Connecting to Bridges2 OnDemand at the Pittsburgh Supercomputing Center (PSC)

Plan for Enhancing Diverse Perspectives (PEDP)

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Competency

• Become proficient in using Bridges2 OnDemand for training sessions, research or both.
Objectives

• Remotely connect to the Bridges2 OnDemand at the Carnegie Mellon University – Pittsburgh Supercomputing Center.

• Define the environment to work with Jupyter notebooks.

• Transfer files between the participant’s local computer and the remote supercomputer for the training sessions.
Target Audience

• This training is addressed to beginners, highly motivated wanting to learn about the Bridges2 OnDemand supercomputer to perform Human Biomolecular Atlas Program (HuBMAP) data analysis on HuBMAP public datasets.
Connect to Bridges2 OnDemand
Type **bridges2 ondemand** in your web browser.

1. Type **bridges2 ondemand** & hit the Enter key or activate the magnifier icon.

2. Activate the **Log in to Bridges2**
Input your **bridges2** access credentials.

1. Type your **Username**

2. Type your **Password**

3. Click in the **Log in** button
Activate My Interactive Sessions.
Activate Jupyter Notebook.
Let’s configure our Jupyter Notebook session.

Number of hours: 1

Account: hivepsc

Extra Slurm Args: -n 8 –meme=16000M

Number of nodes: 1

Partition: RM-shared

Launch
Let’s connect to our Jupyter Notebook.
Let’s create a folder for each training session.
Let’s rename our folder.

1. Select the Untitled Folder

2. Rename
Let’s rename our folder.

**1**

Type

`hubmap_sc_rna_seq`

**2**

Rename

**Rules**

All small caps, no spaces or special characters, and you can use the underscore to separate words.
Let’s create a folder for each training session.

Now let’s create the following folders:
- hubmap_venn_diagrams
- hubmap_string_db
- hubmap_goea
Locate the Jupyter notebooks that on your computer’s **Download** folder.

Our four Jupyter notebooks.
Activate the **hubmap_goea** folder to upload our Jupyter notebook.

1. Activate the **hubmap_goea** link with **one click**.
Upload the HuBMAP_Gene_Ontology_Enrichment_Analysis_(GOEA)_with)goatools_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_goea folder.
Upload the HuBMAP_Gene_Ontology_Enrichment_Analysis_(GOEA)_with)goatools_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_goea folder.

Select the HuBMAP_Gene_Ontology_Enrichment_Analysis_(GOEA)_with)goatools_HBM538_PHSC_677.ipynb Jupyter notebook.

Open
Upload the HuBMAP_Gene_Ontology_Enrichment_Analysis_(GOEA)_with_goatools_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_goea folder.
Let’s exit from our hubmap_goea folder.

1. Click over the folder icon to exit from the hubmap_goea folder.
Activate the **hubmap_sc_rna_seq** folder to upload our Jupyter notebook.

[Image: A screenshot showing a file manager interface with a highlighted folder named 'hubmap_sc_rna_seq'.]

1. Activate the **hubmap_sc_rna_seq** link with one click.
Upload the HuBMAP_scRNAseq_HBM538_PHSC_677_Bridges2_Jupyter_Notebook_version_02.ipynb Jupyter notebook into our hubmap_sc_rna_seq folder.
Upload the HuBMAP_scRNAseq_HBM538_PHSC_677_Bridges2_Jupyter_Notebook_version_02.ipynb Jupyter notebook into our hubmap_sc_rna_seq folder.

Select the HuBMAP_scRNAseq_HBM538_PHSC_677_Bridges2_Jupyter_Notebook_version_02.ipynb Jupyter notebook.

Open
Upload the HuBMAP_scRNAseq_HBM538_PHSC_677_Bridges2_Jupyter_Notebook_version 02.ipynb Jupyter notebook into our hubmap_sc_rna_seq folder.
Upload the HuBMAP_scRNAseq_HBM538_PHSC_677_Bridges2_Jupyter_Notebook_version_02.ipynb Jupyter notebook into our hubmap_sc_rna_seq folder.

Click over the folder icon to exit from the hubmap_sc_rna_seq folder.
Activate the `hubmap_string_db` folder to upload our Jupyter notebook.
Upload the HuBMAP_String_Database_protein_protein_interaction_networks_version_03_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_string_db folder.
Upload the HuBMAP_String_Database_protein_protein_interaction_networks_version_03_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_string_db folder.

Select the HuBMAP_String_Database_protein_protein_interaction_networks_version_03_HBM538_PHSC_677.ipynb Jupyter notebook.
Upload the HuBMAP_String_Database_protein_protein_interaction_networks_version_03_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_string_db folder.
Upload the HuBMAP_String_Database_protein_protein_interaction_networks_version_03_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_string_db folder.

Click over the folder icon to exit from the hubmap_string_db folder.
Activate the **hubmap_venn_diagrams** folder to upload our Jupyter notebook.

1. Activate the **hubmap_venn_diagrams** link with one click.
Upload the Super_Venn_Diagram_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_string_db folder.
Upload the Super_Venn_Diagram_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_venn_diagrams folder.

Select the Super_Venn_Diagram_HBM538_PHSC_677.ipynb Jupyter notebook.

Open
Upload the Super_Venn_Diagram_HBM538_PHSC_677.ipynb Jupyter notebook into our hubmap_venn_diagrams folder.
Upload the *Super_Venn_Diagram_HBM538_PHSC_677.ipynb* Jupyter notebook into our *hubmap_venn_diagrams* folder.

Click over the folder icon to exit from the *hubmap_venn_diagrams* folder.
Now we are ready to start with the **hubmap_sc_rna_seq** data analysis.

Activate the **hubmap_venn_diagrams** link with one click.
Now we are ready to start with the **hubmap_sc_rna_seq** data analysis.

Activate the Jupyter notebook

HuBMAP_scRNAseq_HBM538_PHSC_677_Bridges2_Jupyter_Notebook_version_02.ipynb

link with one click.
Title: Introduction to Single-Cell RNA-Seq (scRNA-seq) Data Analysis

Competency

- Become proficient in single cell RNA-seq data analysis from HuBMAP.

Objectives

- Import HuBMAP preprocessed data into an anndata object with the Python library scanpy.
- Filter cell outliers based on the number of genes expressed for raw data.
- Normalize and log transform raw data.
- Generate clusters and visualize via UMAP dimensional reduction.
- Find cluster-specific marker genes with scanpy.

Install the required Python libraries to conduct the scRNA-seq analysis.