | echo "Going to sleep for 30 seconds, but when I wake up, I'll greet you!" |
| 5 | sleep 30 |
| 6 | echo "Hello from Open OnDemand!" |
| 7 | |



A Widget For Talking to the Scheduler

- 7. After we have made our edits to the job script, we can close this tab and return to the job composer page. Now all that remains is to select this job and hit submit!
 - After this point the status of the job updates from "Not Submitted" to "Running", and when the job terminates, this will update finally to "Completed"

Jobs





A Widget For Talking to the Scheduler

- 8. After the job completes, we can view the job details along the right-hand side of the page
 - We see that the "Folder Contents" has been updated with a new output file: "slurm-2677561.out"
 - If we click the link to this file, we will see that our job successfully generated the expected output:

Save /home/x-derue/ondemand/data/sys/myjobs/projects/default/1/slurm-1677976.out Going to sleep for 30 seconds, but when I wake up, I'll greet you! Hello from Open OnDemand!

3

| 1677976 | |
|-----------------|--|
| Job Name: | |
| (default) Sin | nple Sequential Job |
| Submit to: | |
| Anvil | |
| Account: | |
| asc170016 | |
| | ue/ondemand/data/sys/myjobs/projects/default/1 |
| Script name: | |
| main_job.sh | |
| | |
| Folder Contents | : |
| main_job.sh | |
| slurm-167797 | '6 out |



00D 101

Conclusions



Conclusions

- Open OnDemand helps to lower the barrier of entry to HPC for domain scientists seeking to do computational work
- We can use Open OnDemand to manage our directories as well as transfer files to/from the cluster
- Open OnDemand is especially useful for running interactive style jobs that require a graphical user interface
- We can use Open OnDemand to manage our non-interactive jobs as well



00D 101

Questions?



THANK YOU

Feel free to reach out to rderue@purdue.edu with questions.

Slides are posted at: https://www.rcac.purdue.edu/training/

