Matlab on the Biowulf Cluster

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BIOWULF
HIGH PERFORMANCE COMPUTING AT THE NIH

Download these slides from:

https://hpc.nih.gov/training/handouts/matlab4biowulf.pdf

Outline

- Motivation
- Quick review of the Biowulf cluster
- Matlab Institute Wide License
- Running Matlab scripts interactively
- Running Matlab scripts as batch jobs
  - Running single job with *sbatch*
  - Running job array with *swarm*
  - Monitoring jobs
  - Limits, pitfalls and caveats
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- We have implemented a new licensing model for Matlab
- This new model gives Biowulf users access to virtually UNLIMITED Matlab licenses and ALL toolboxes
- Users do not need to compile their Matlab code to submit batch jobs to the cluster

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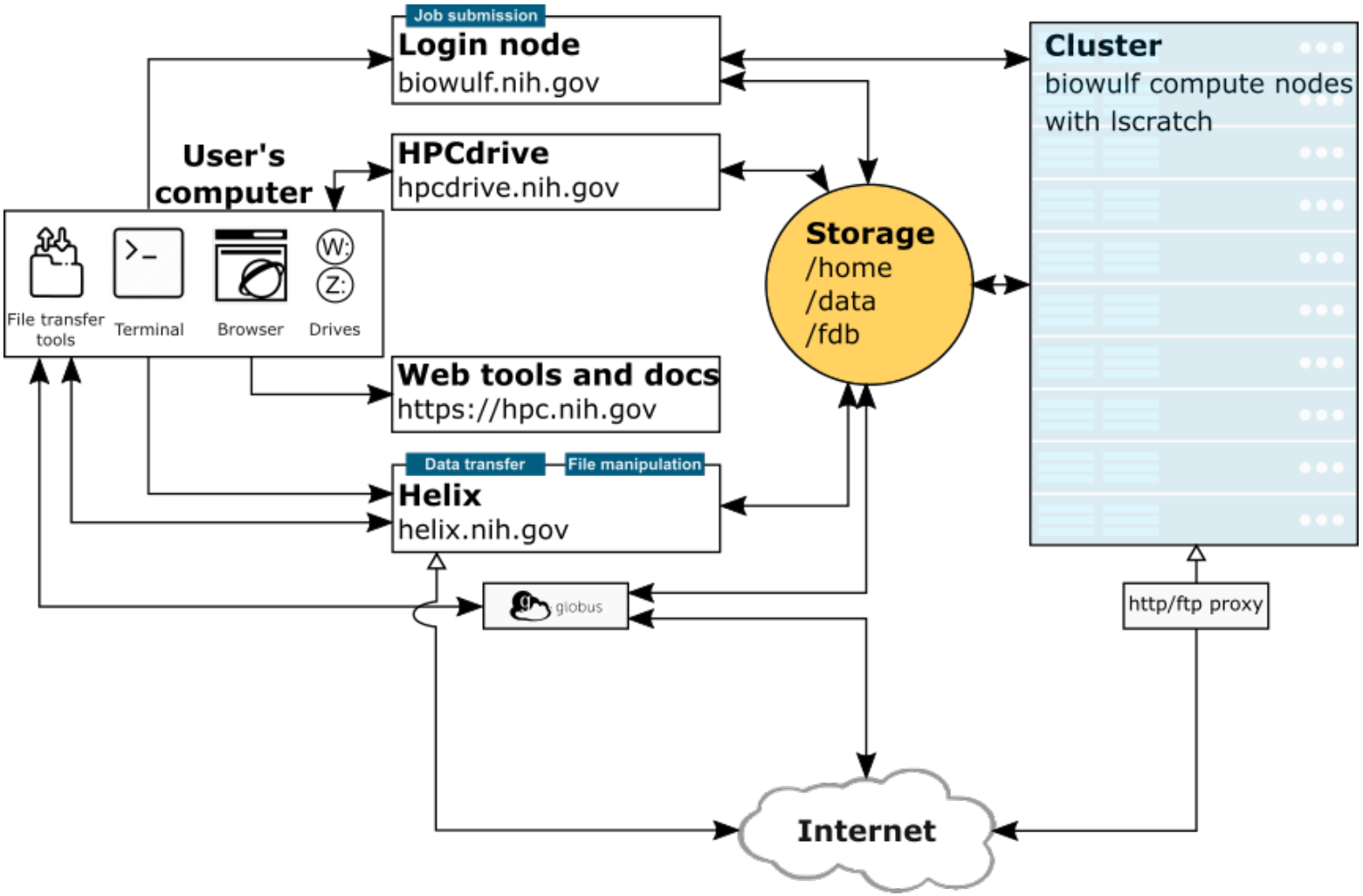

Source: https://hpc.nih.gov/systems

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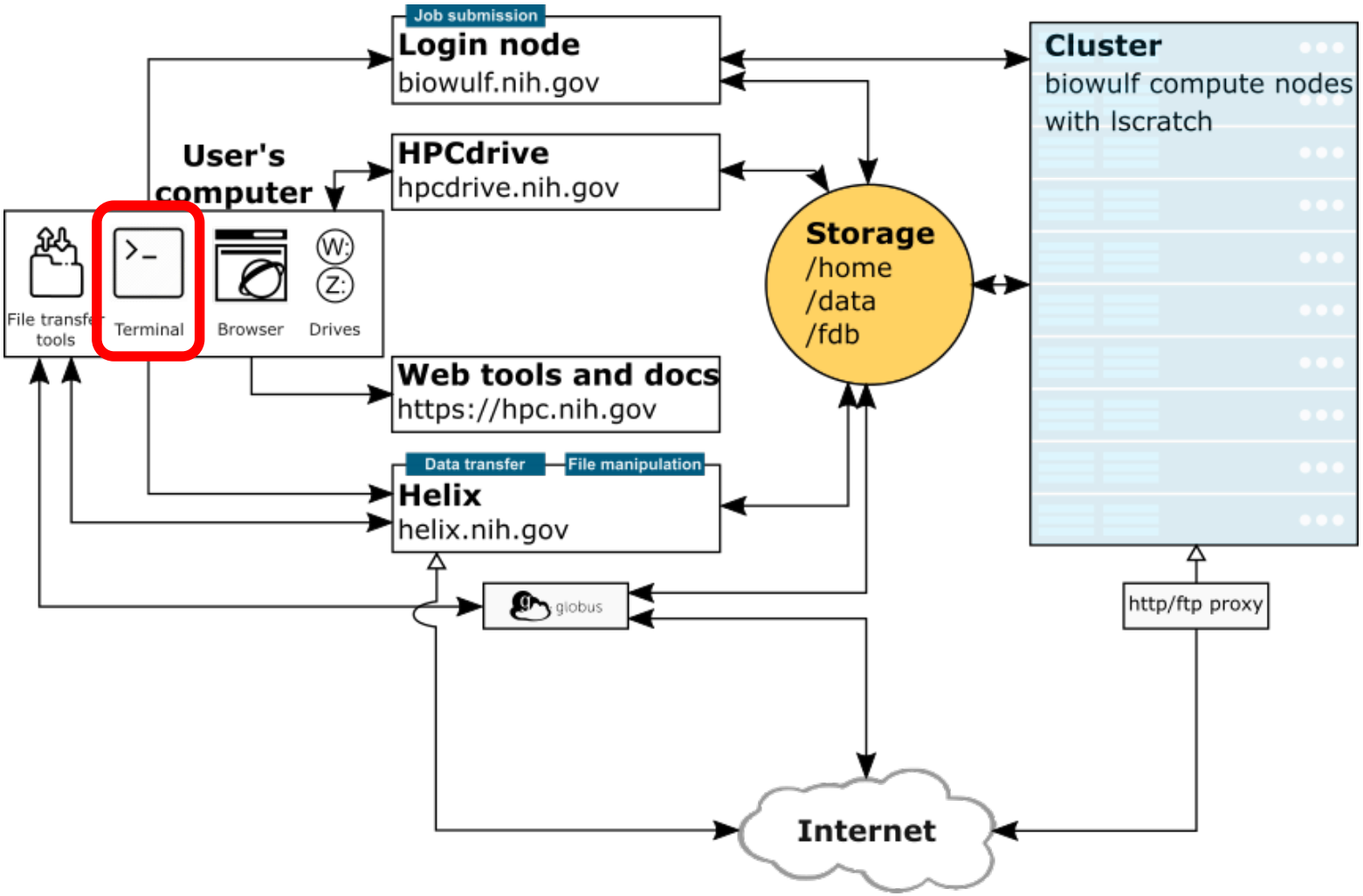

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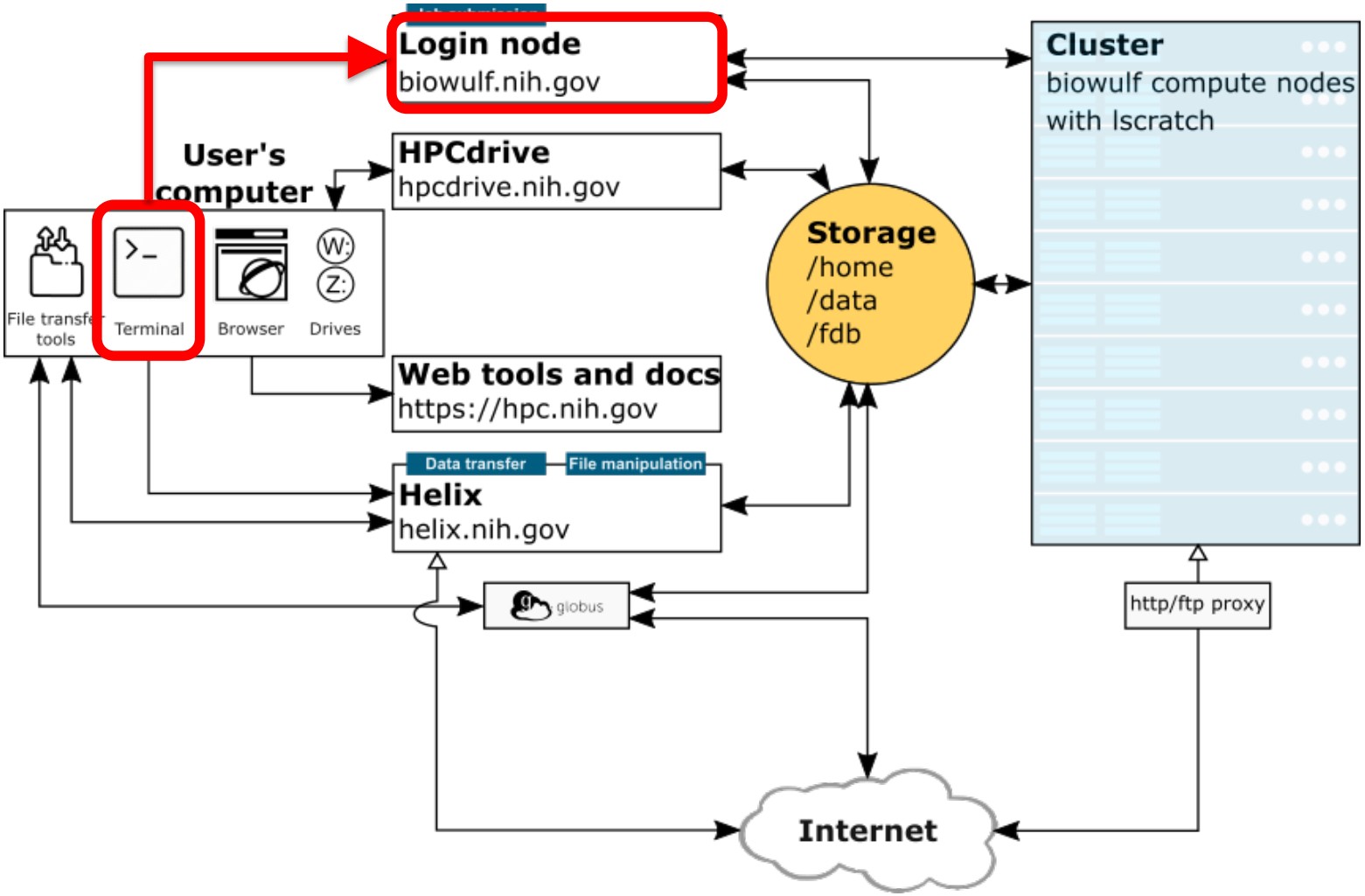

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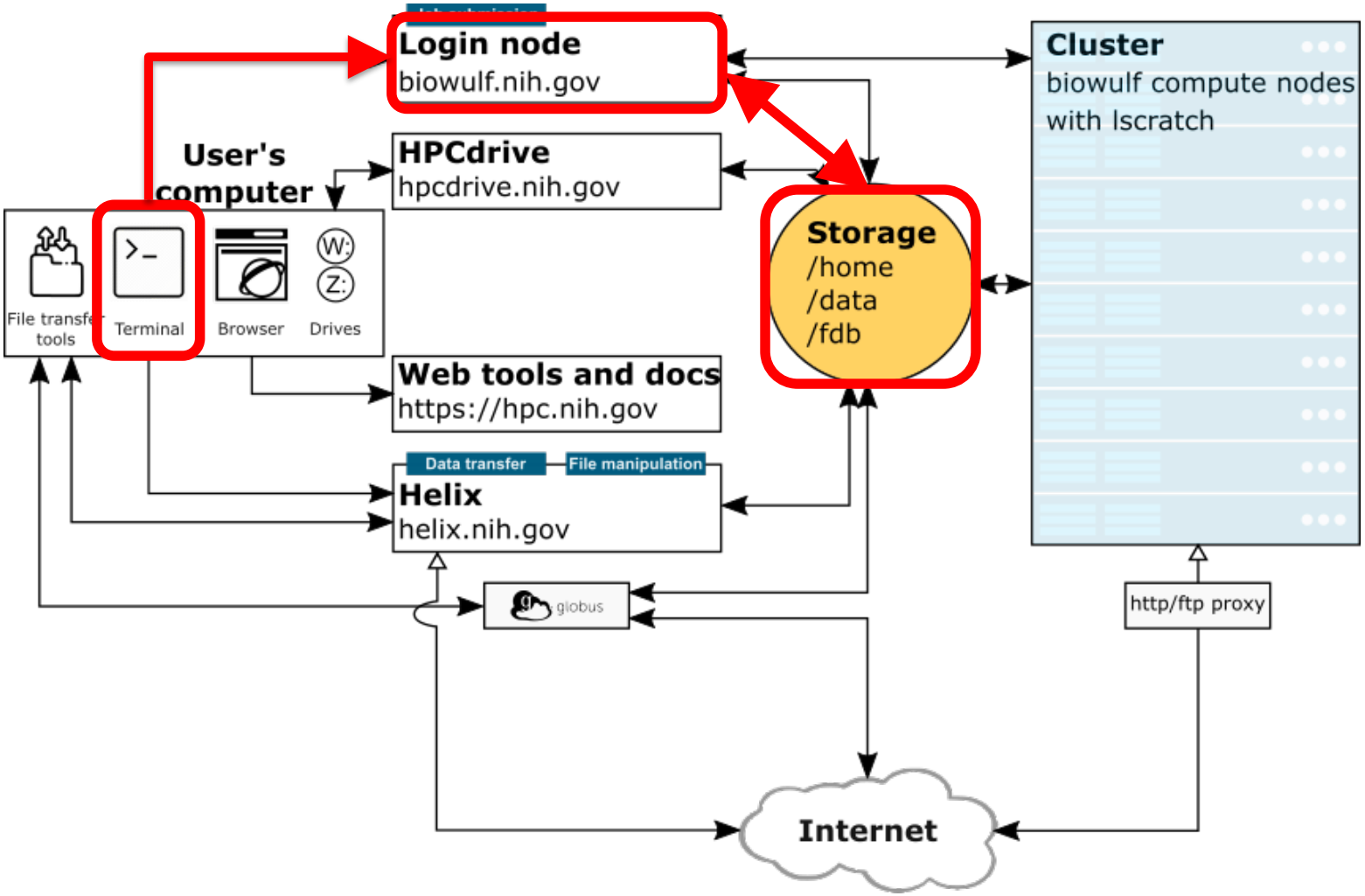

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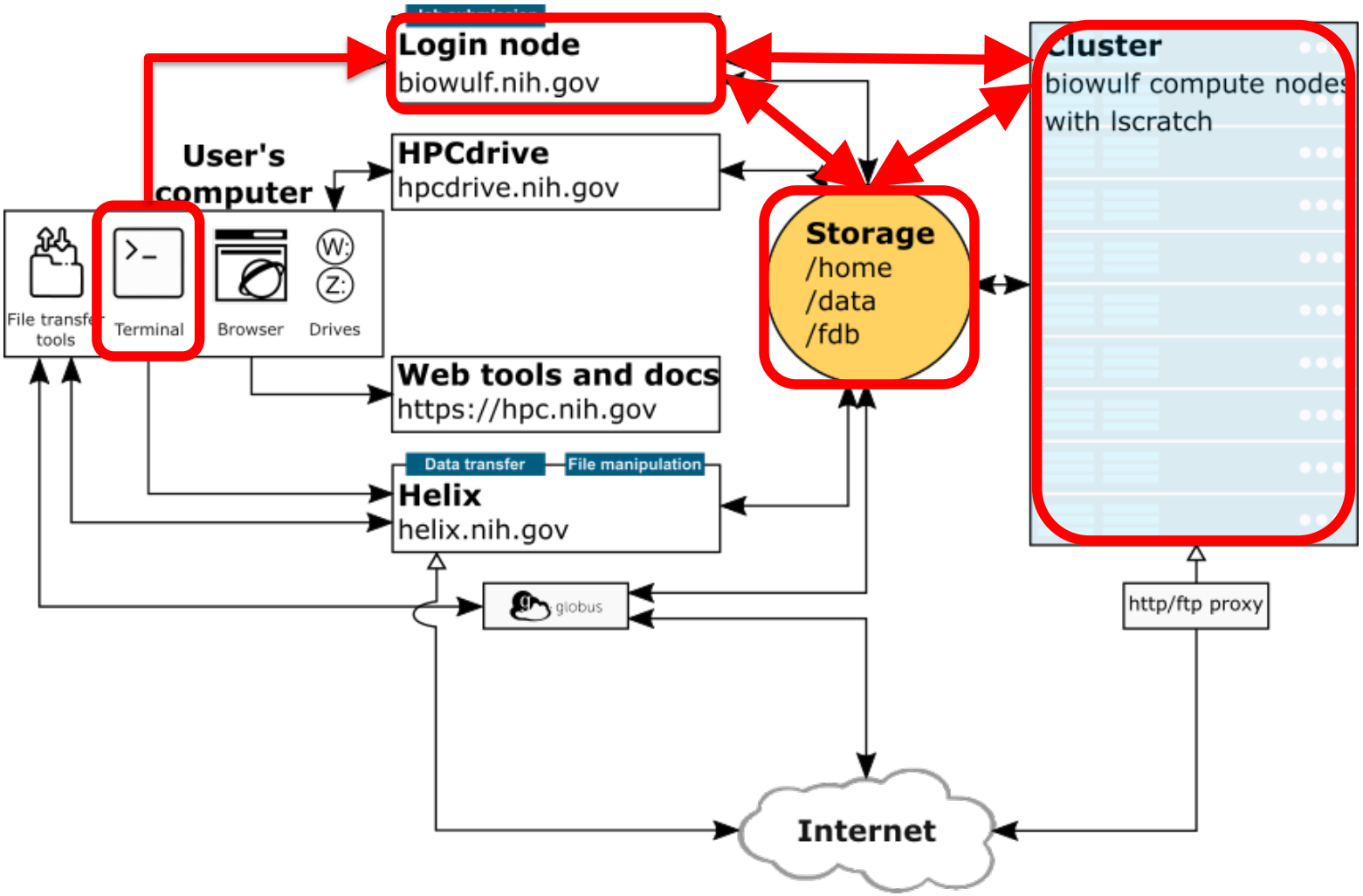

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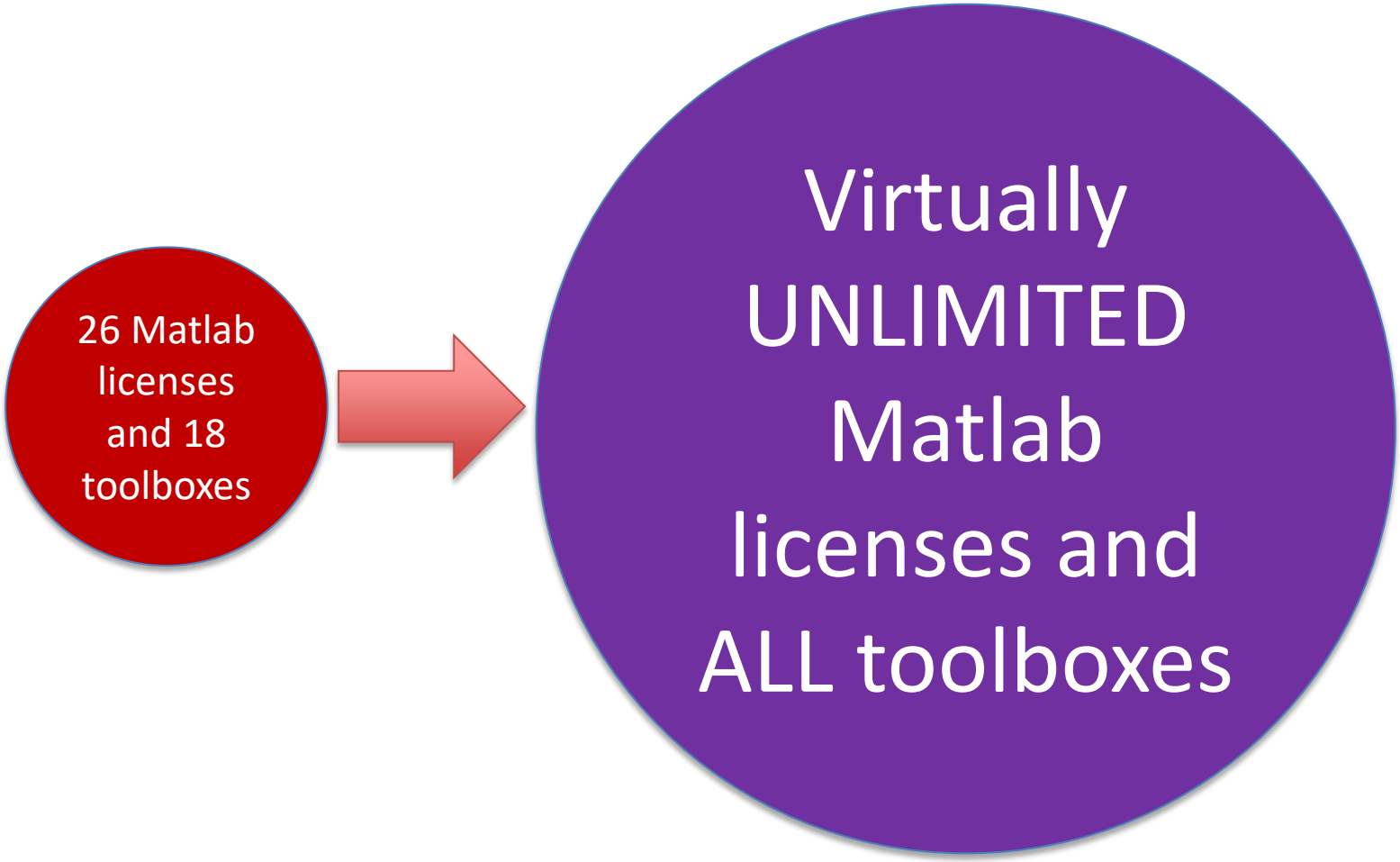
Matlab Institute Wide License (IWL)



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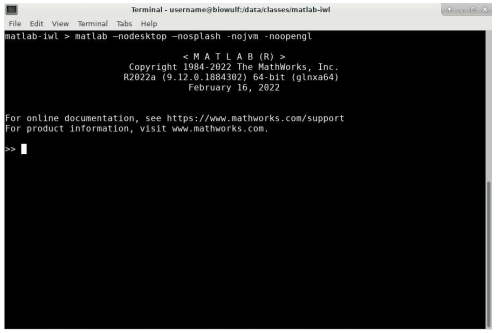
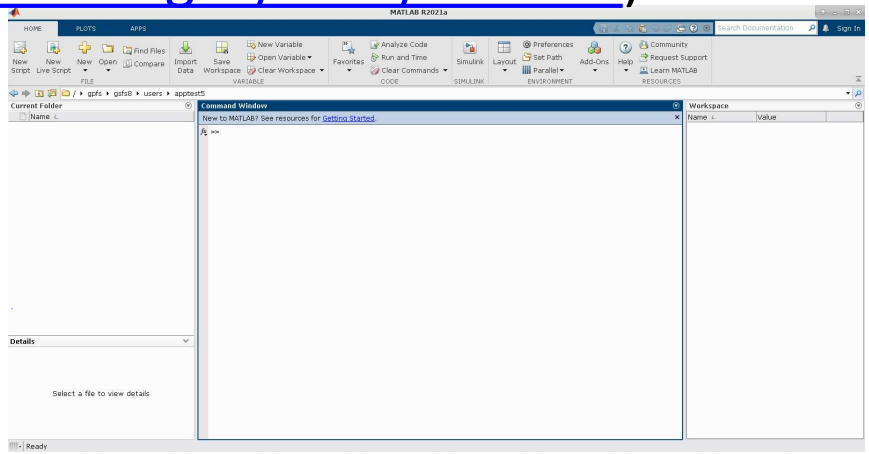
Command-line Matlab:



Graphical Matlab using nomachine NX (see https://hpc.nih.gov/docs/nx.html):



Source: https://hpc.nih.gov/apps/Matlab.html

Running Matlab scripts interactively

```
local-computer> ssh username@biowulf.nih.gov
biowulf> sinteractive
cn1234> cd /data/$USER
cn1234> cp -r /data/classes/matlab-iwl .
cn1234> cd matlab-iwl
cn1234> module load matlab
[+] Loading Matlab  2022a  on cn1234
cn1234> matlab -nodesktop -nosplash -nojvm -noopengl

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local-computer> ssh username@biowulf.nih.gov
biowulf> sinteractive --mem=4g
cn1234> cd /data/$USER
cn1234> cp -r /data/classes/matlab-iwl .
cn1234> cd matlab-iwl
cn1234> module load matlab
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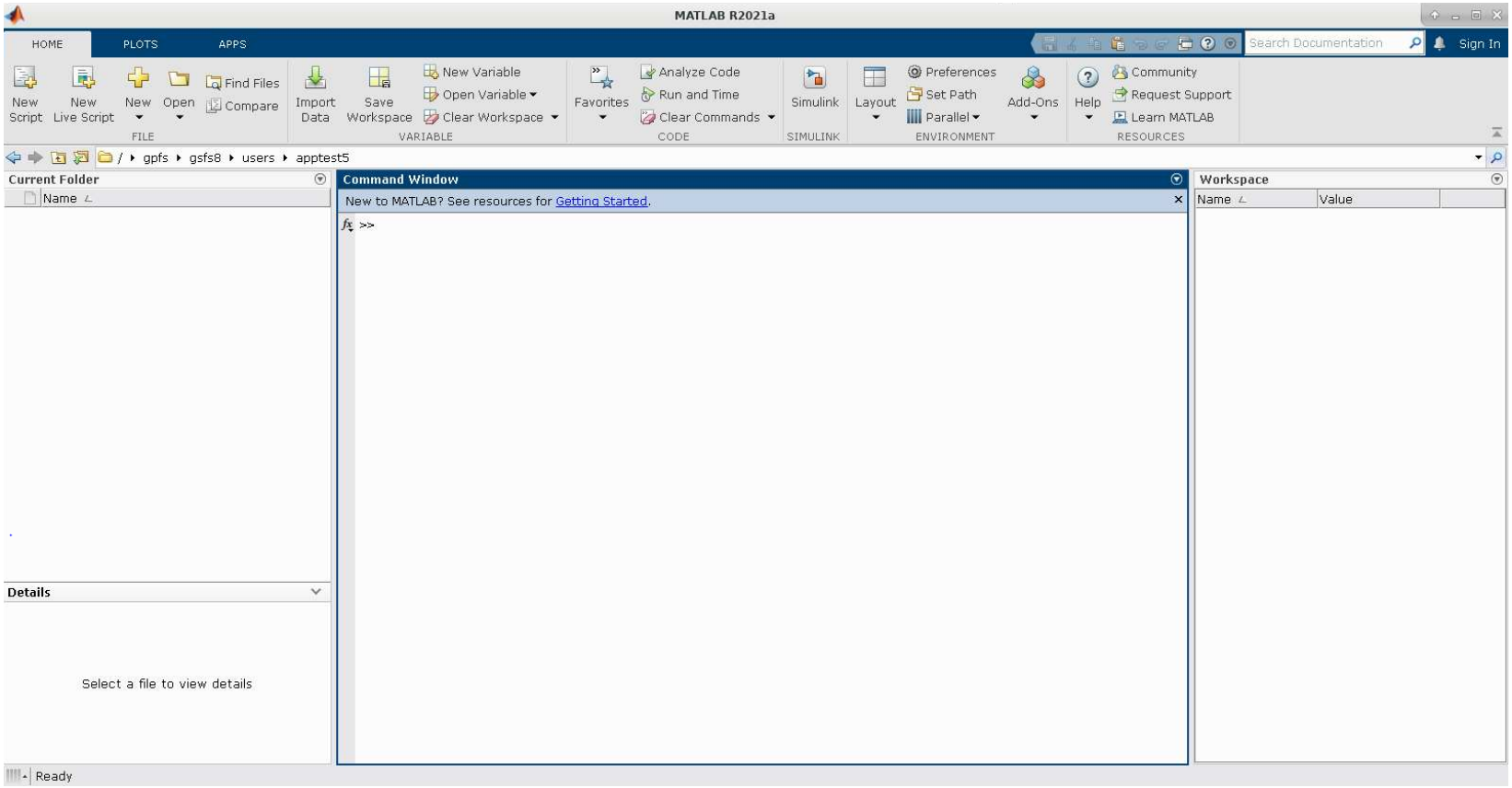

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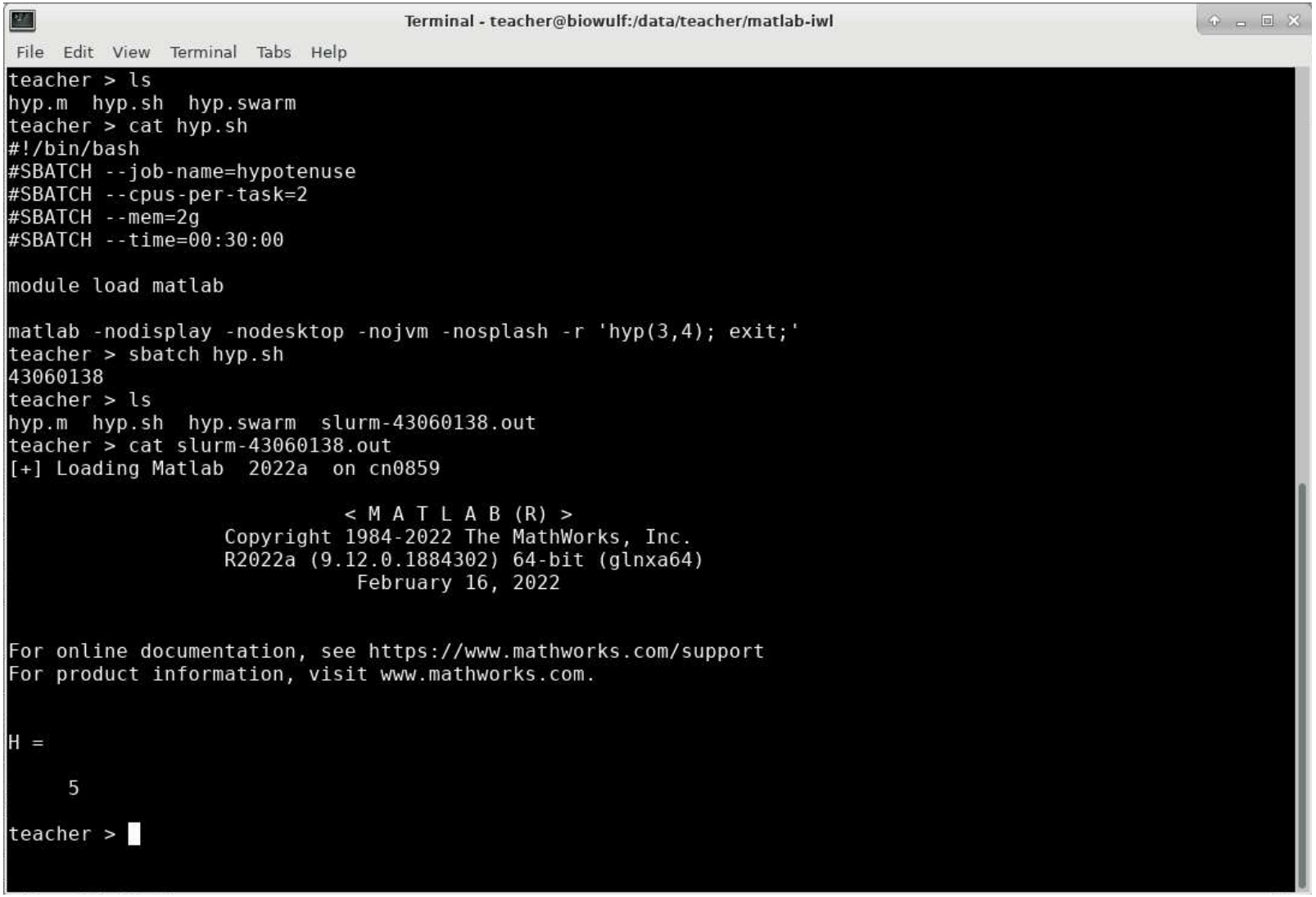

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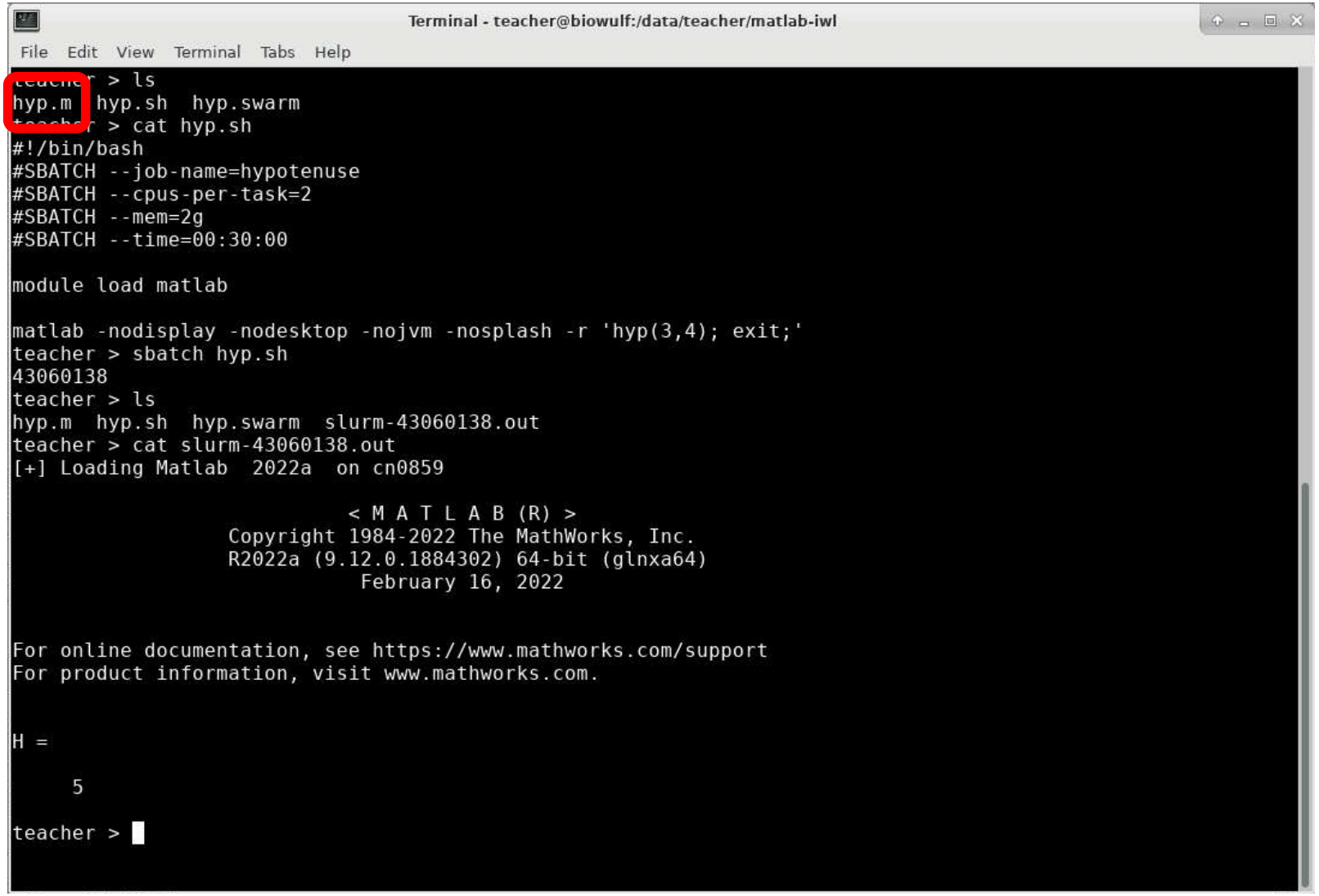

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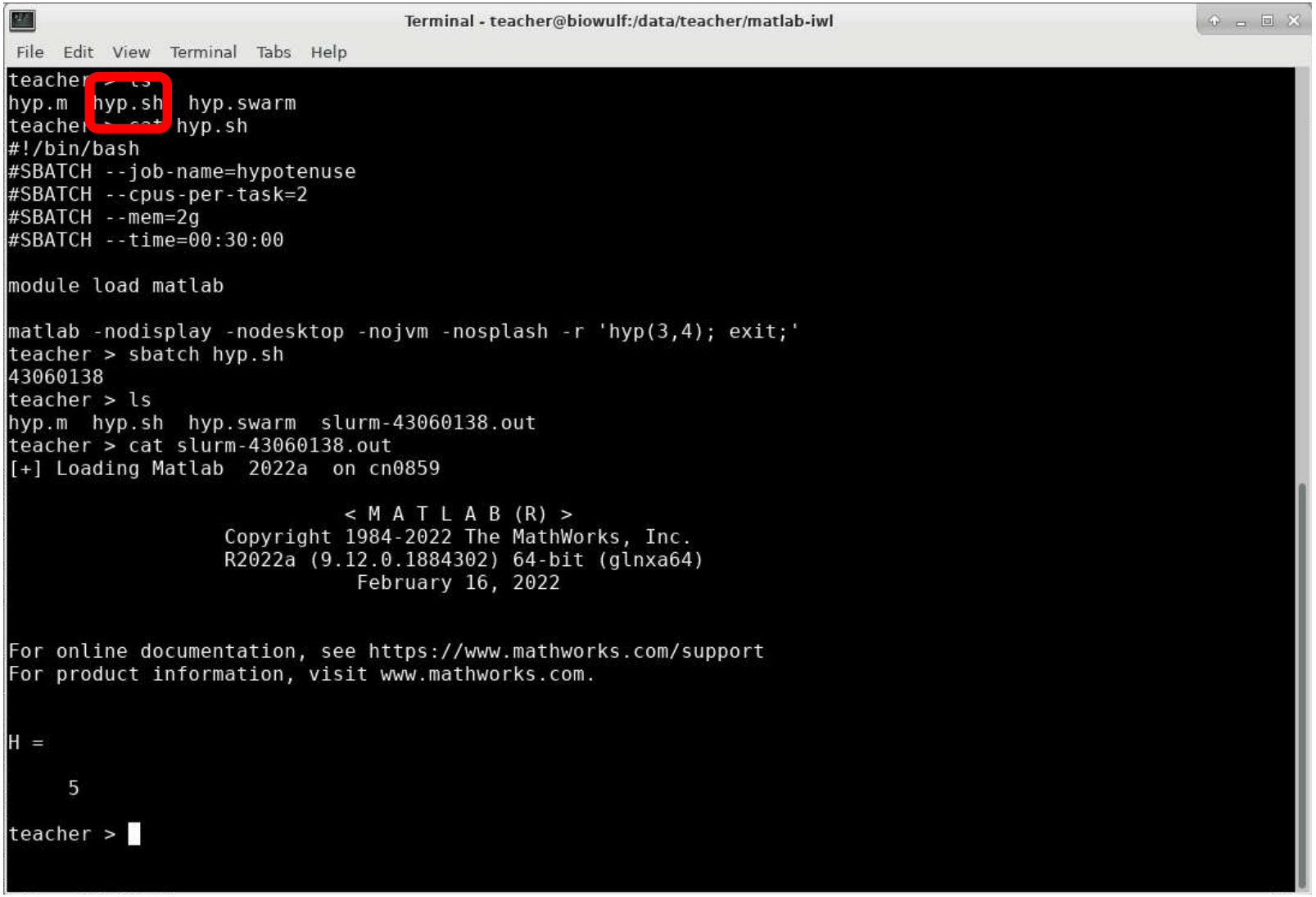

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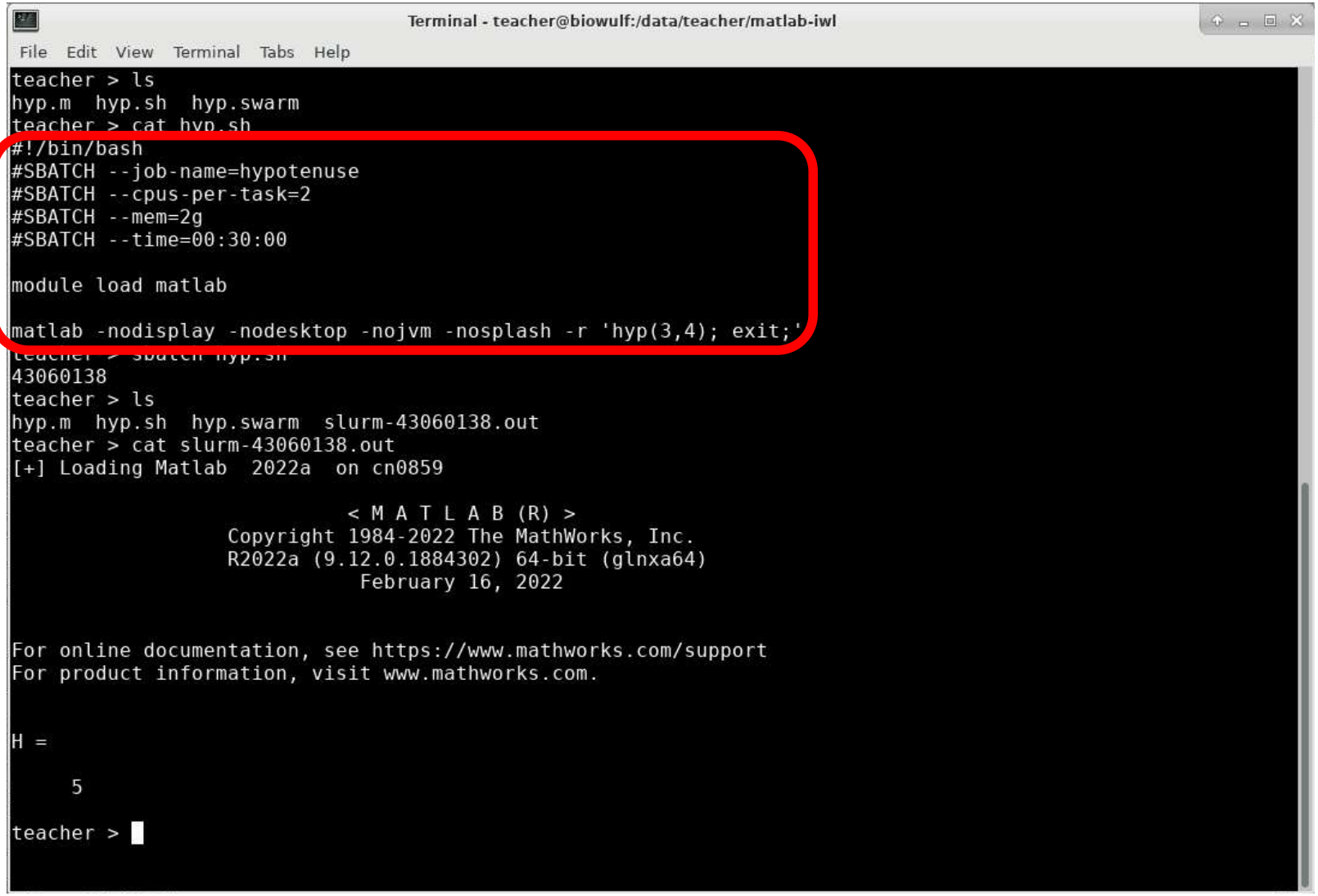

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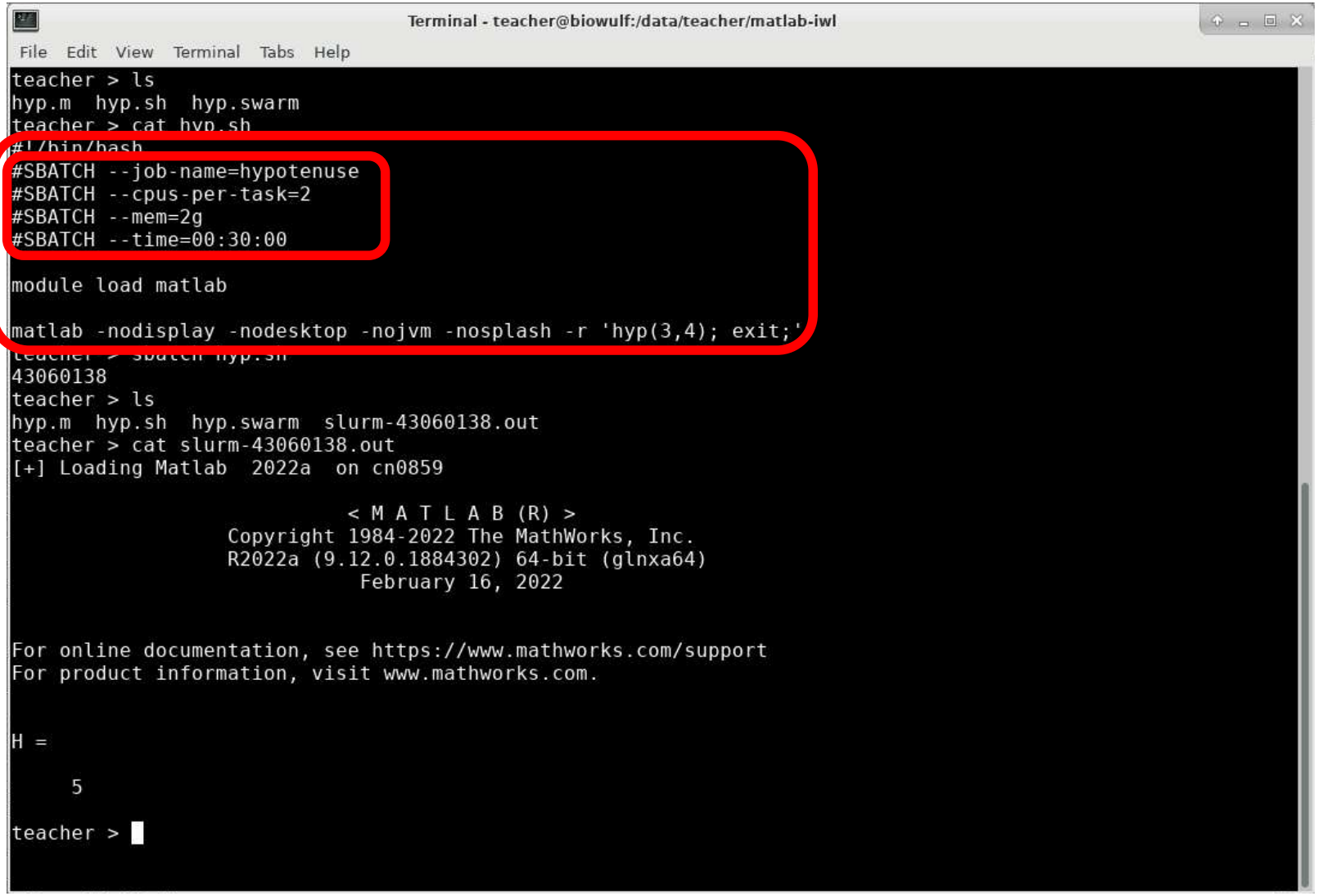

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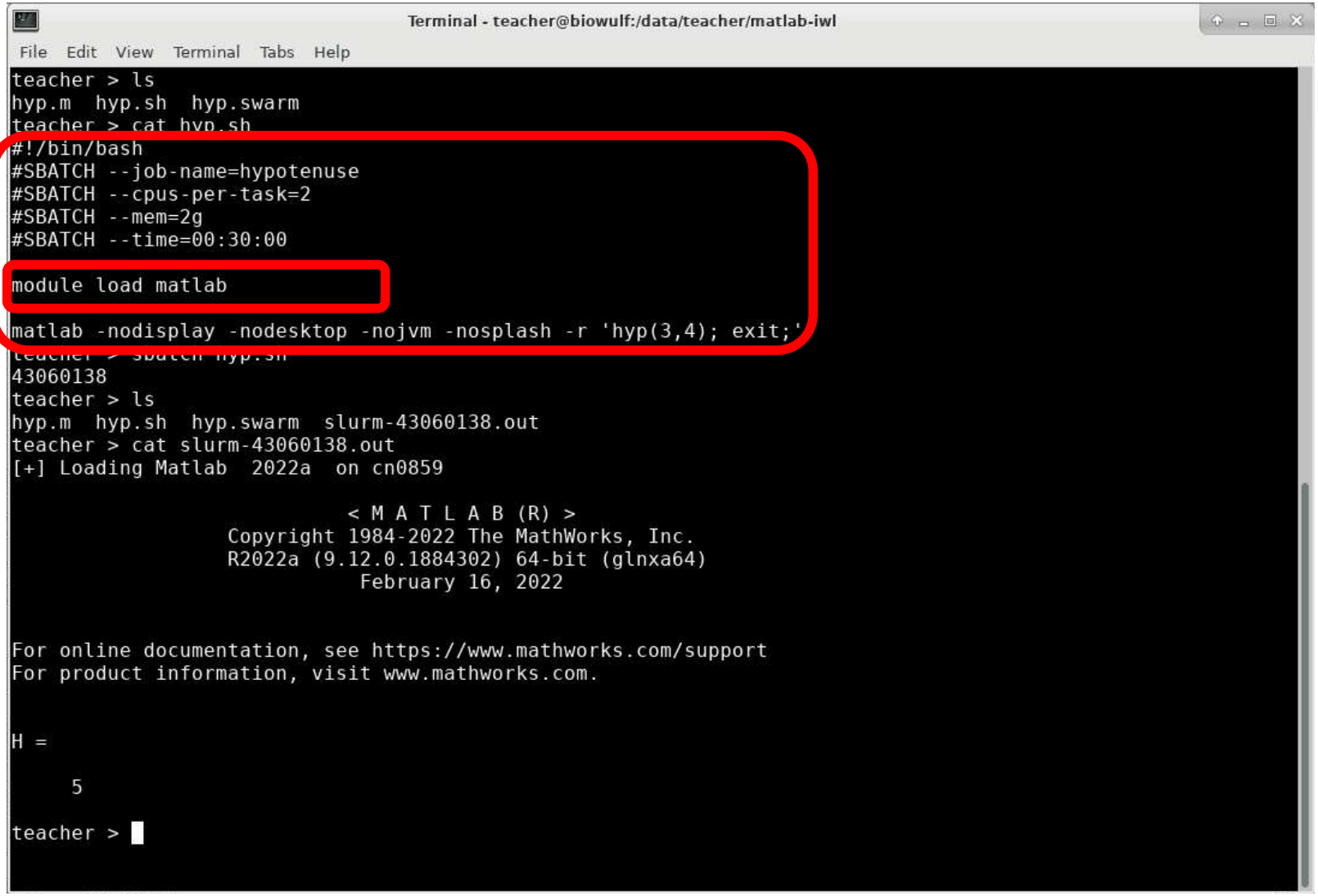

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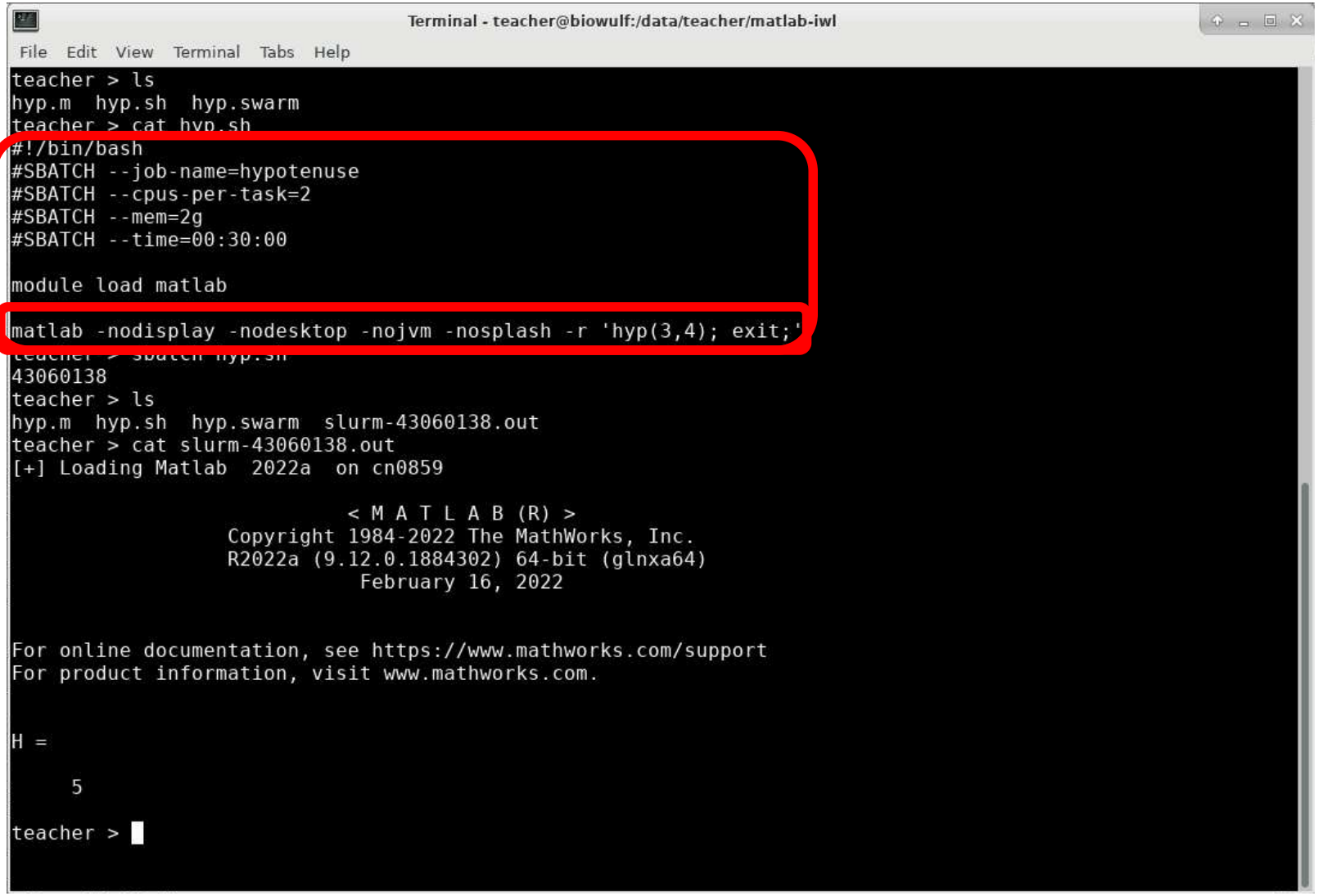

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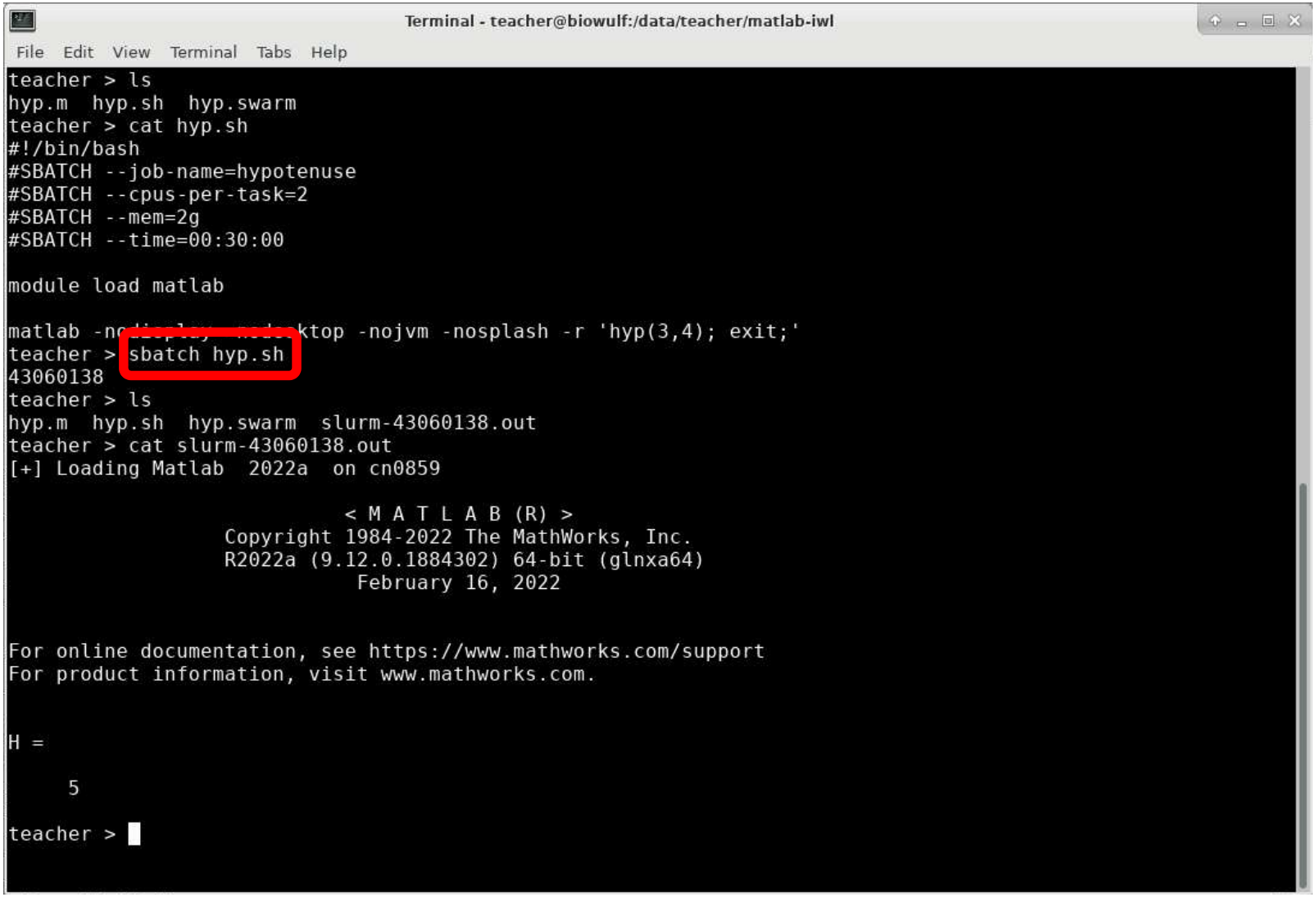

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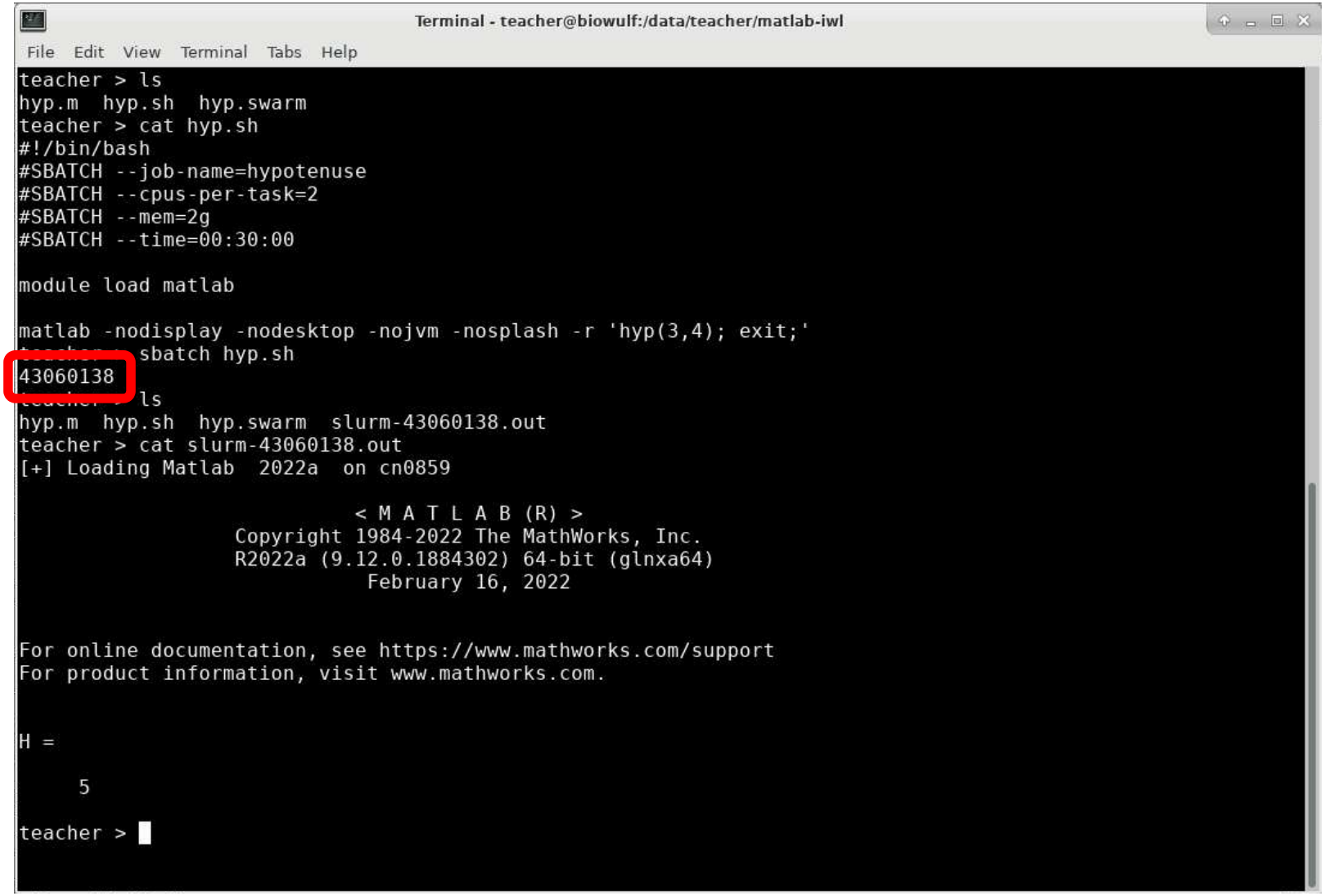

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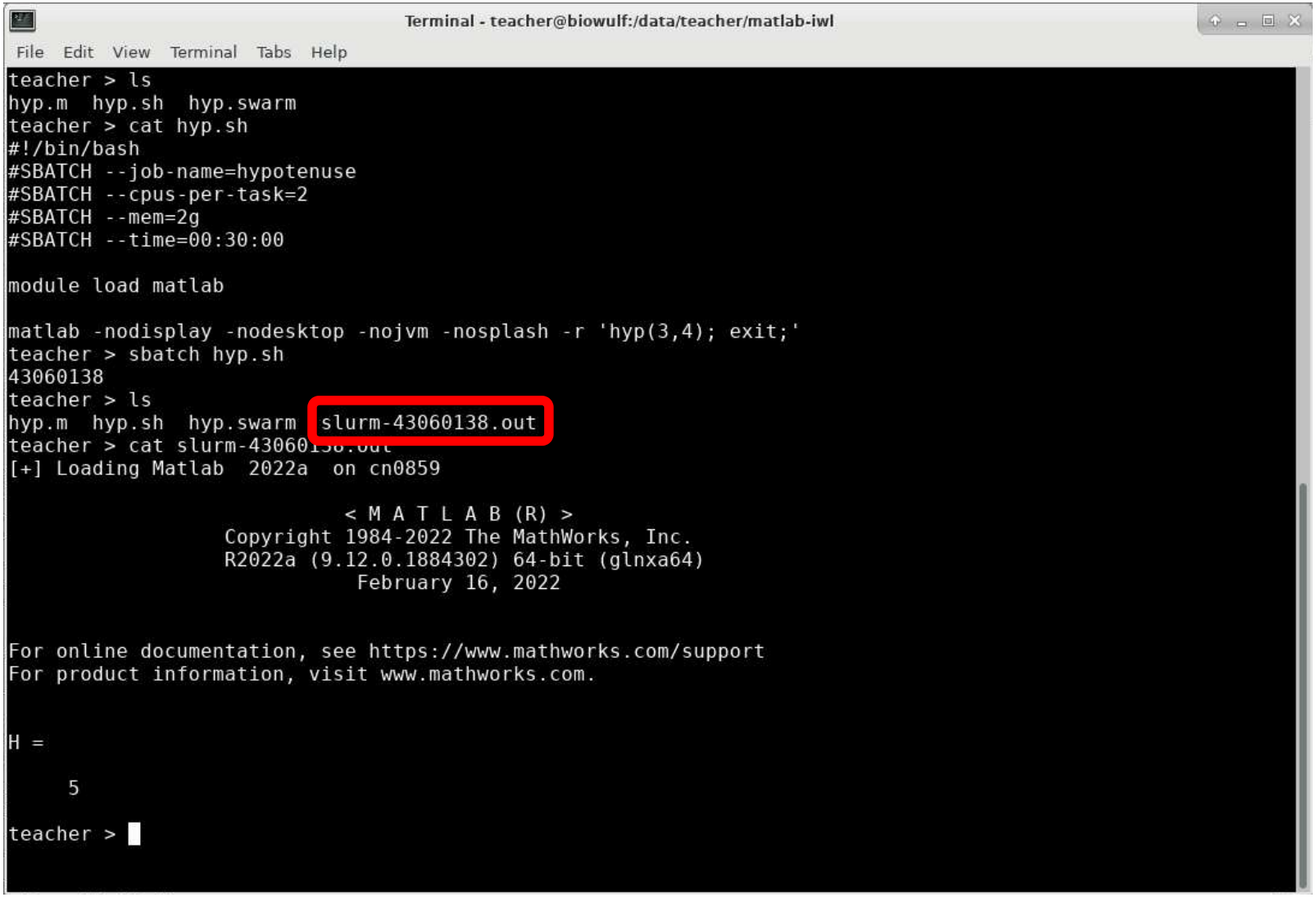

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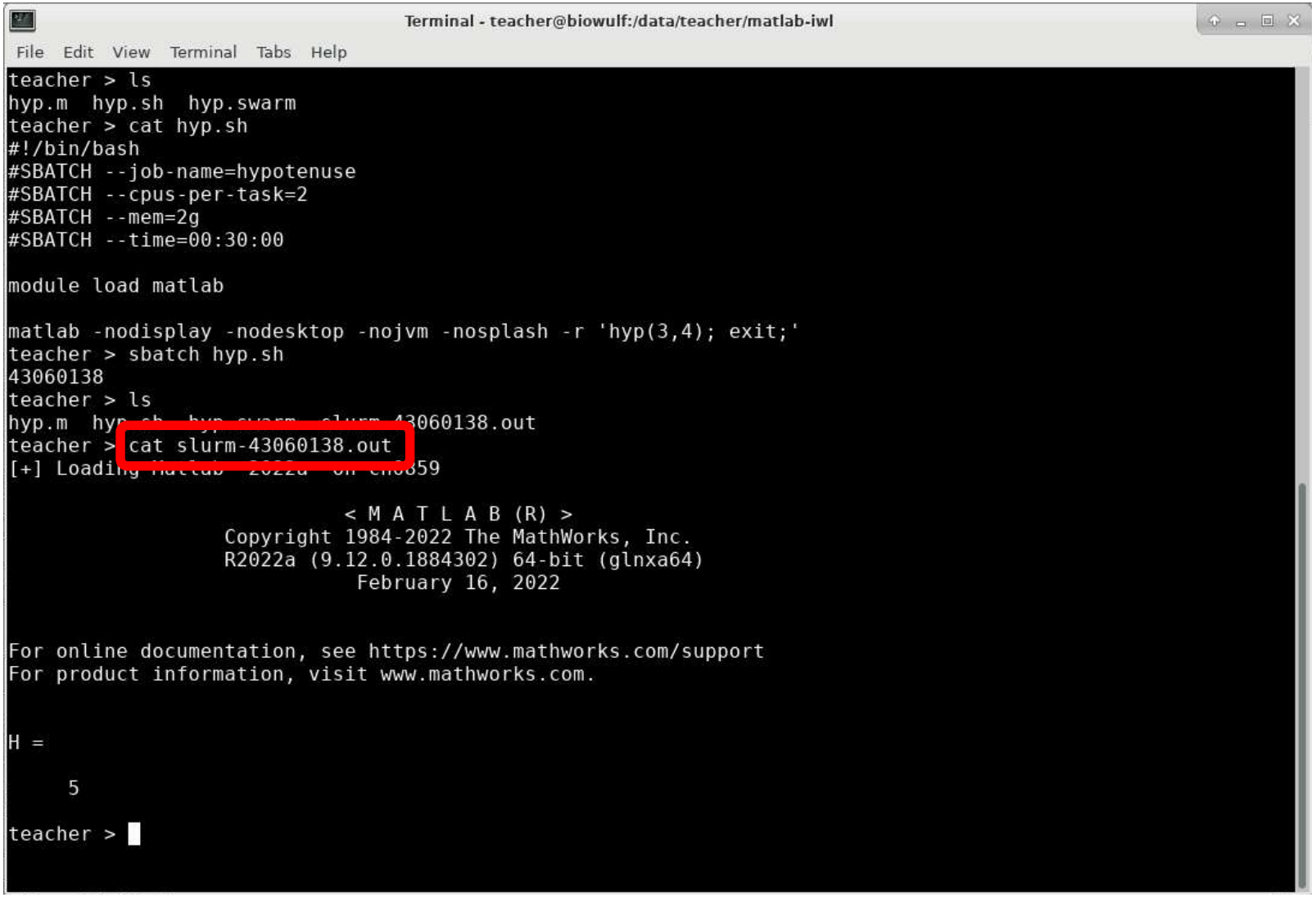

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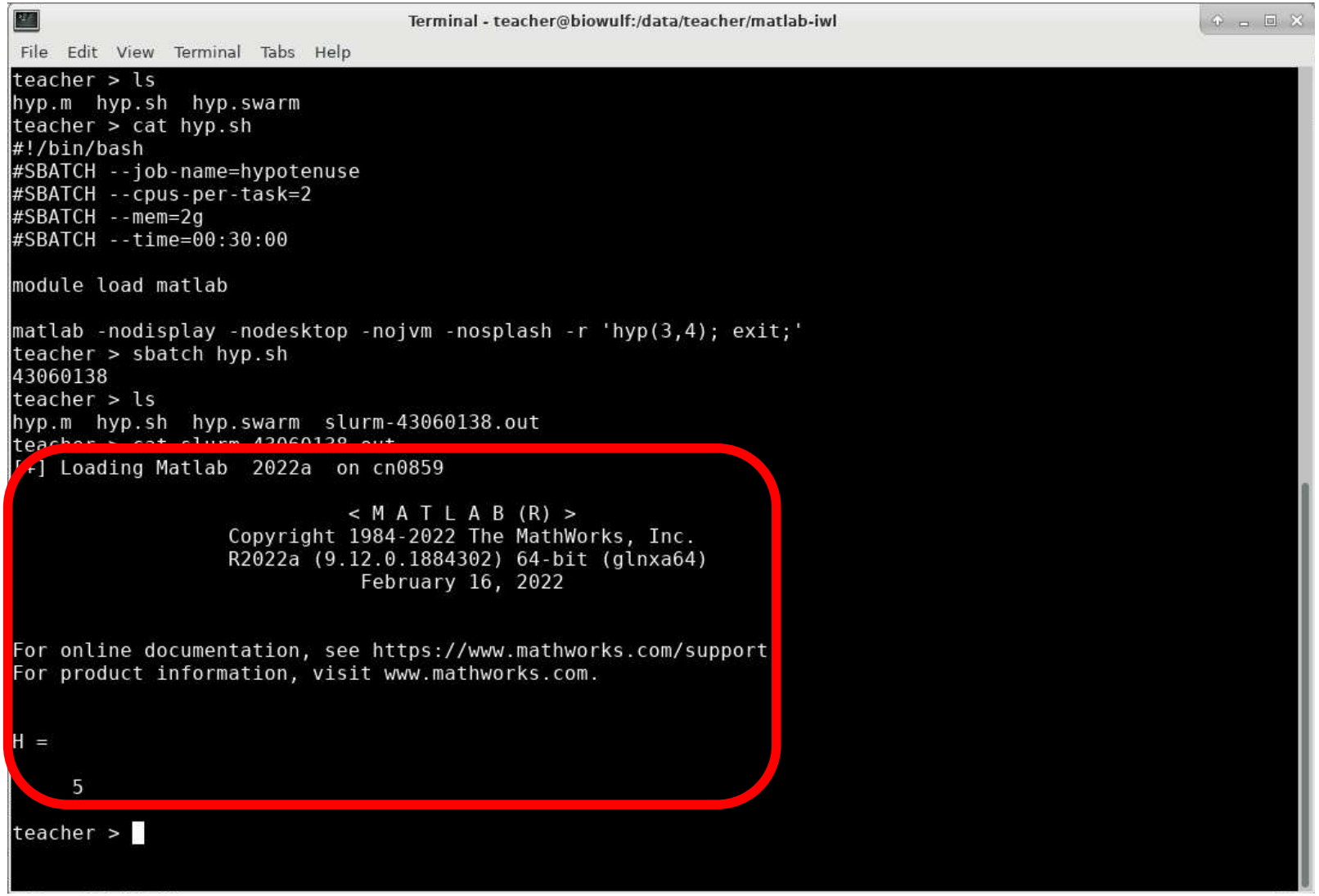

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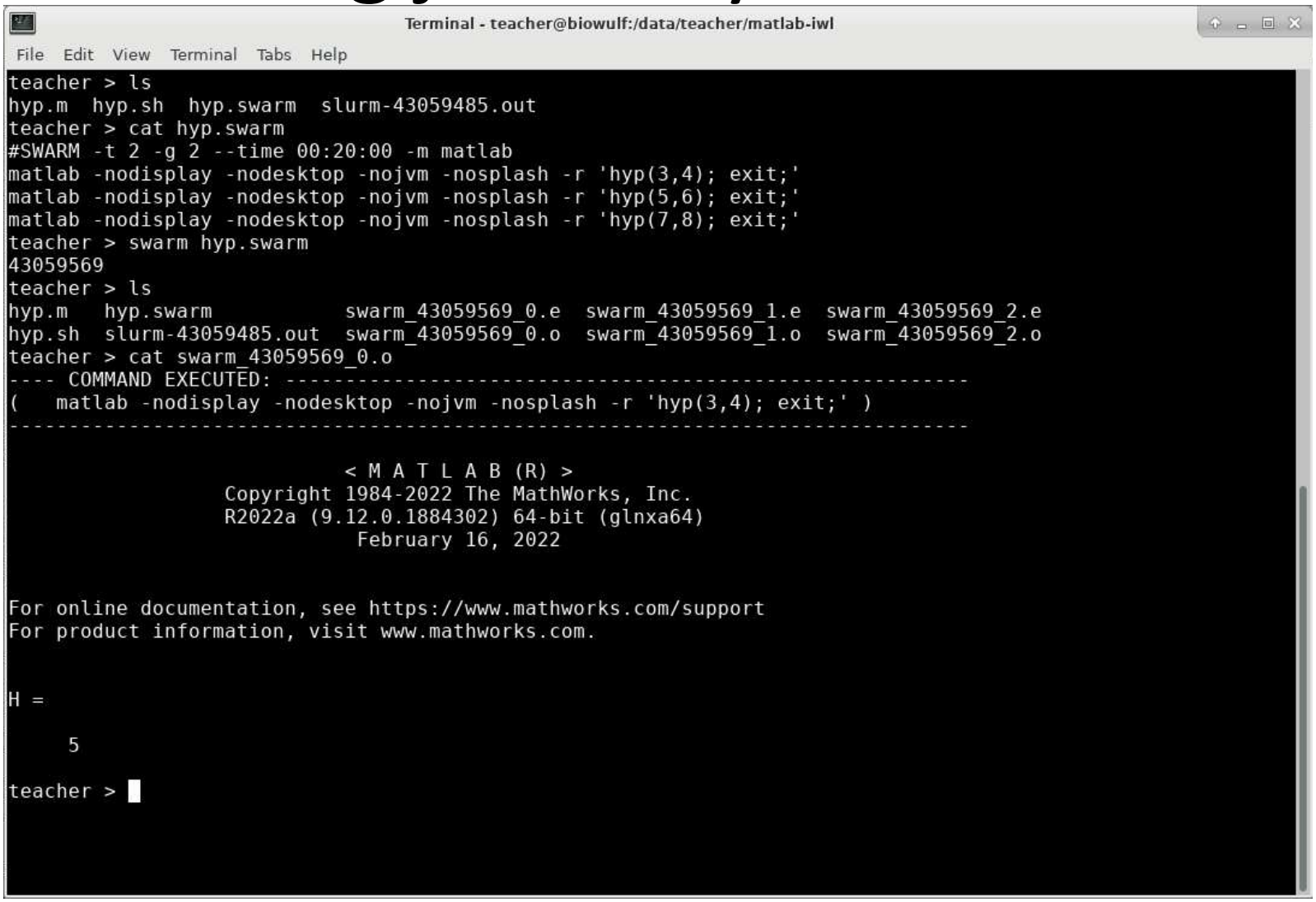

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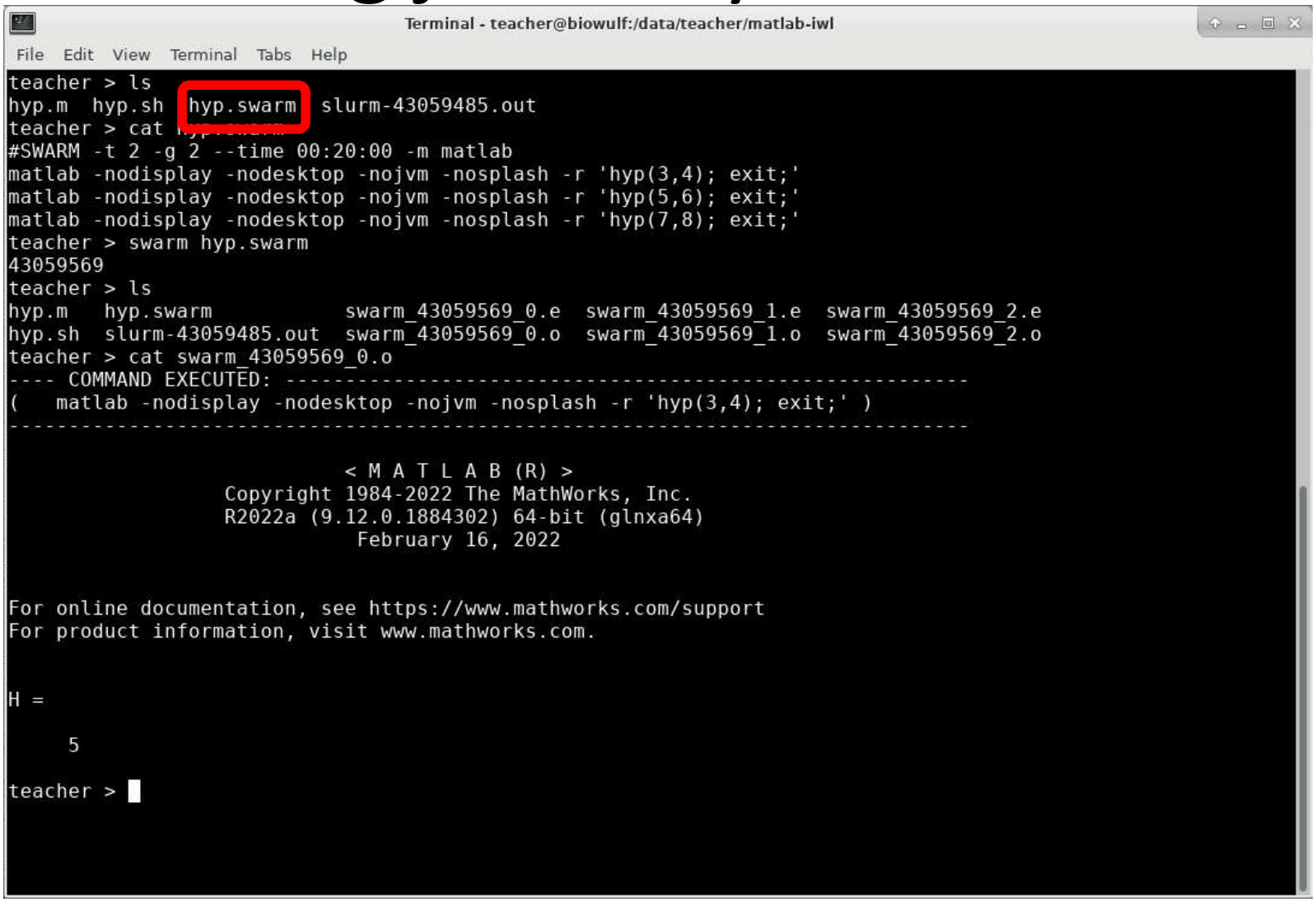

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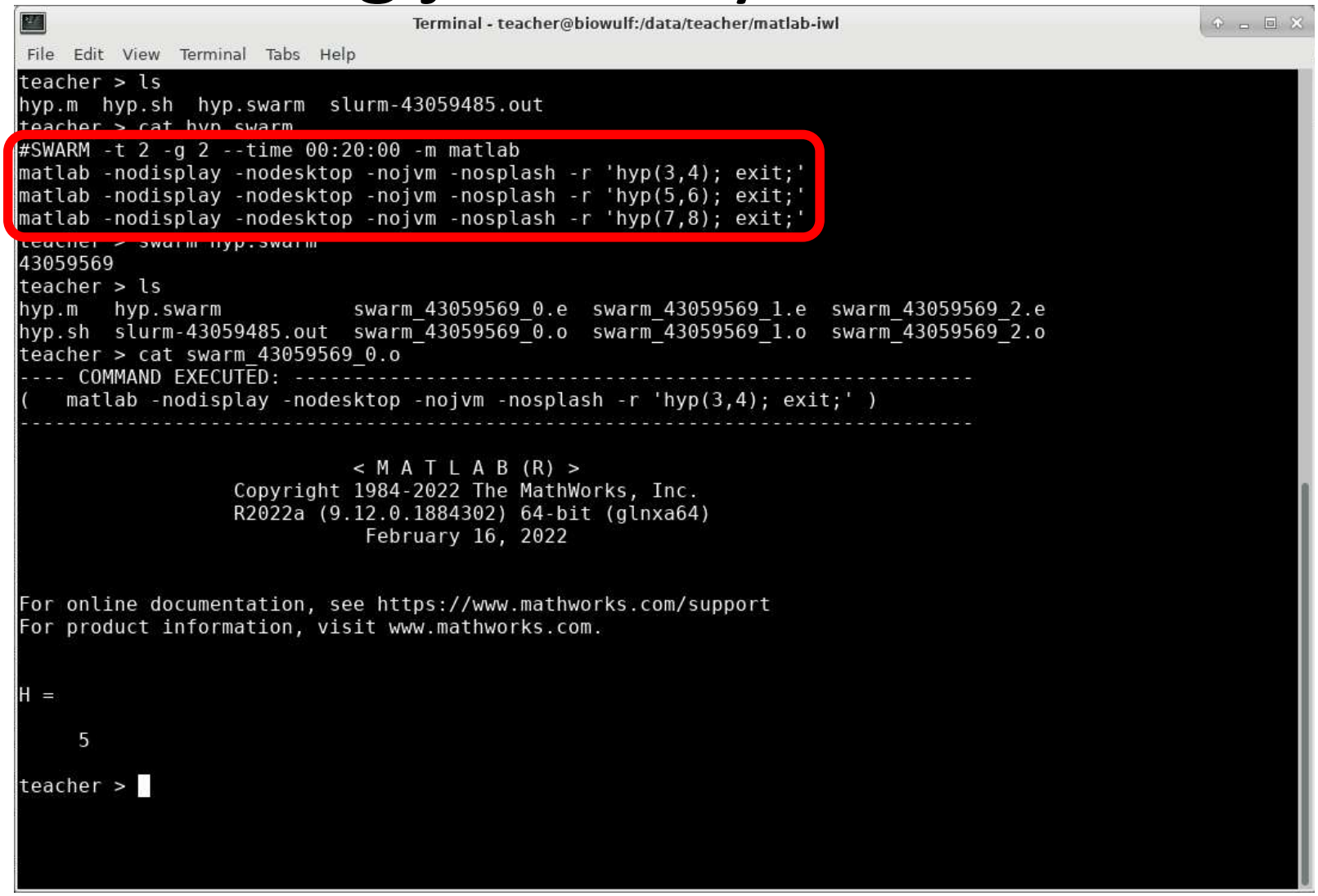

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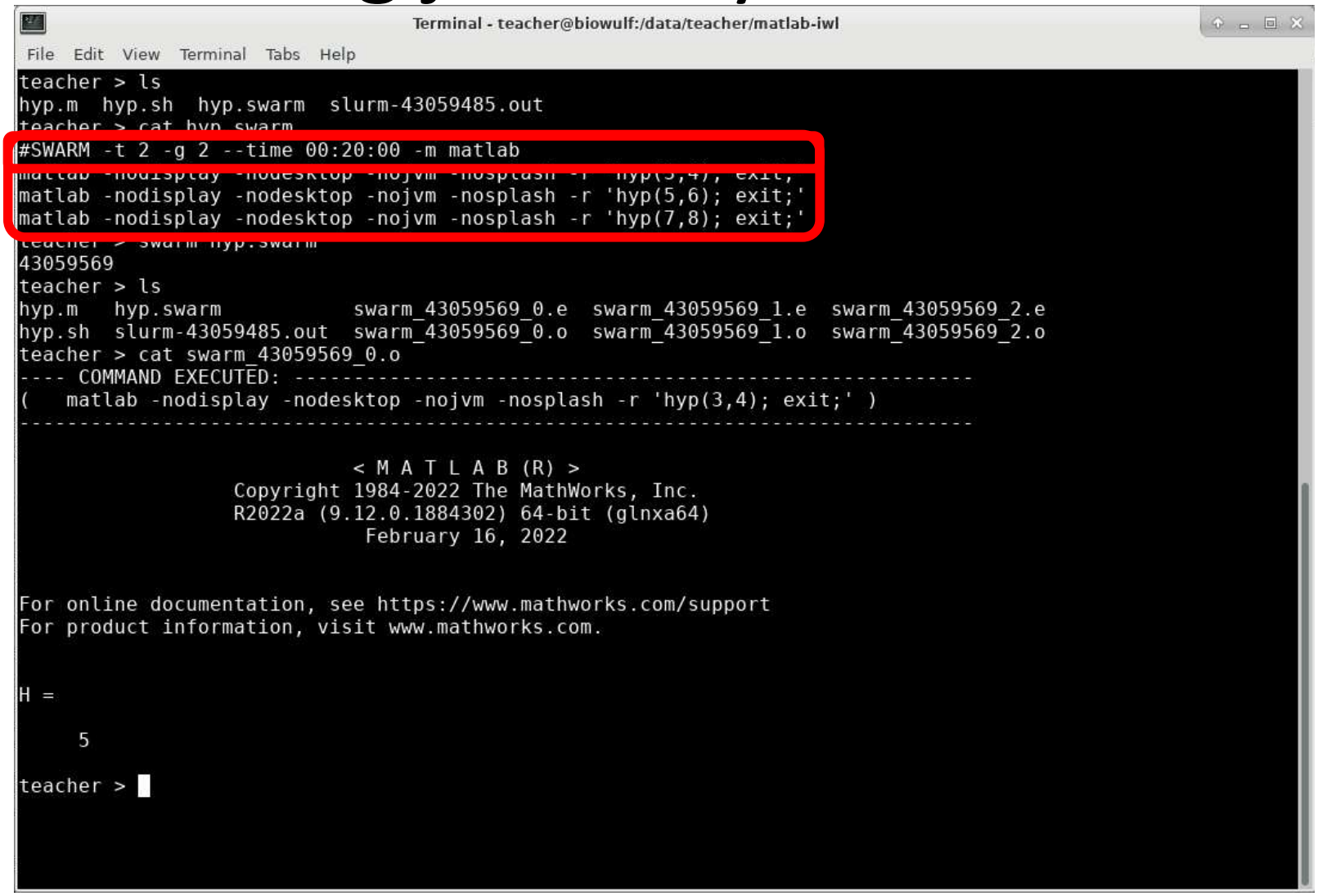

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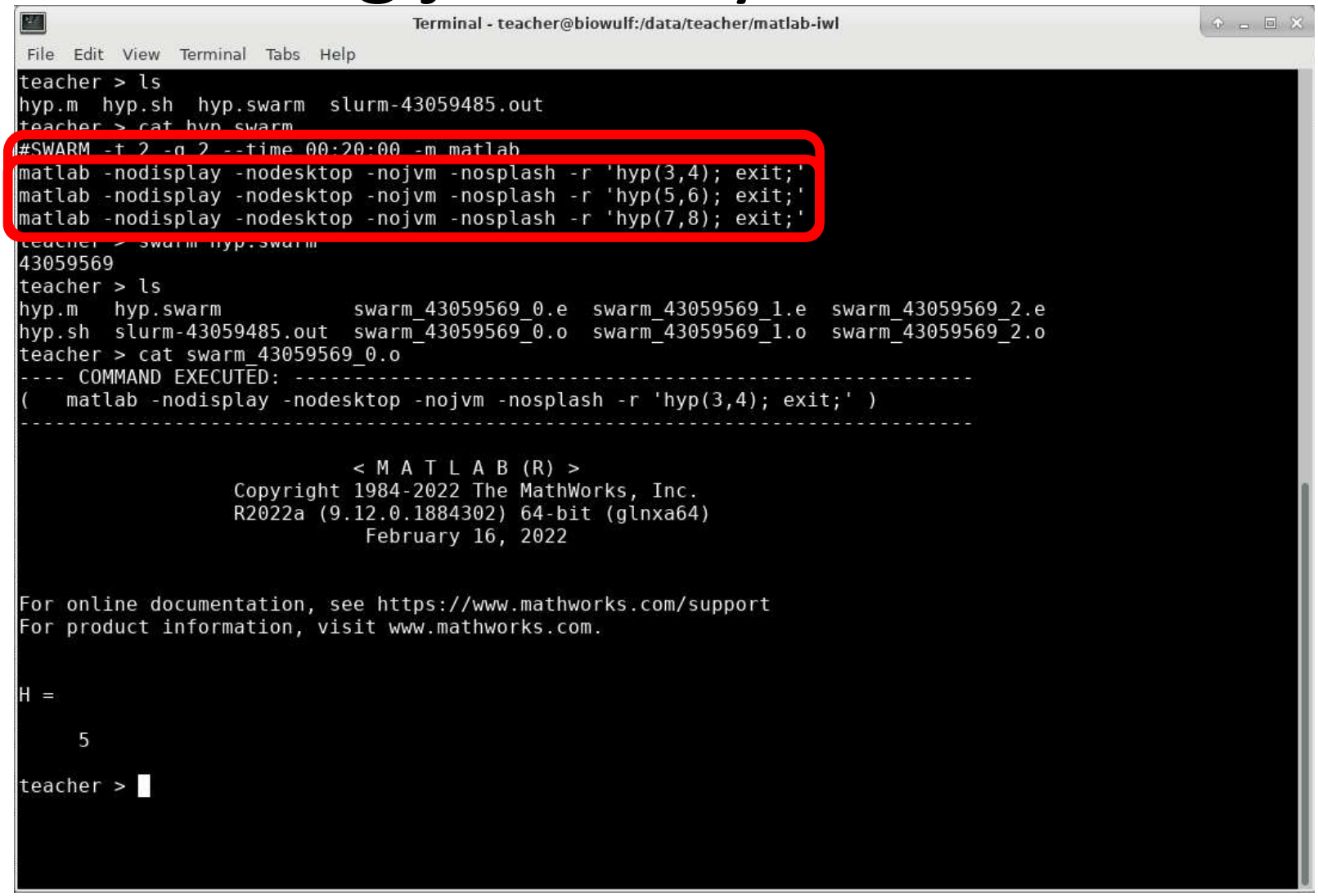

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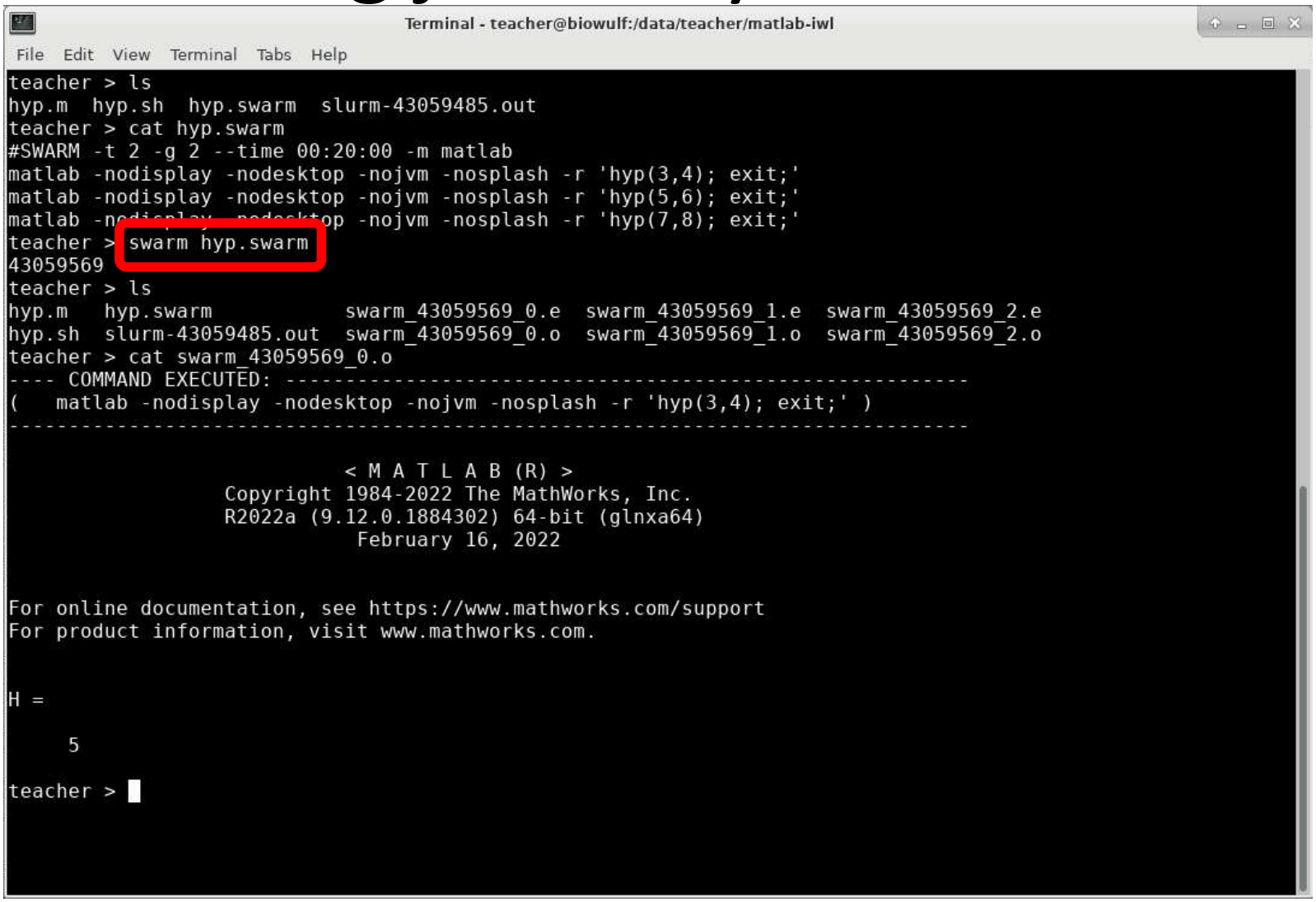

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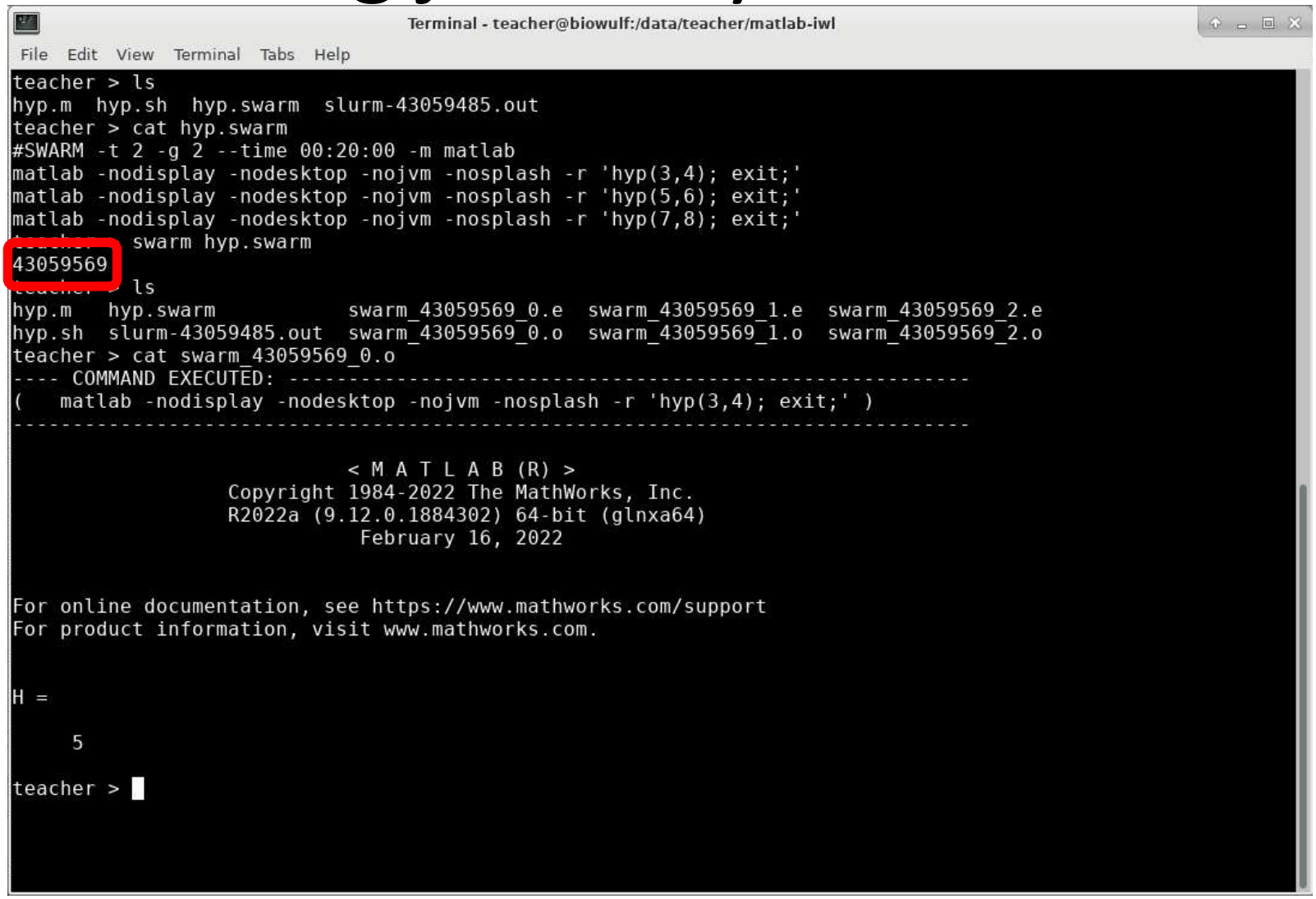

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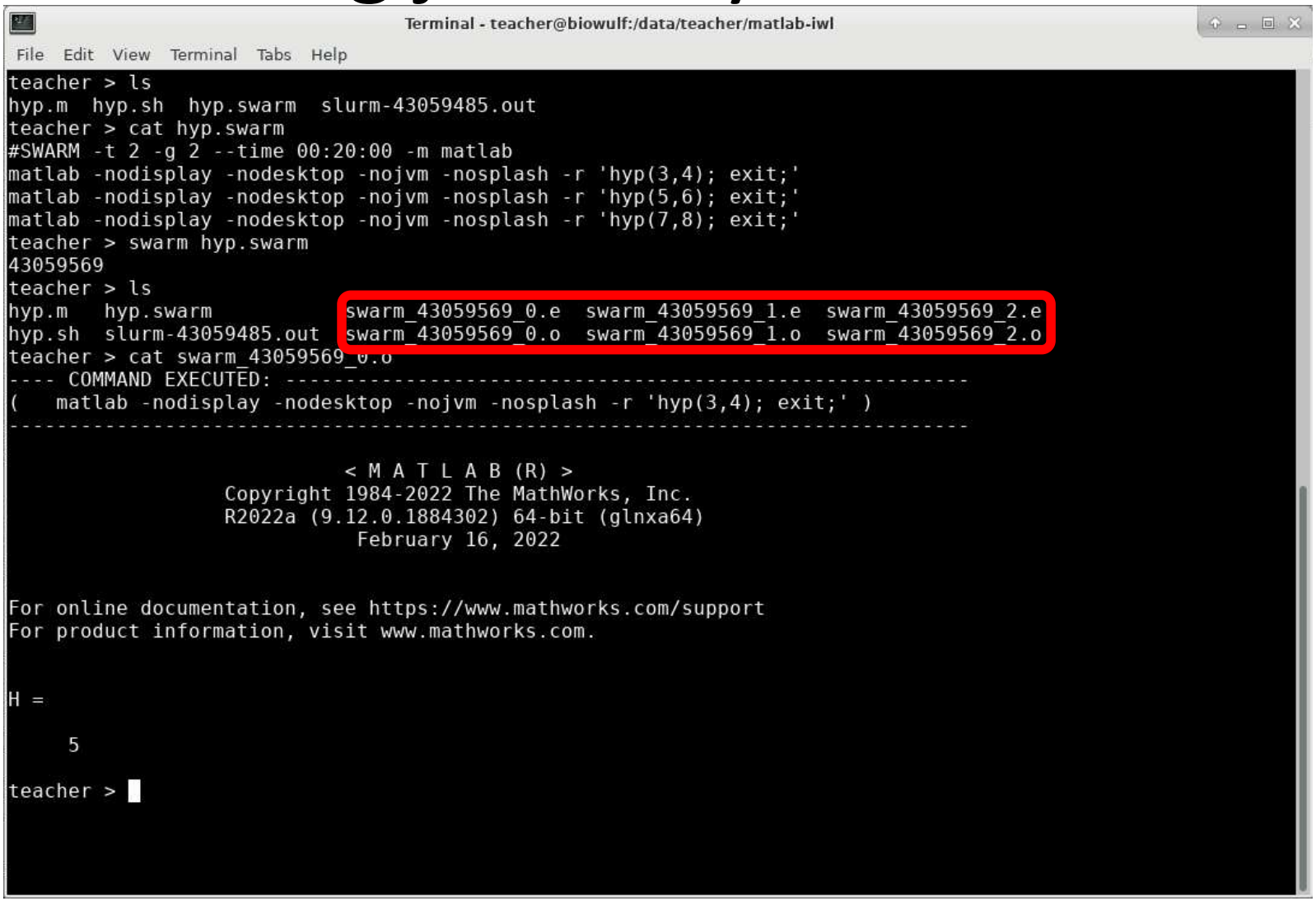

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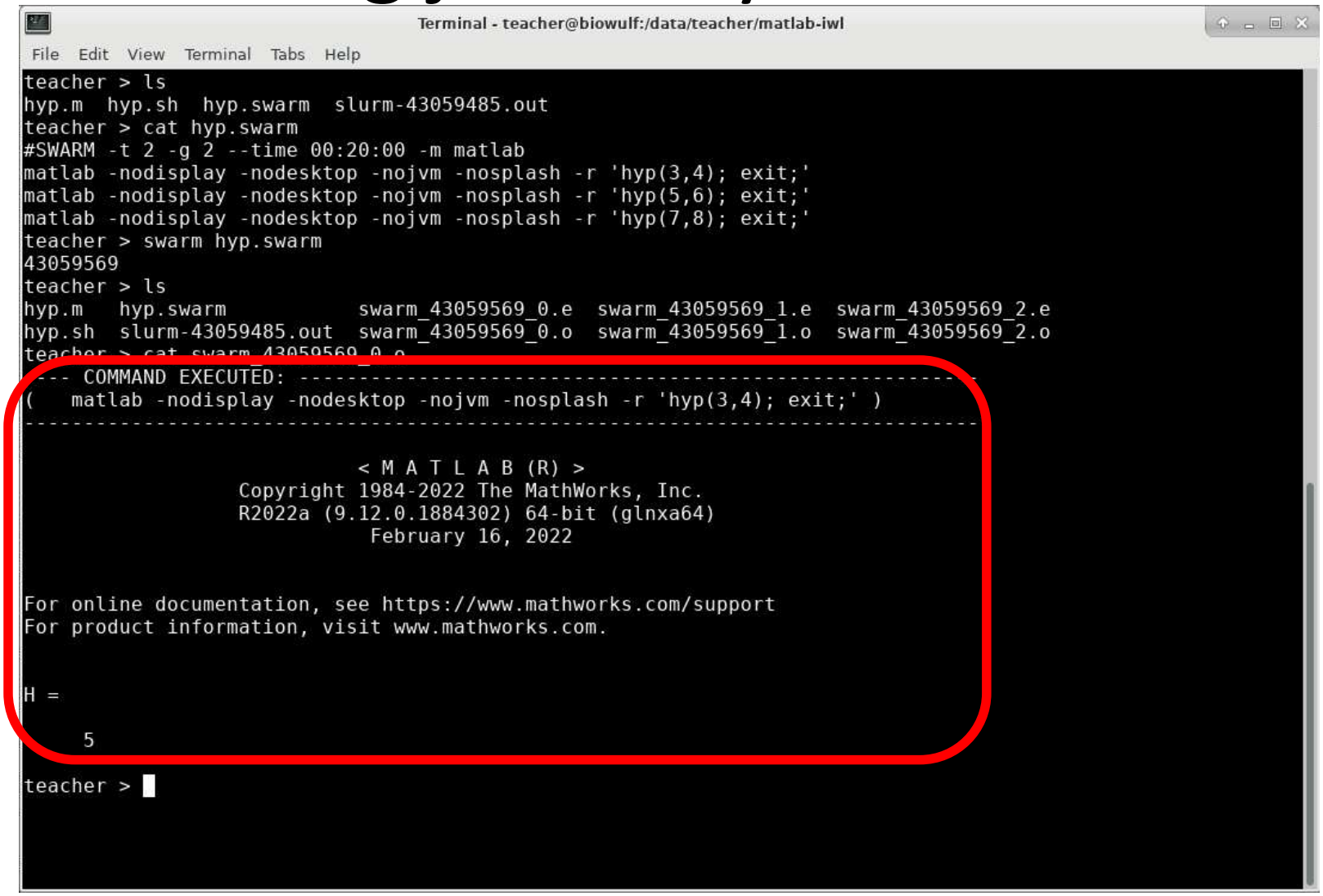

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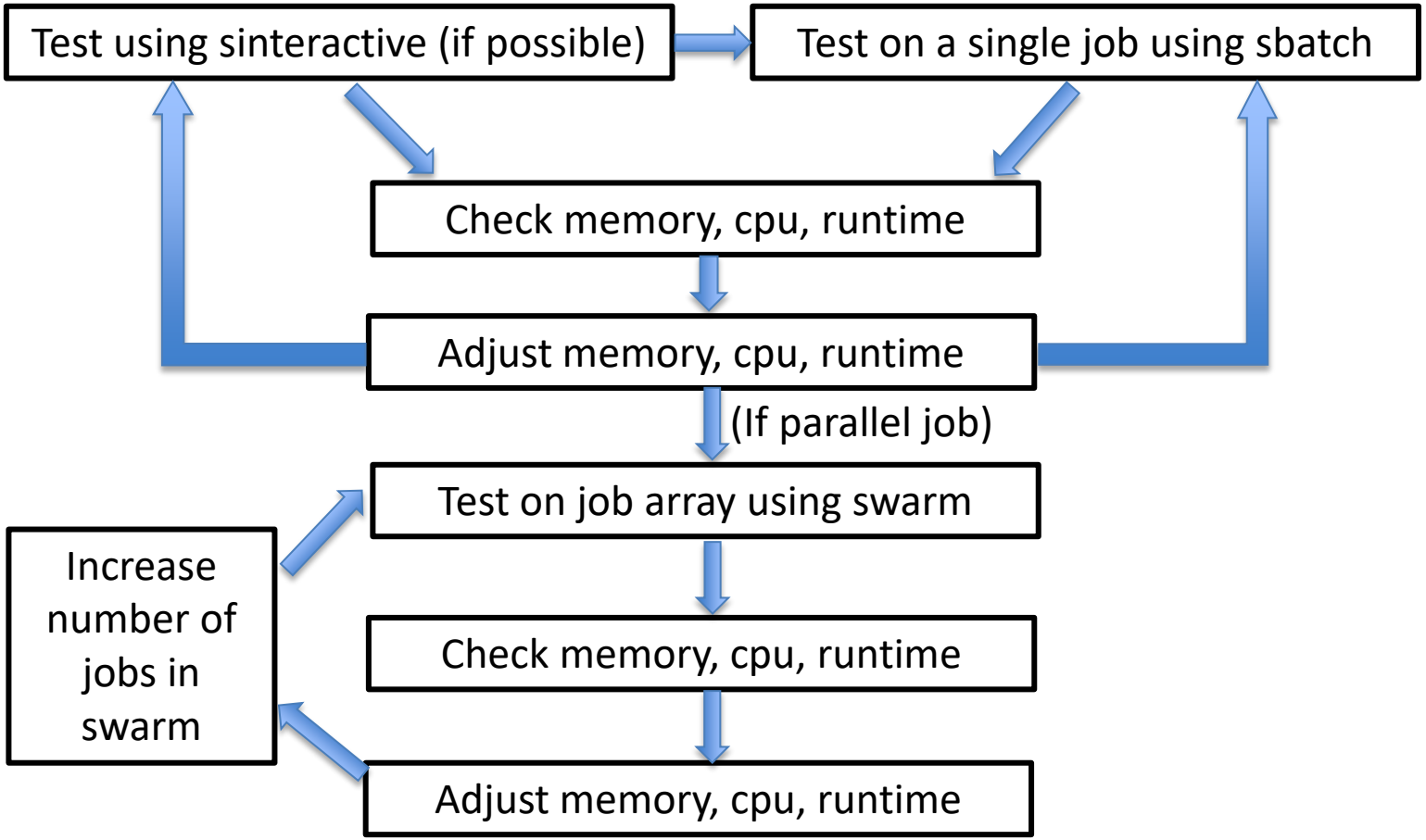

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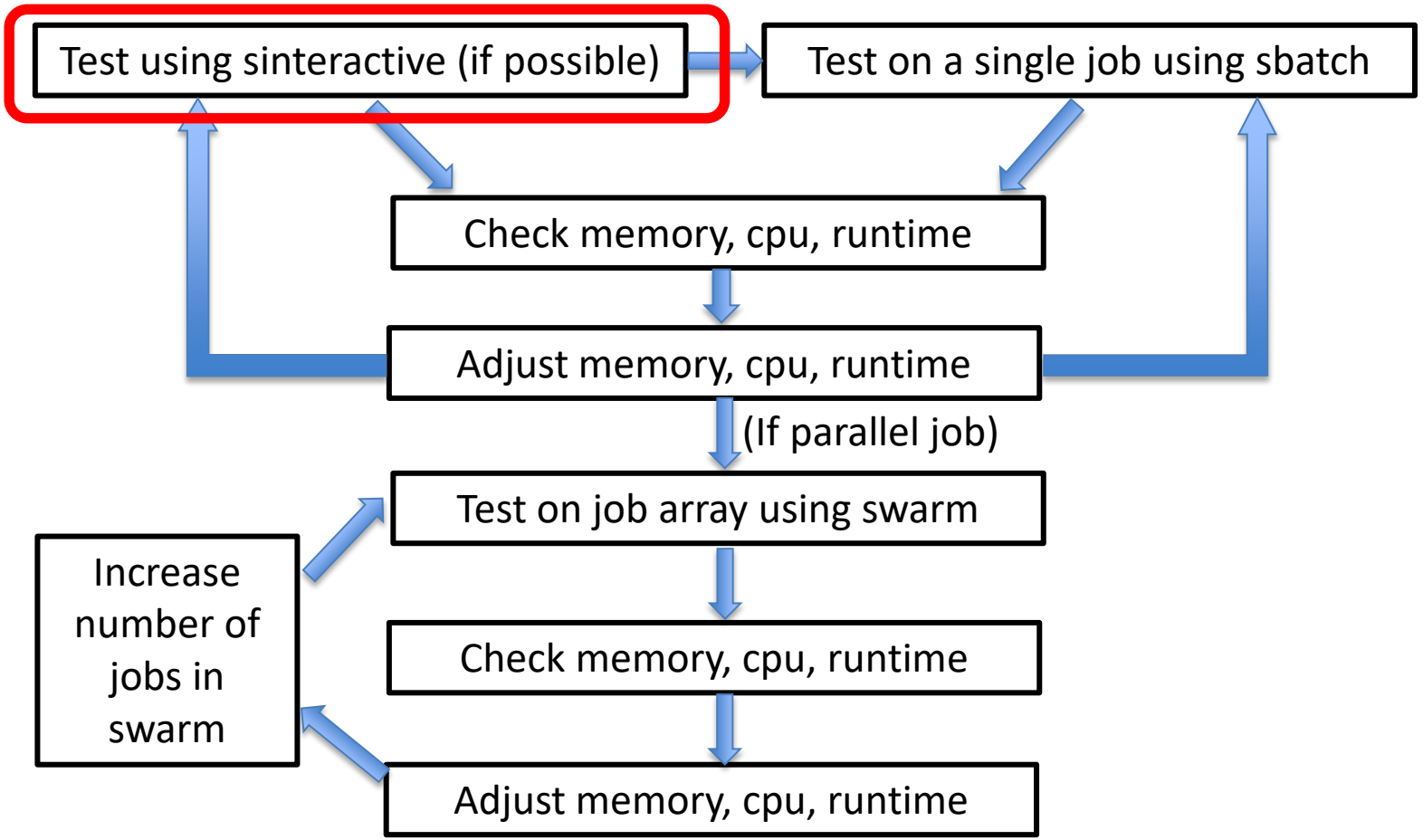

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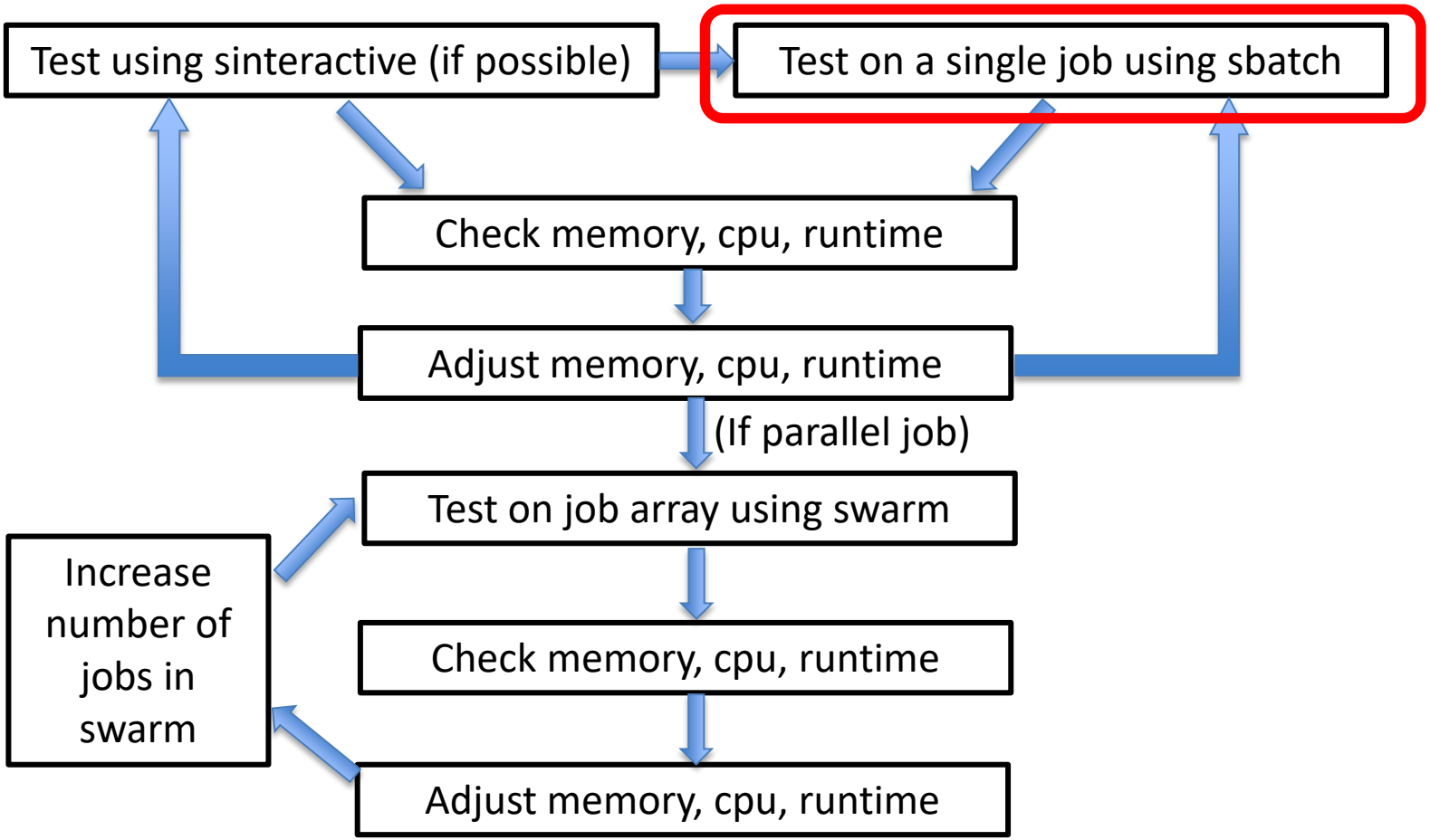

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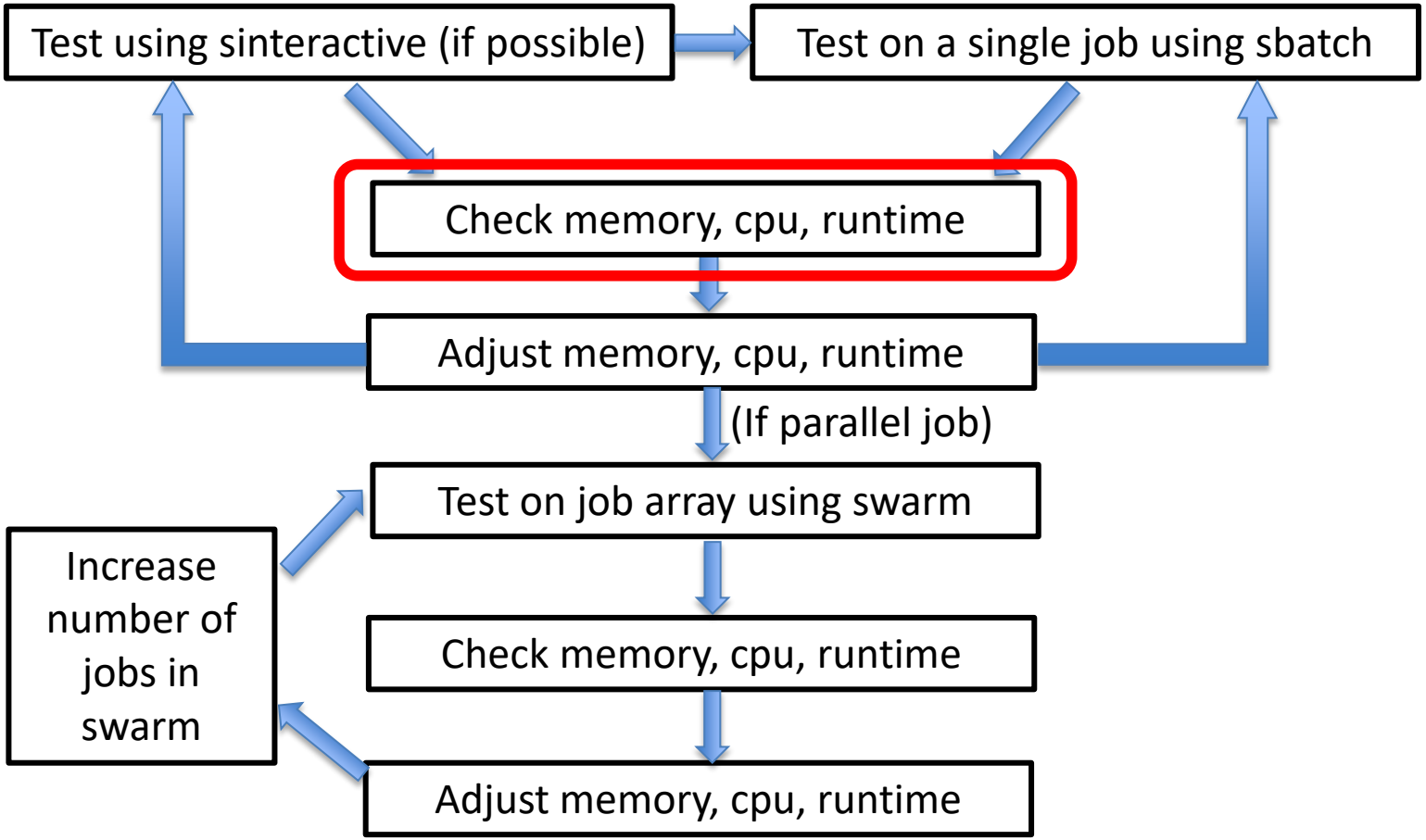

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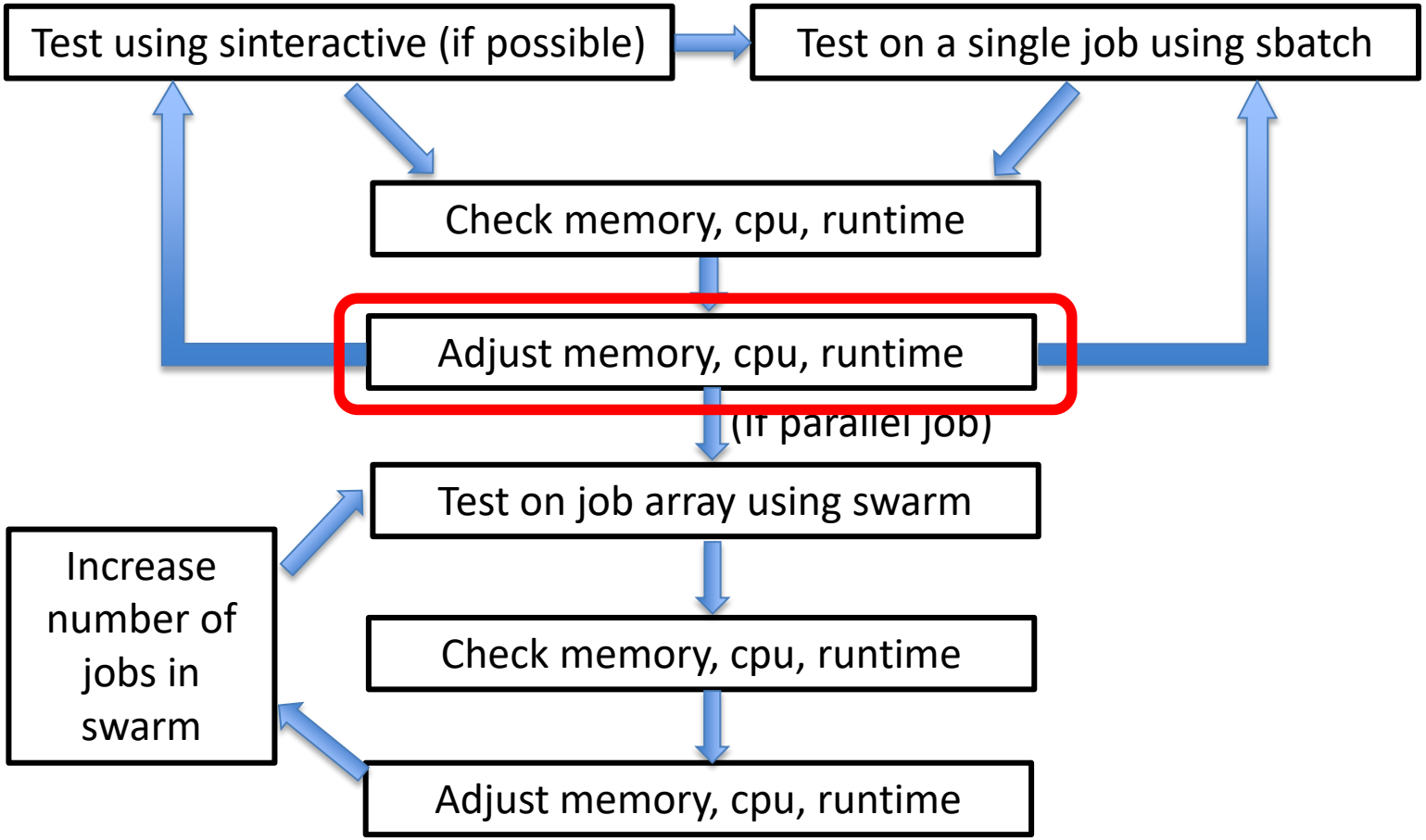

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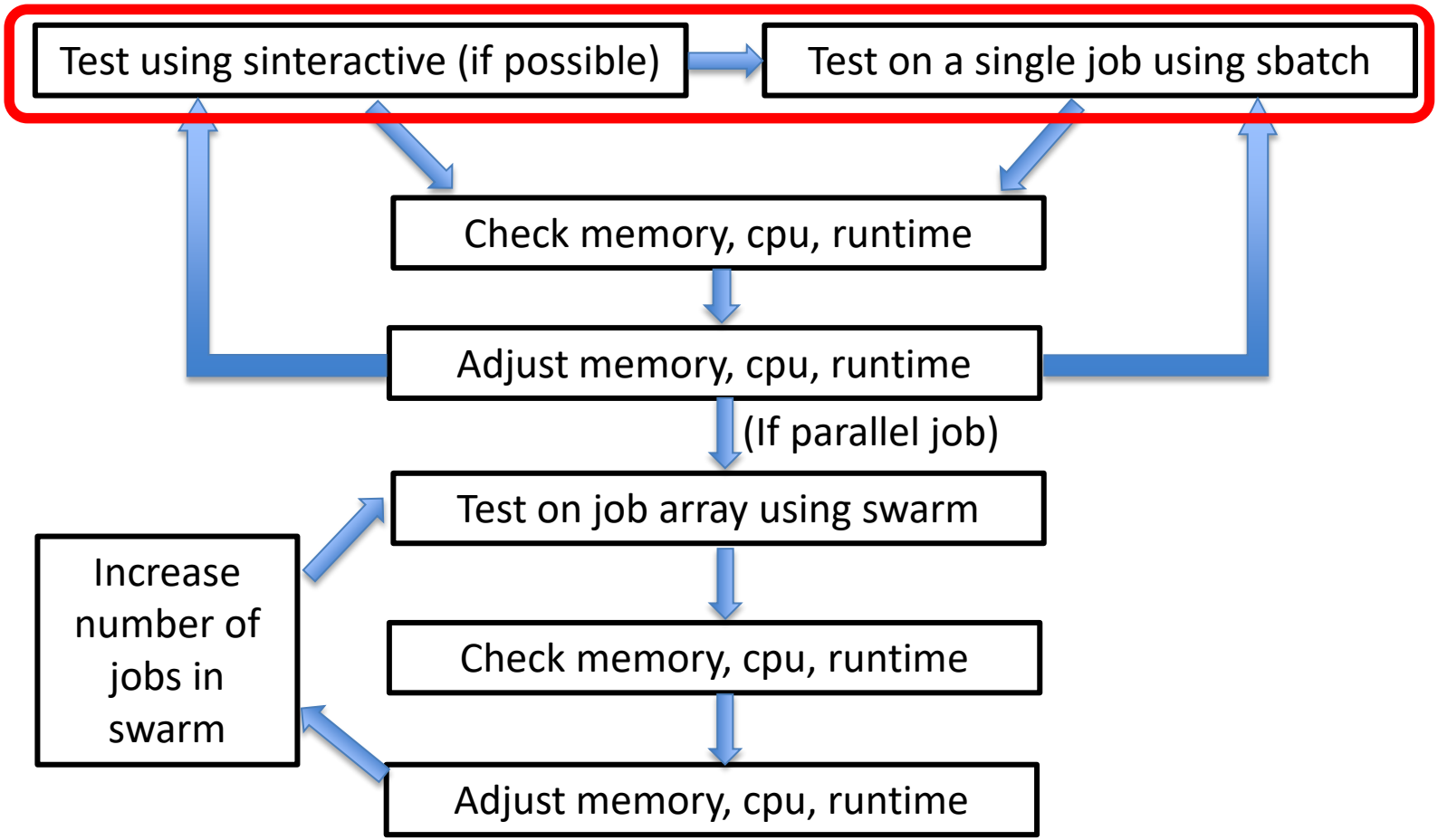

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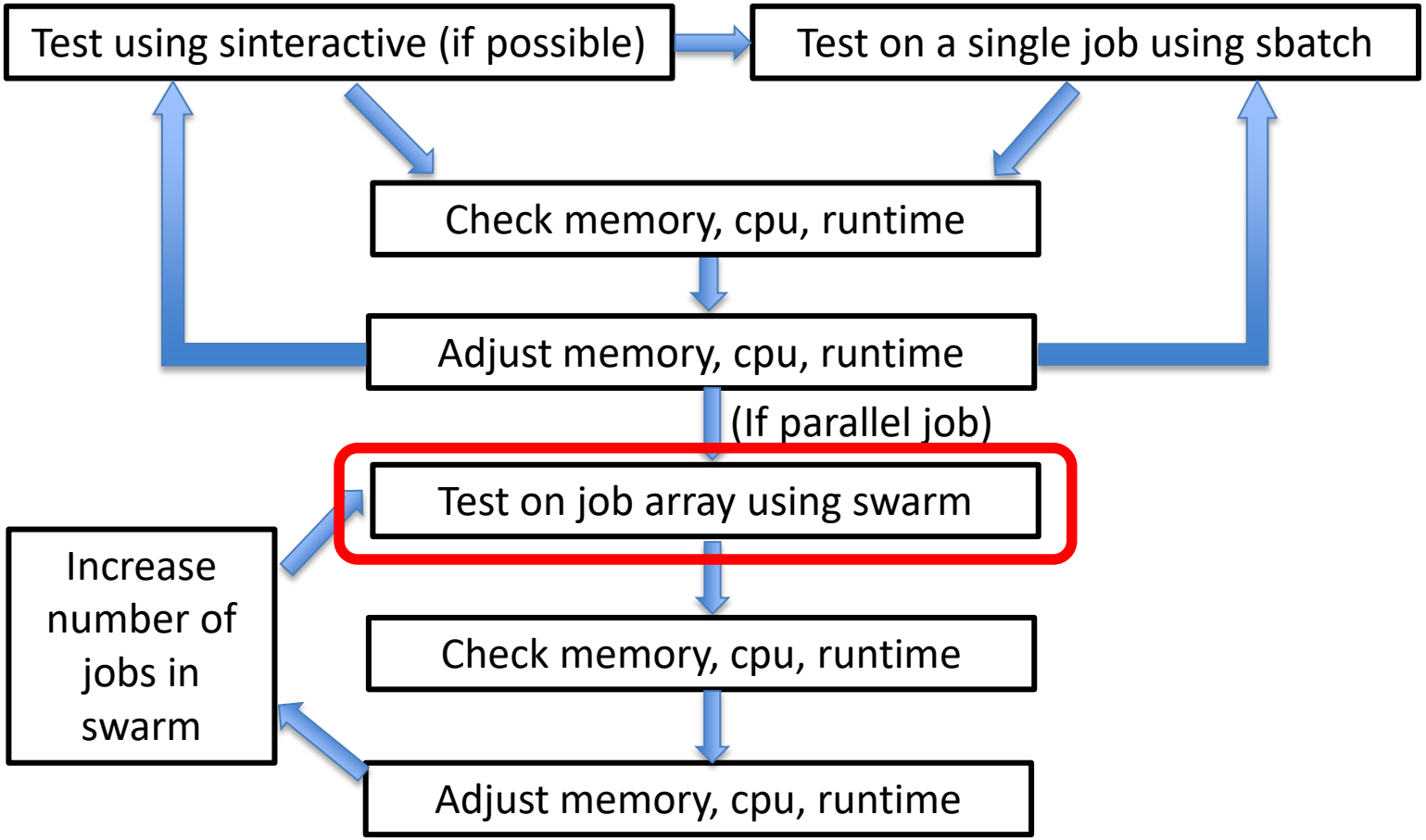

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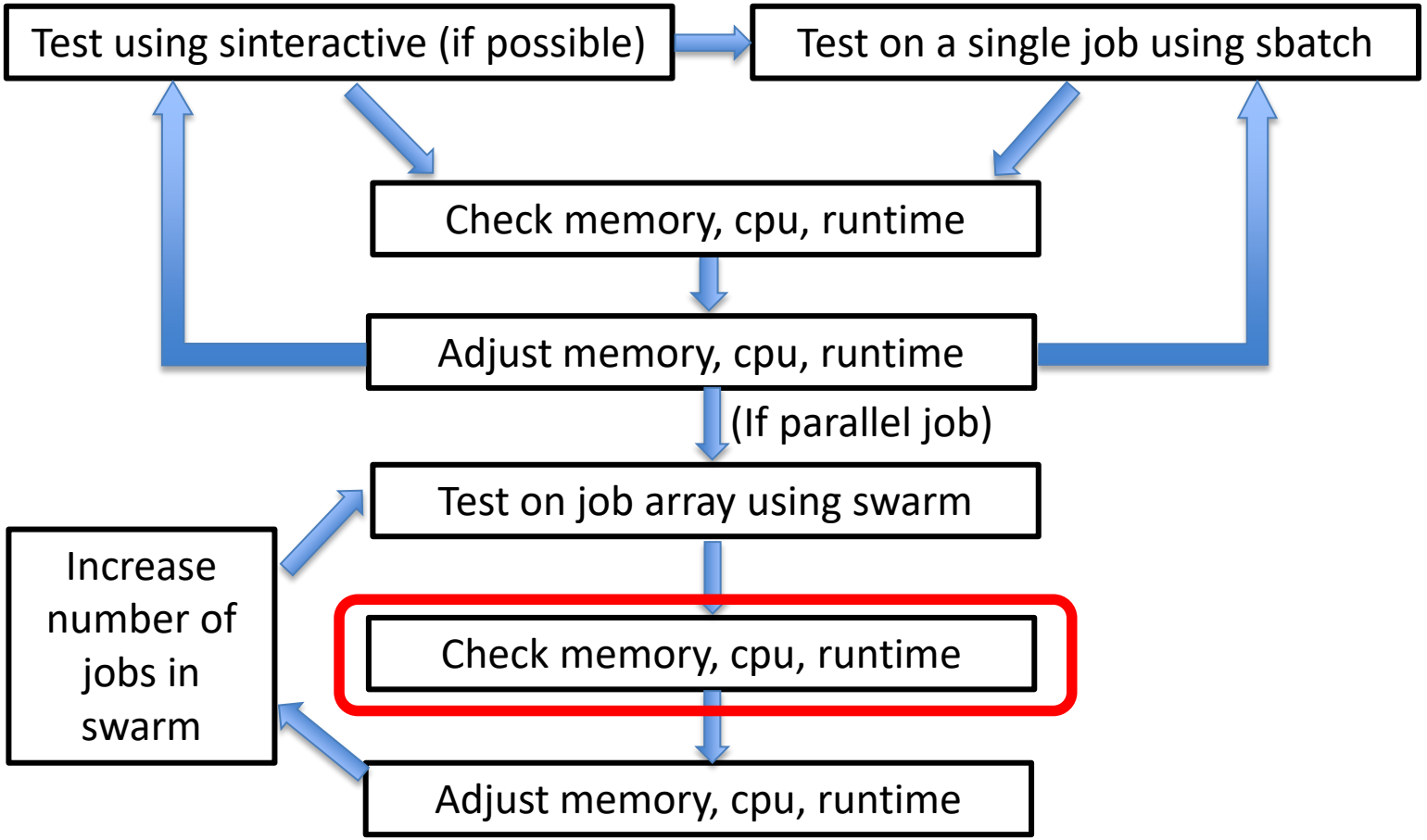

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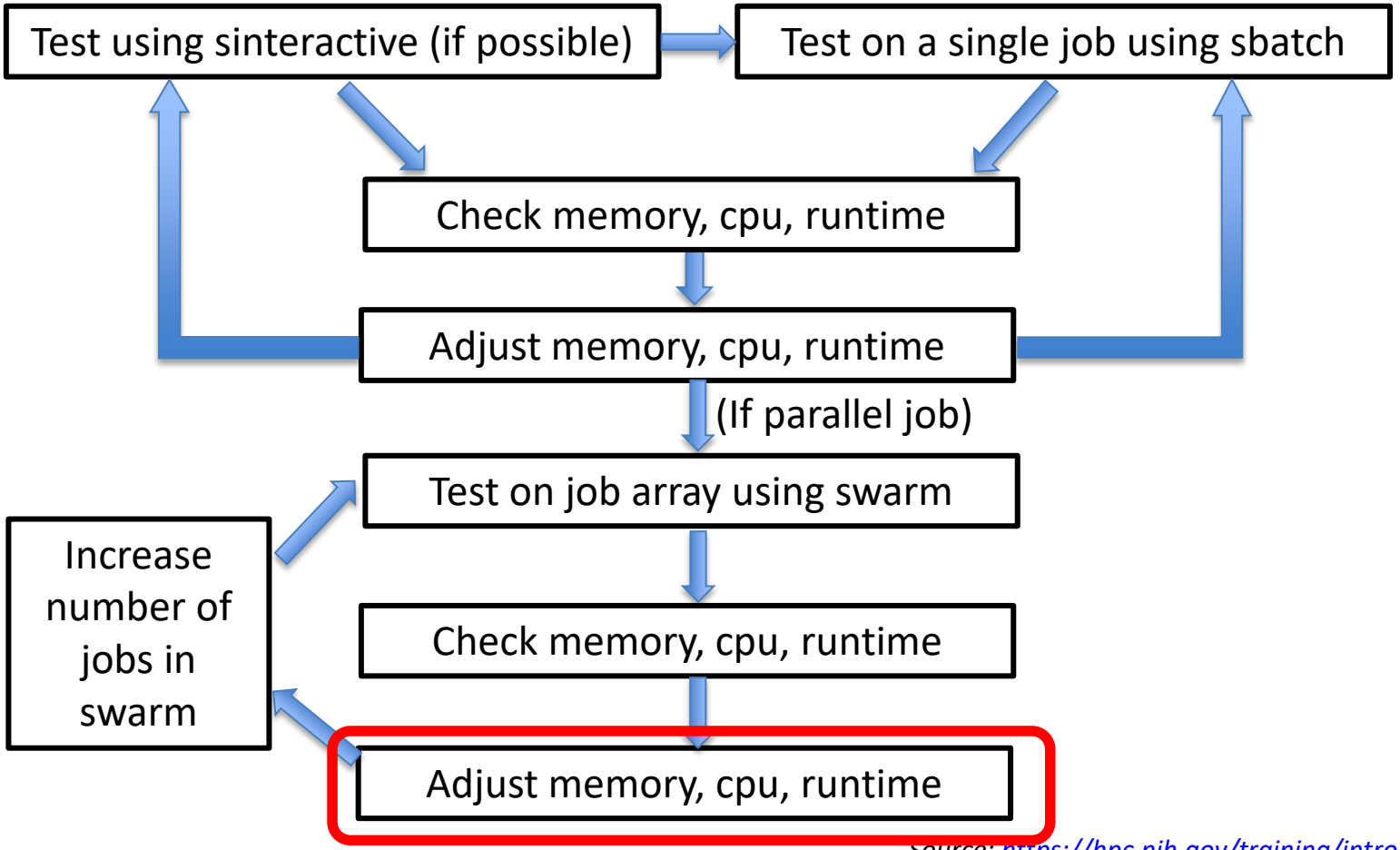

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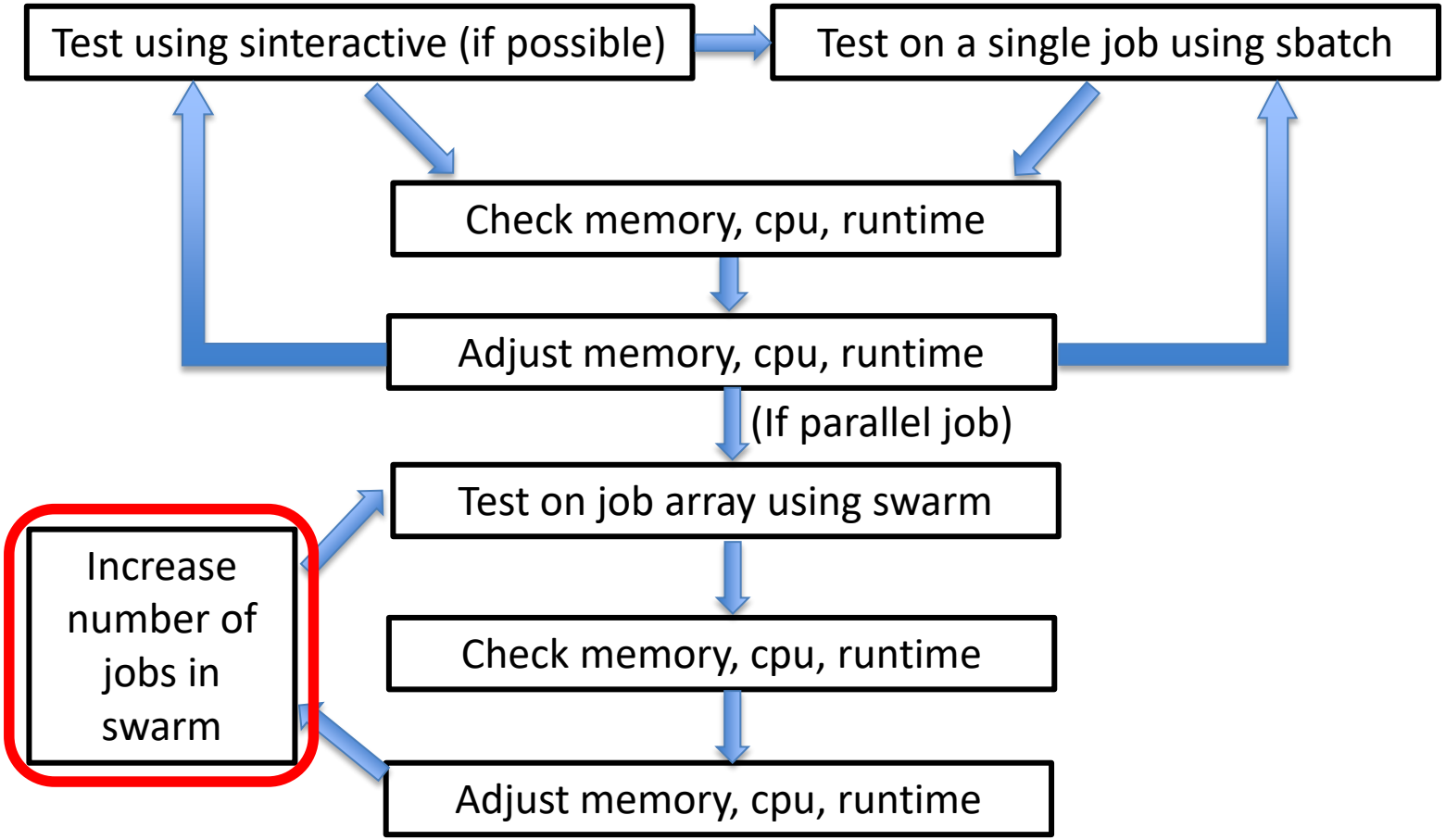

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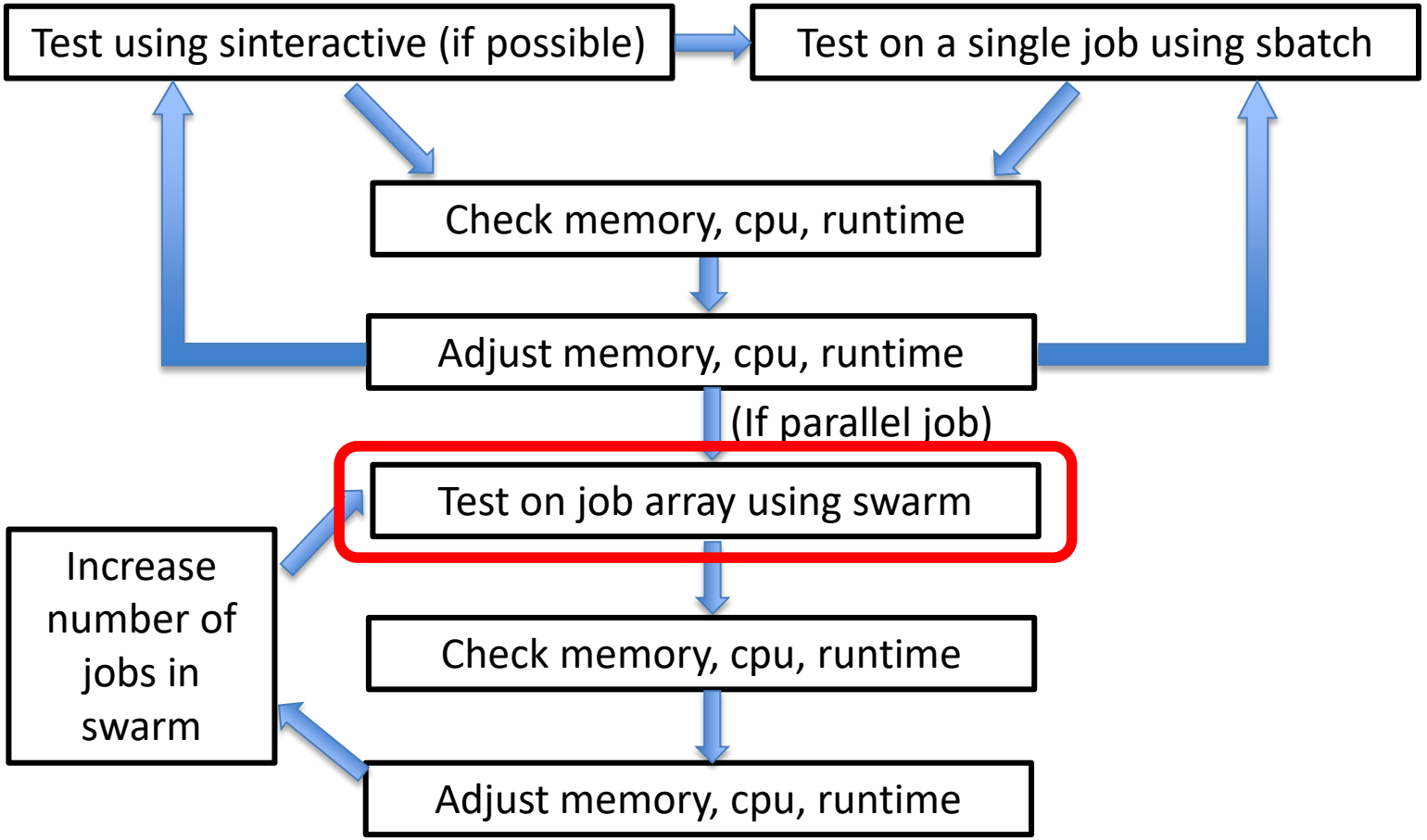

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Outline

- Motivation
- Quick review of the Biowulf cluster
- Matlab Institute Wide License
- Running Matlab scripts interactively
- Running Matlab scripts as batch jobs
  - Running single job with *sbatch*
  - Running job array with *swarm*
  - Monitoring jobs
  - Limits, pitfalls and caveats
- Conclusion

Monitoring Matlab jobs

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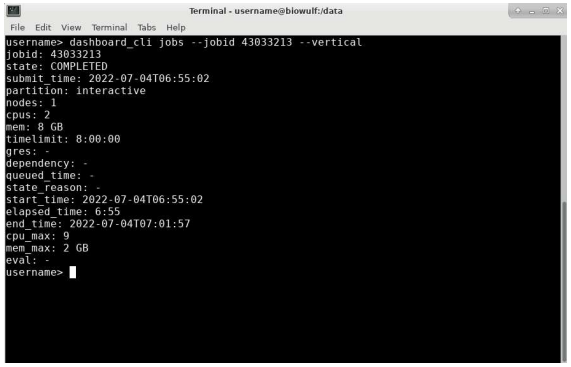
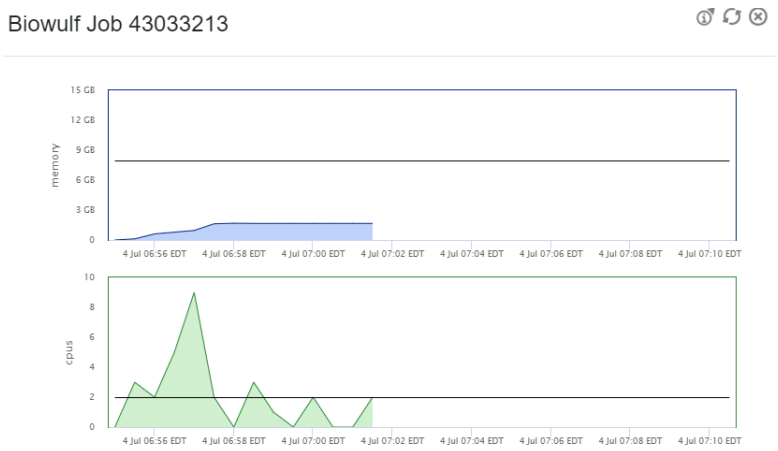
- Users are responsible for monitoring their own jobs

Monitoring Matlab jobs

Command-line tools (see hpc.nih.gov/docs/userguide.html)



Graphical dashboard (hpc.nih.gov/dashboard):



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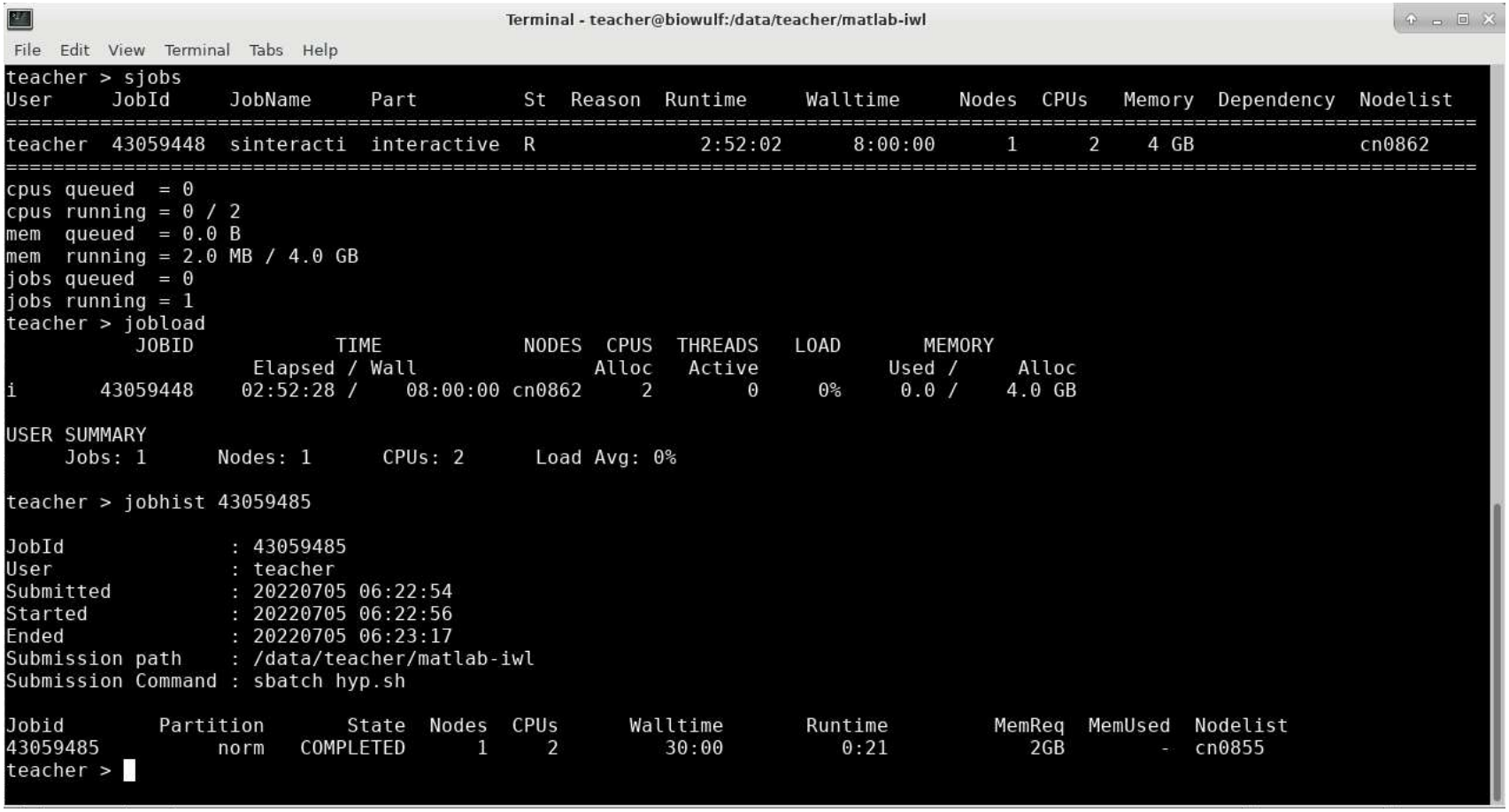

Source: https://hpc.nih.gov/docs/userguide.html#monitor

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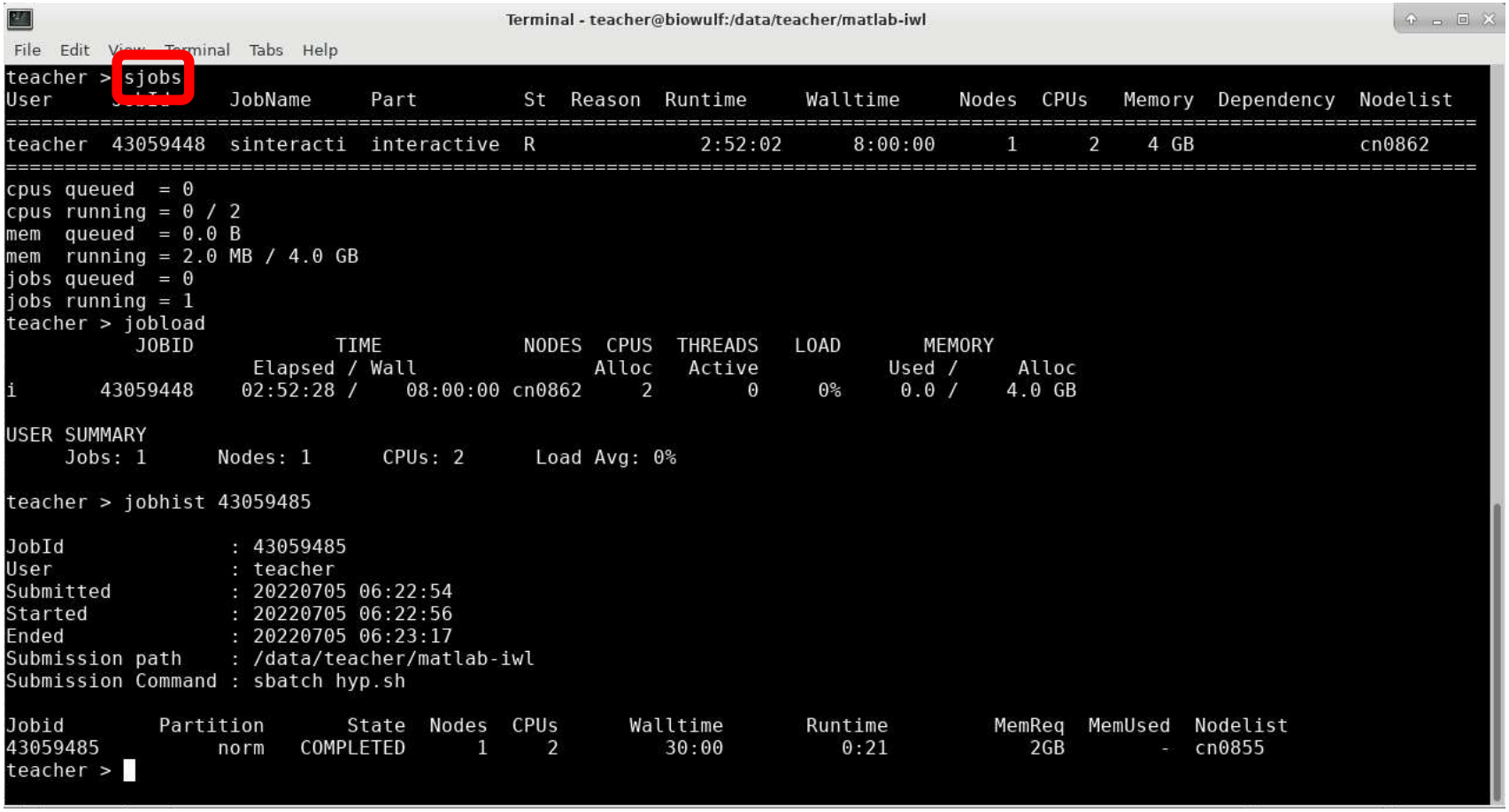

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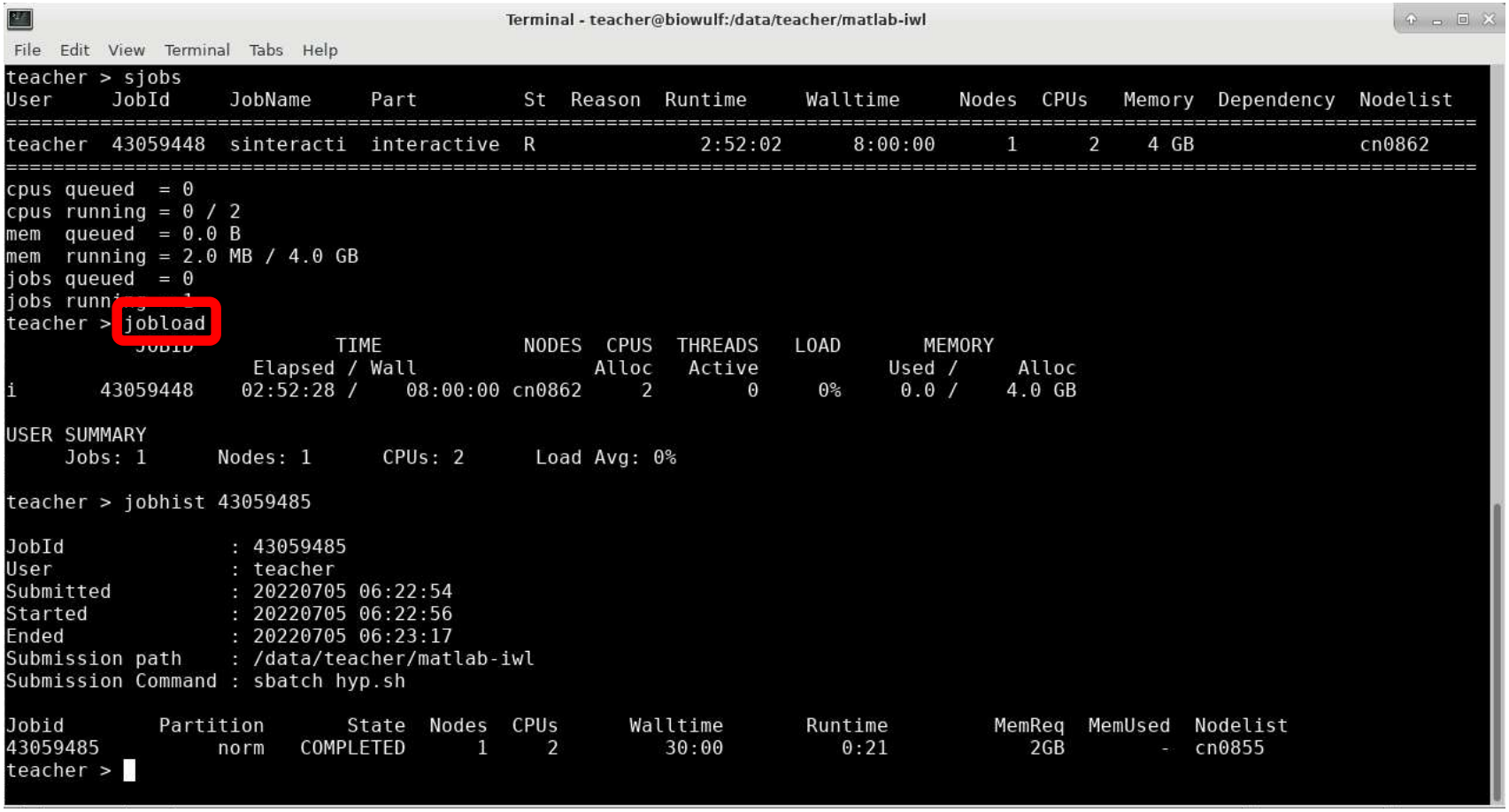

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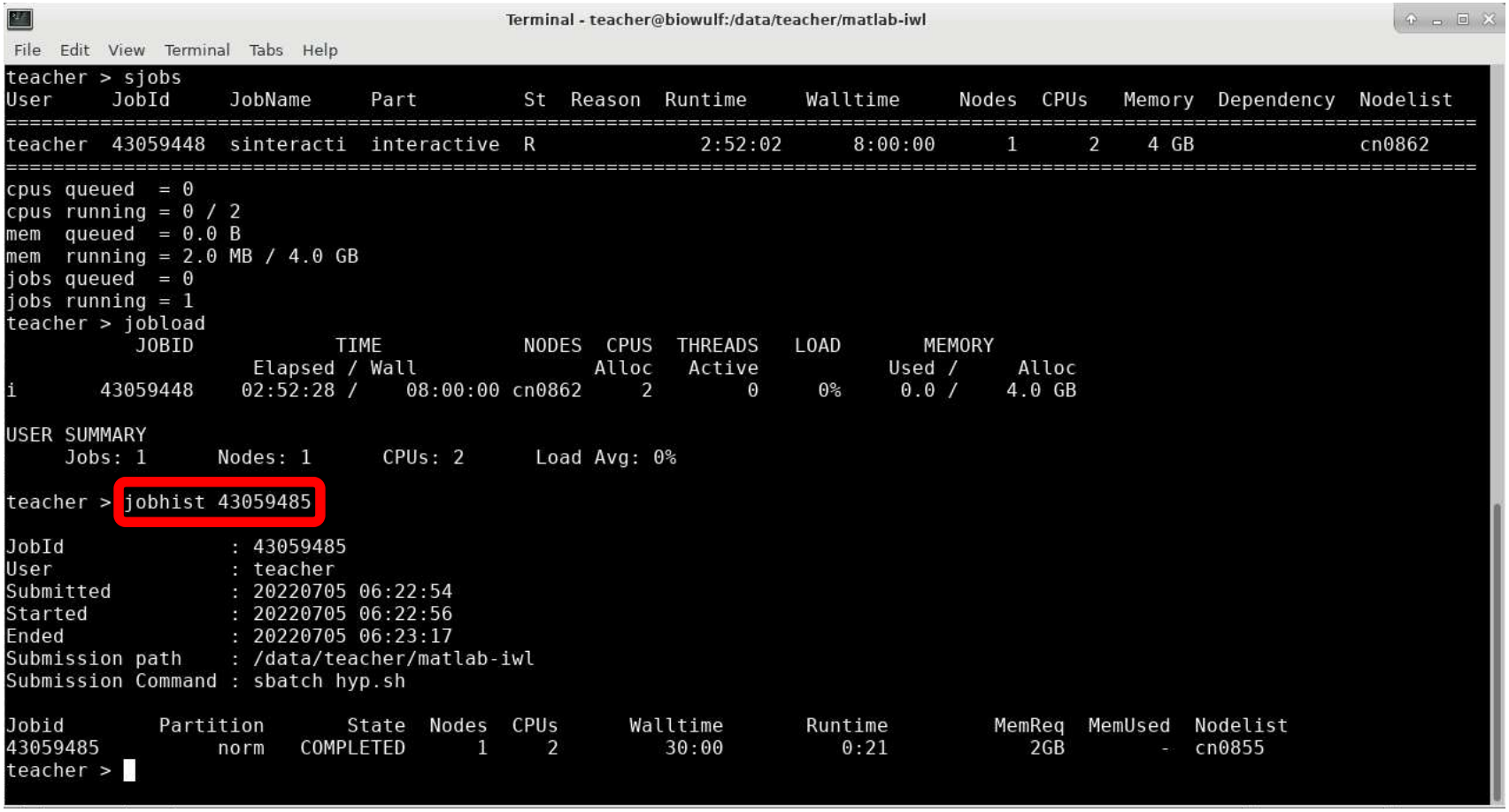

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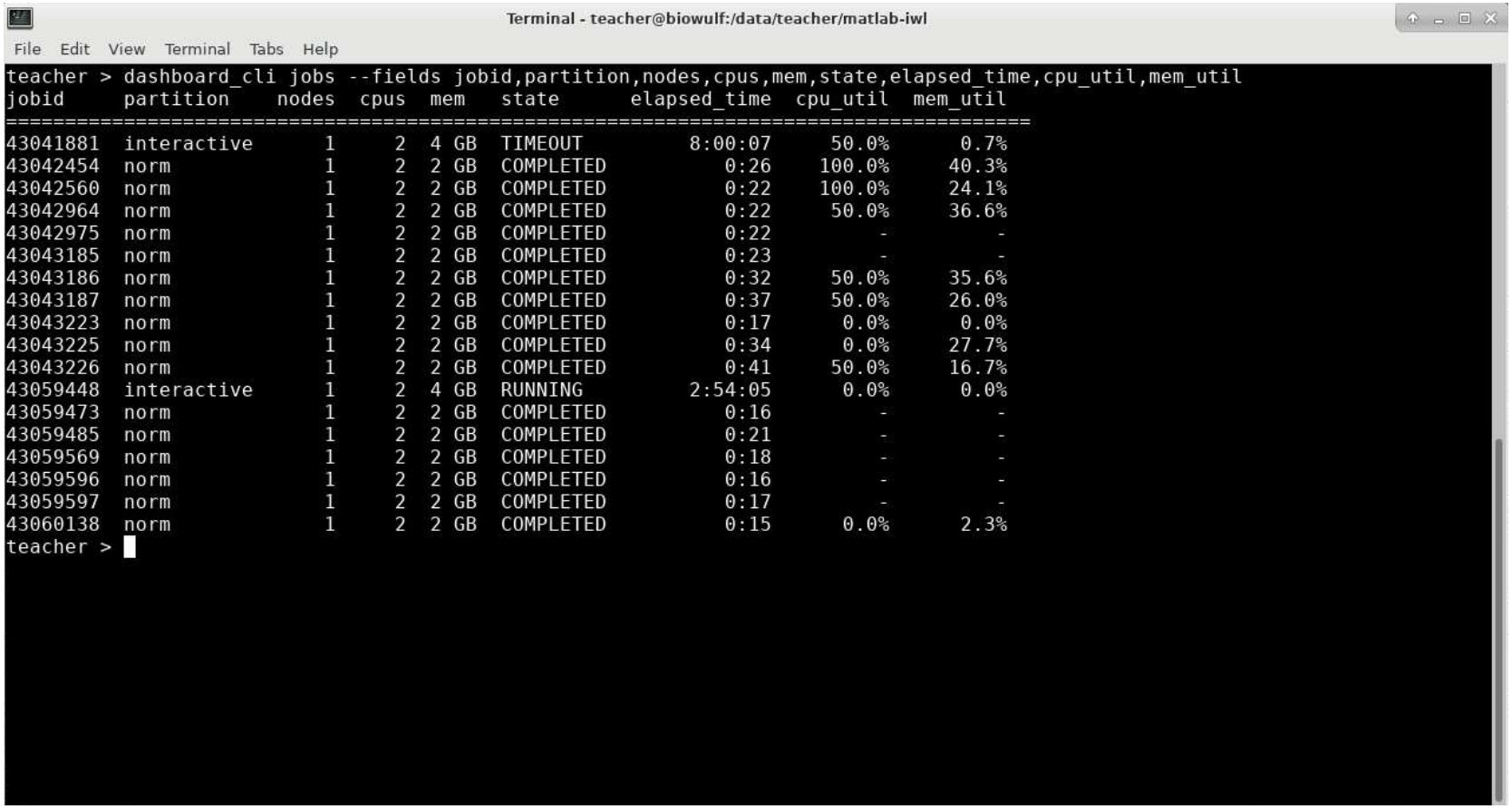

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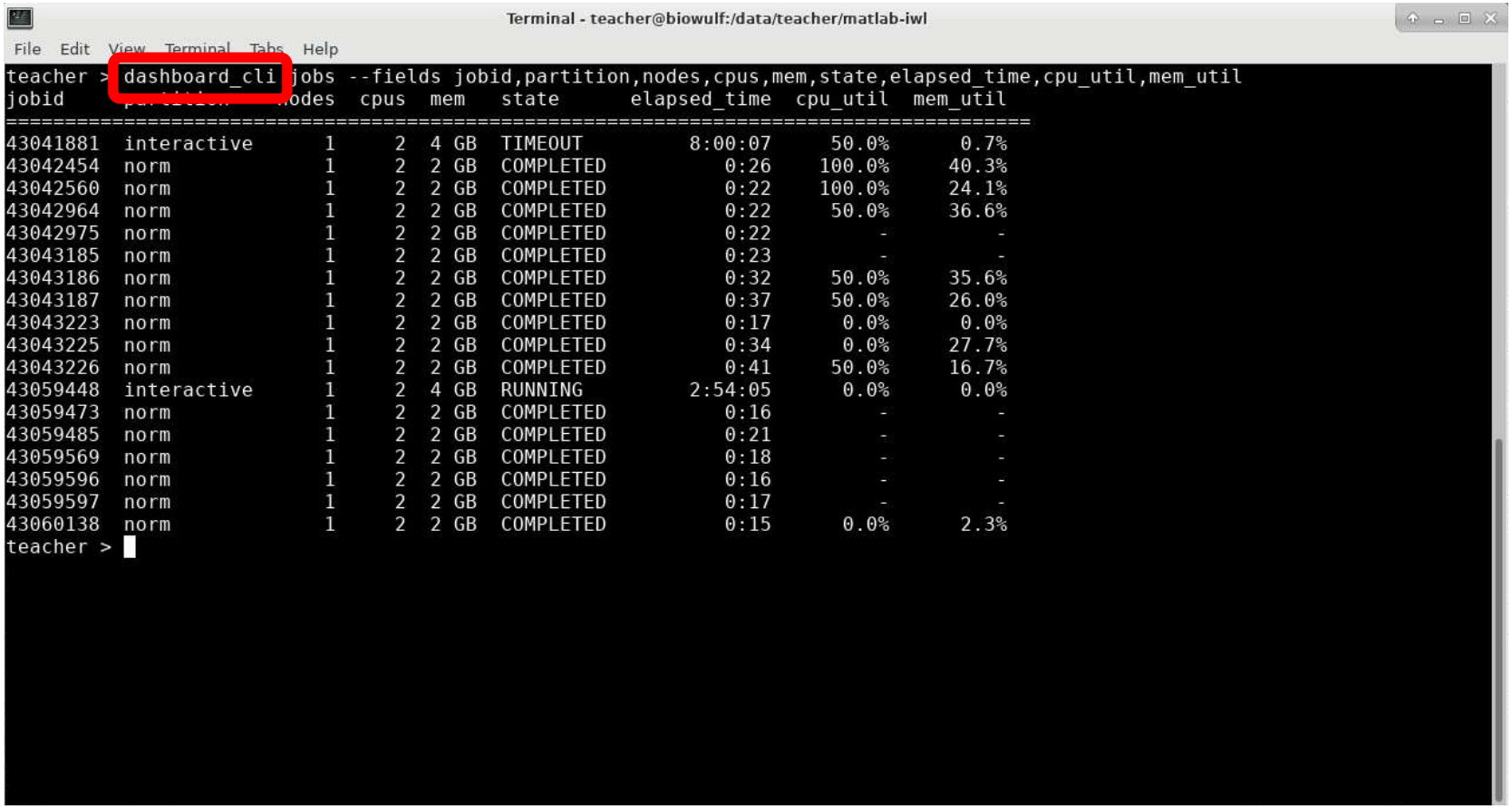

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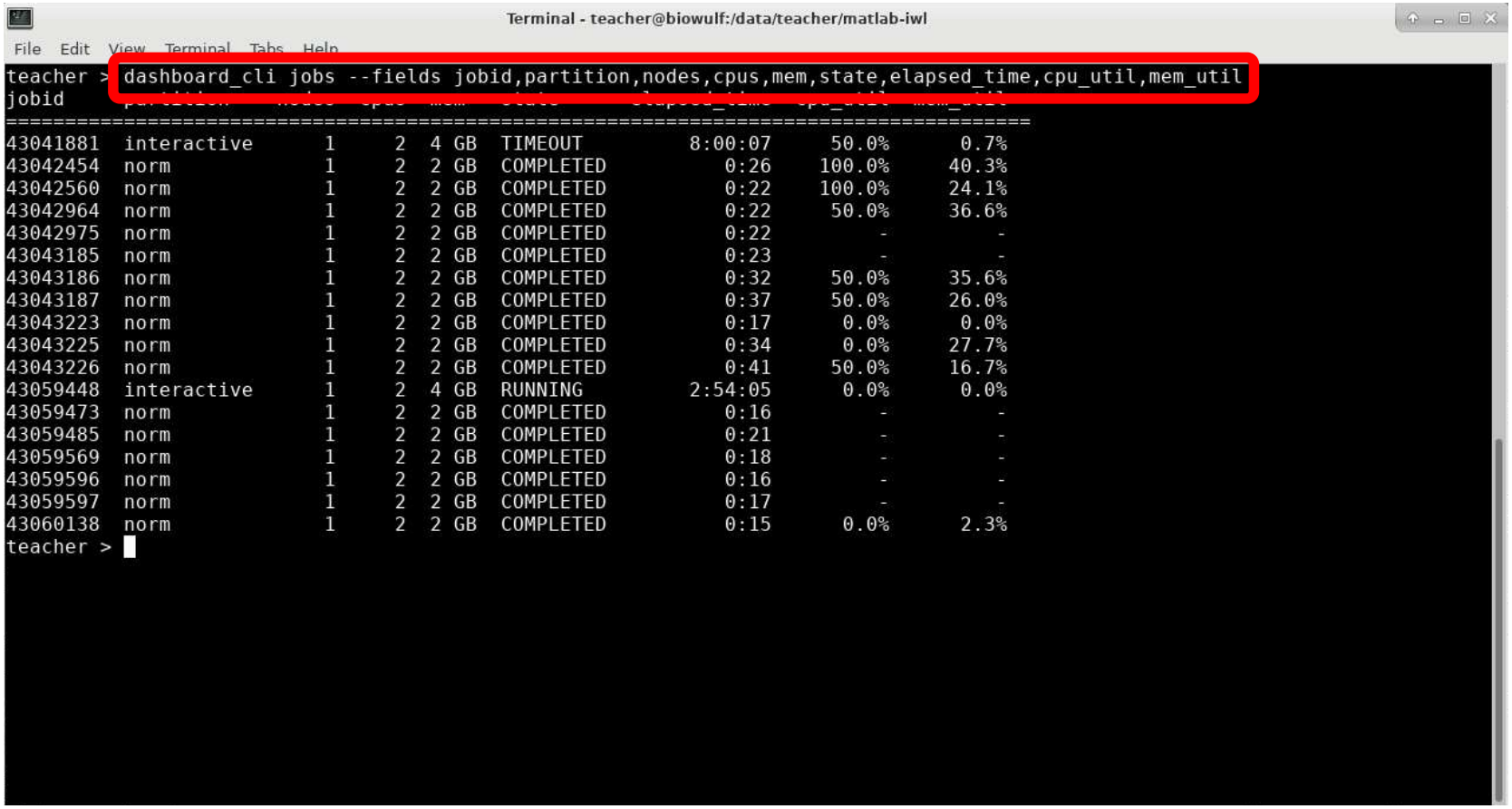

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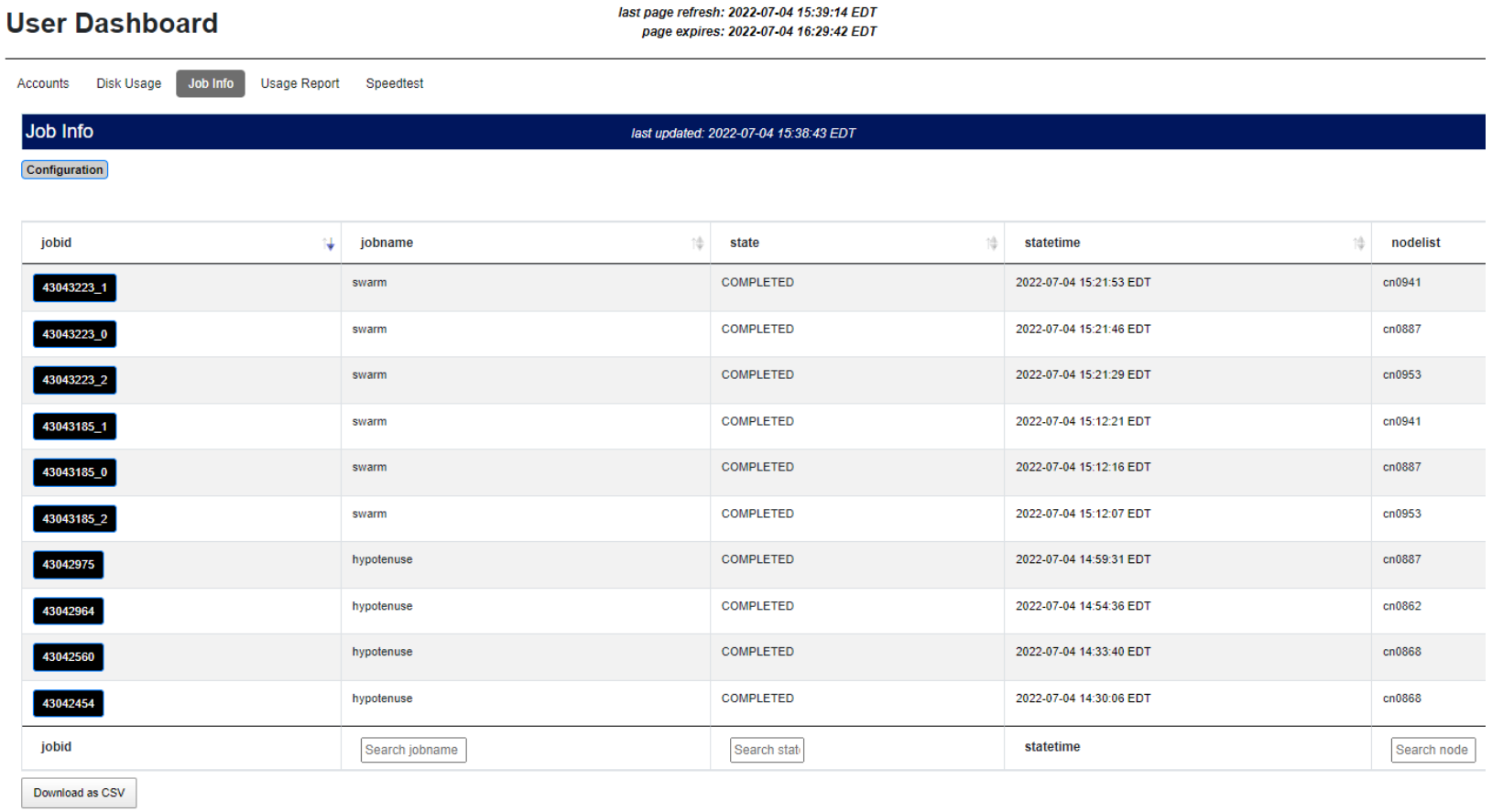

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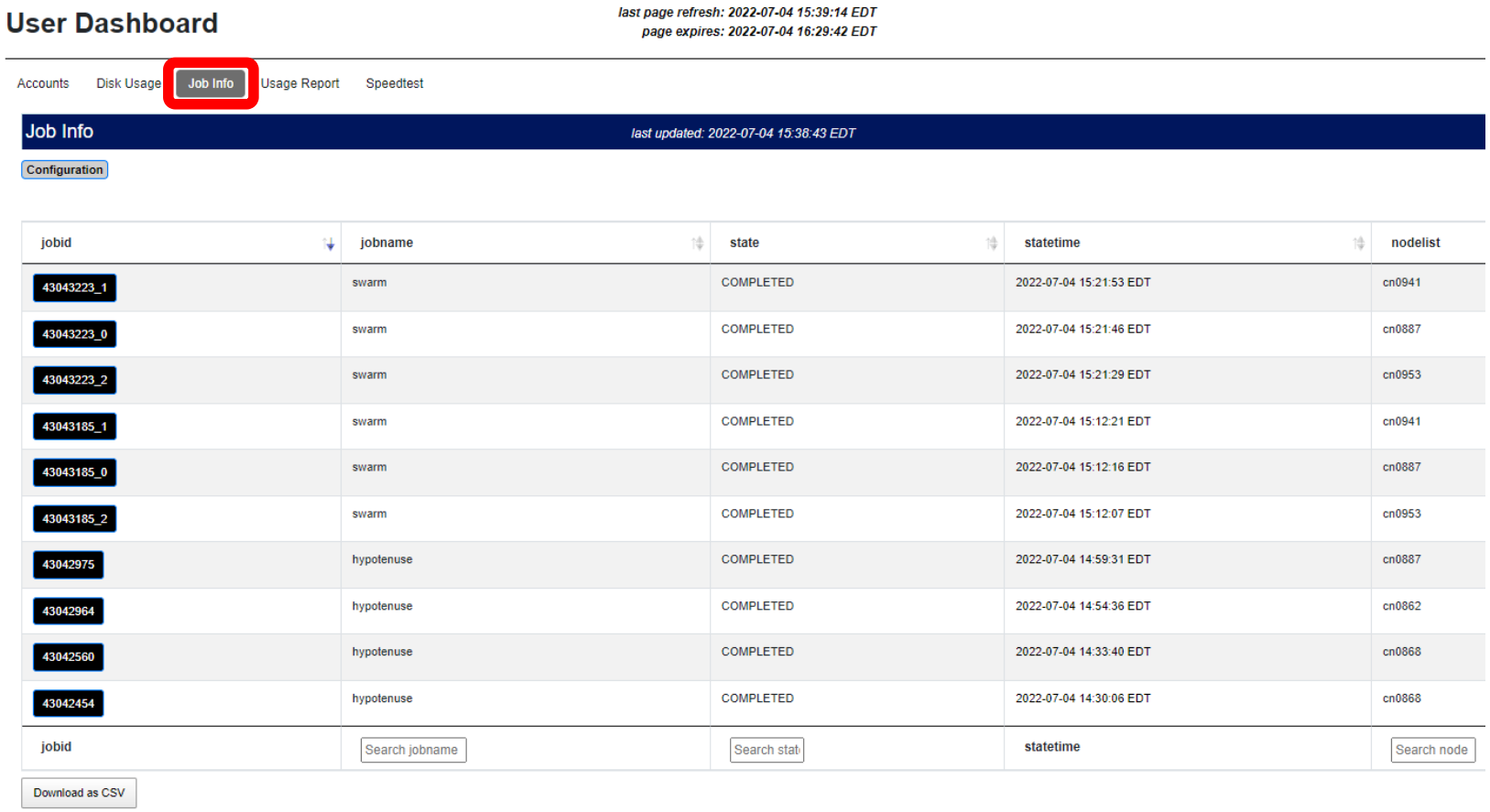

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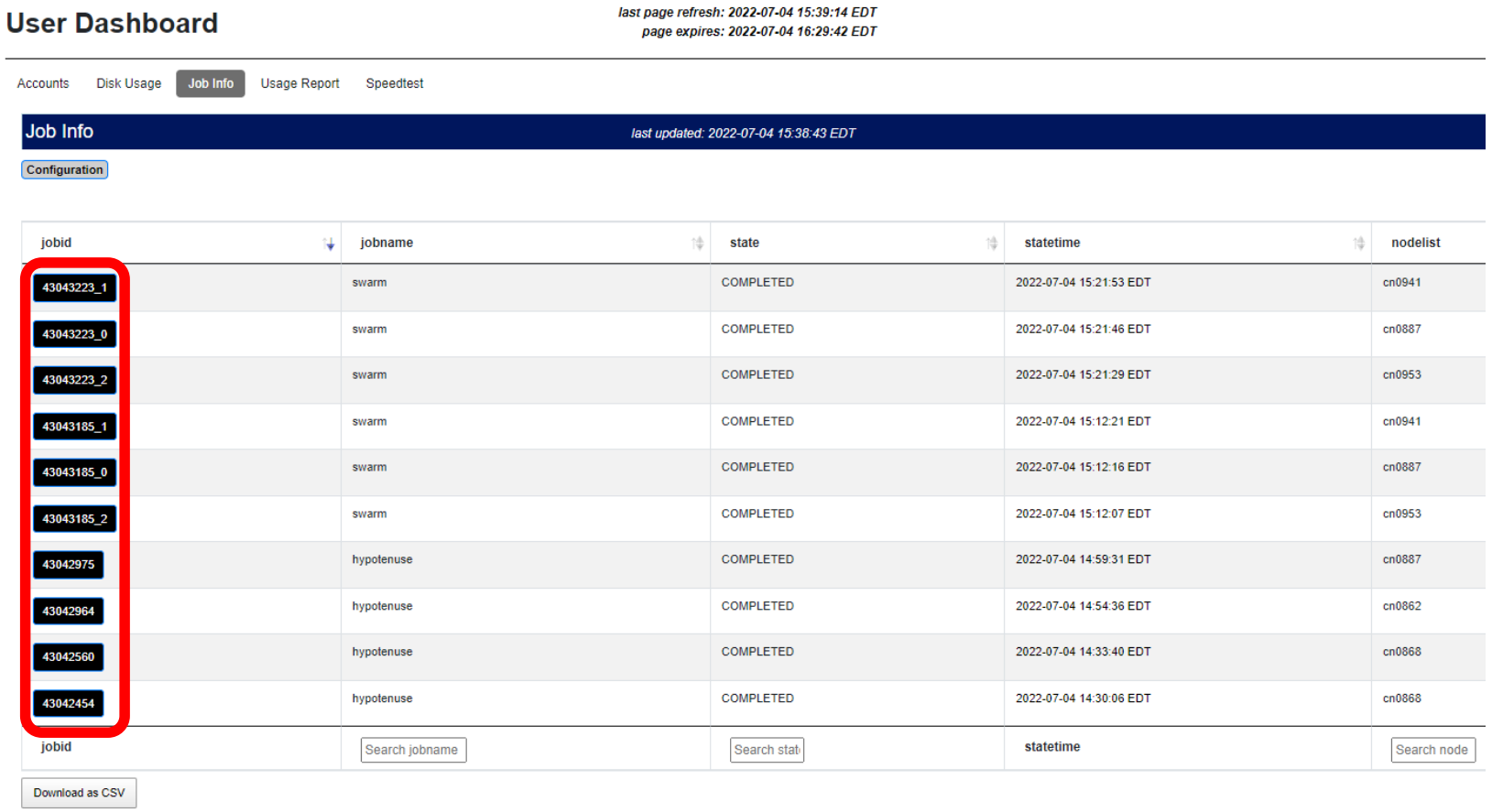

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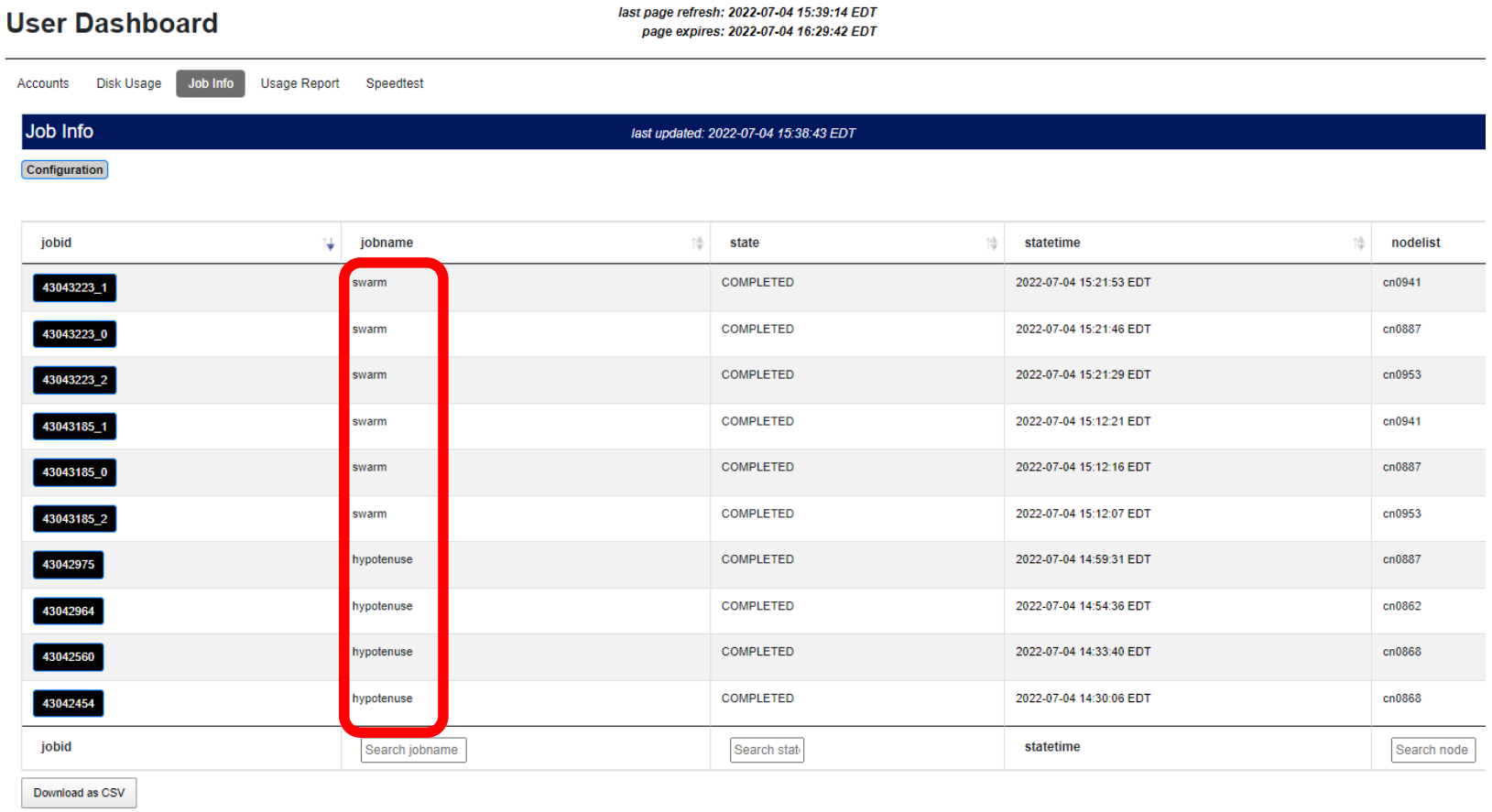

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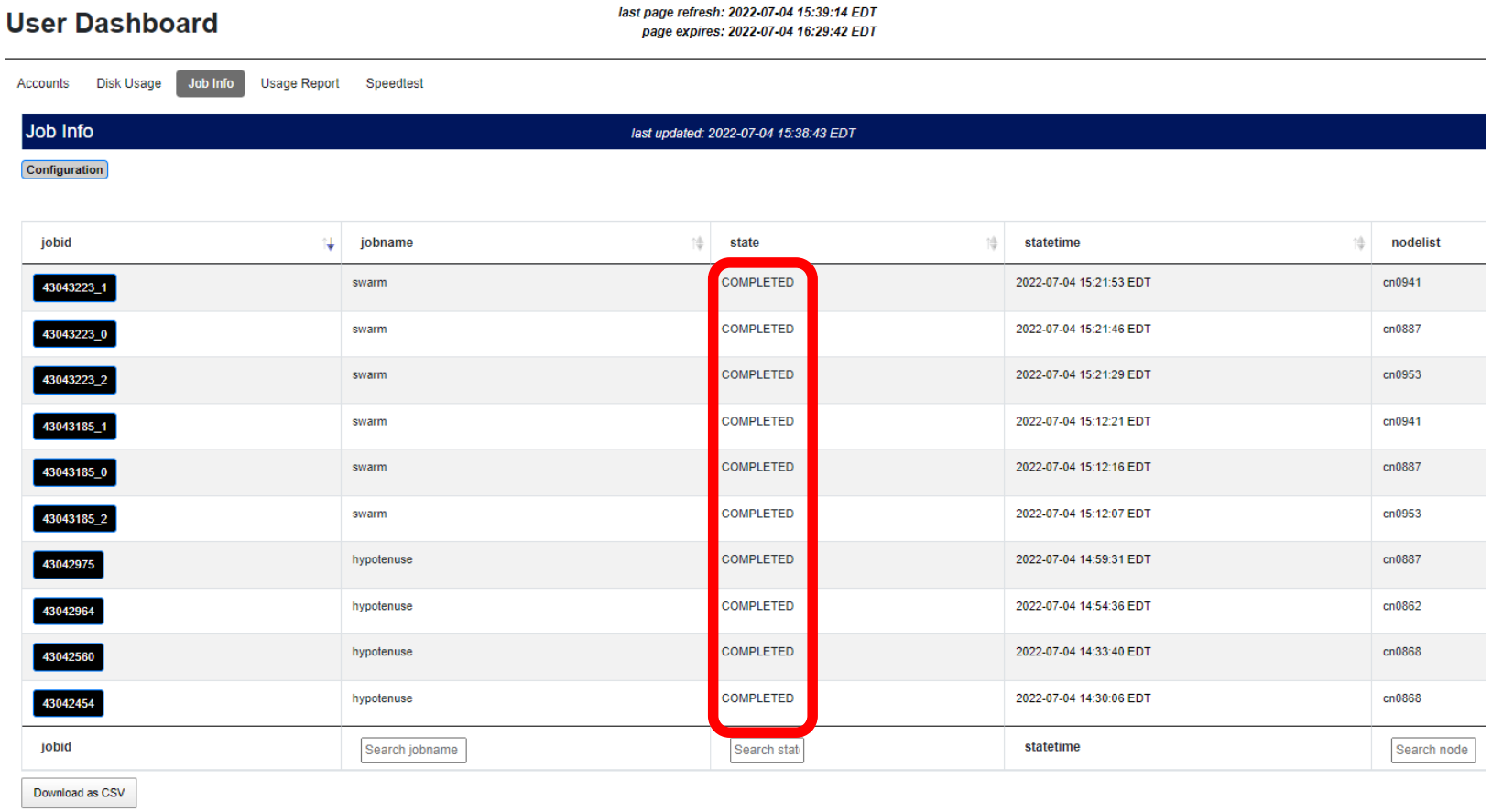

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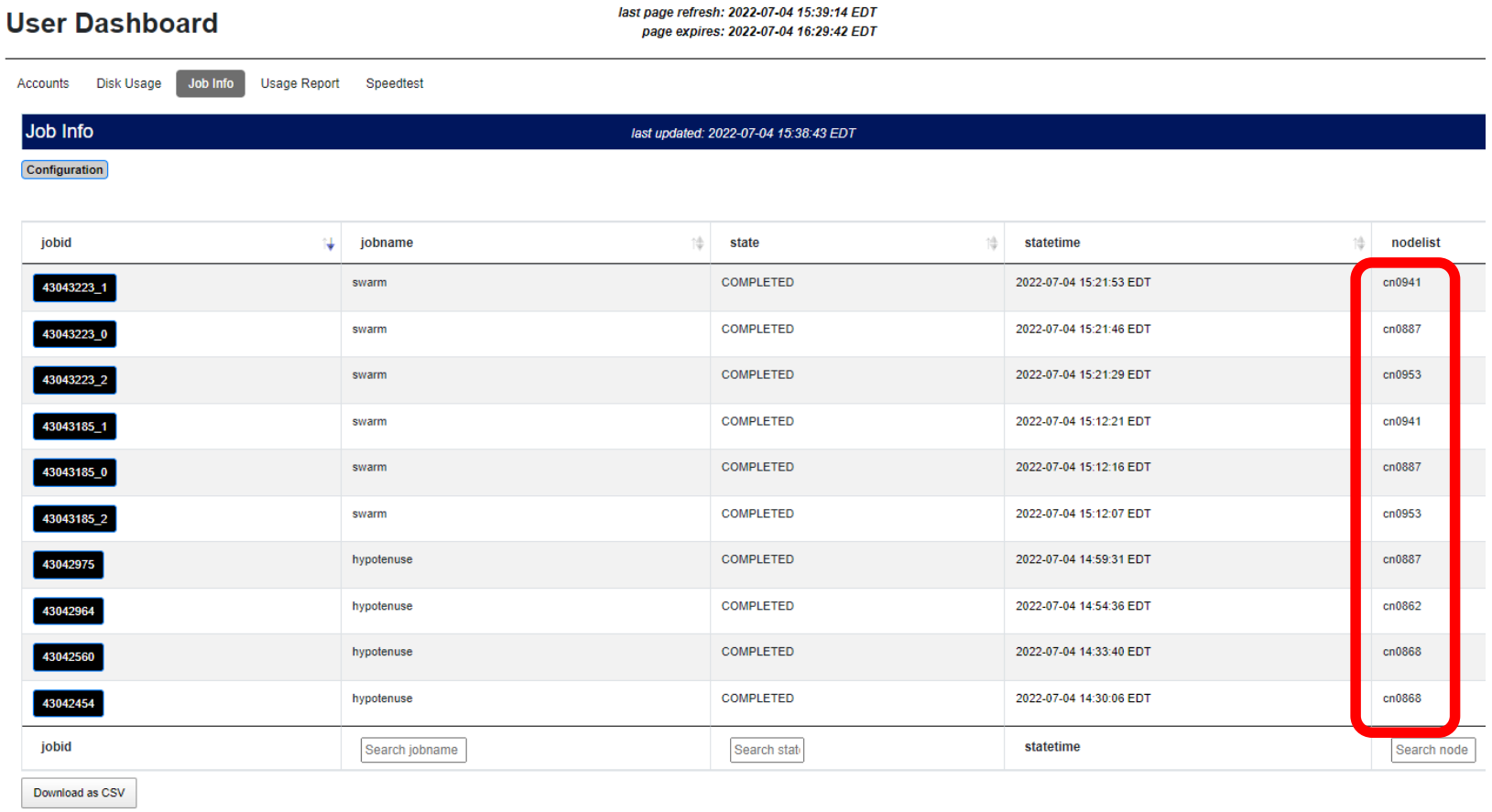

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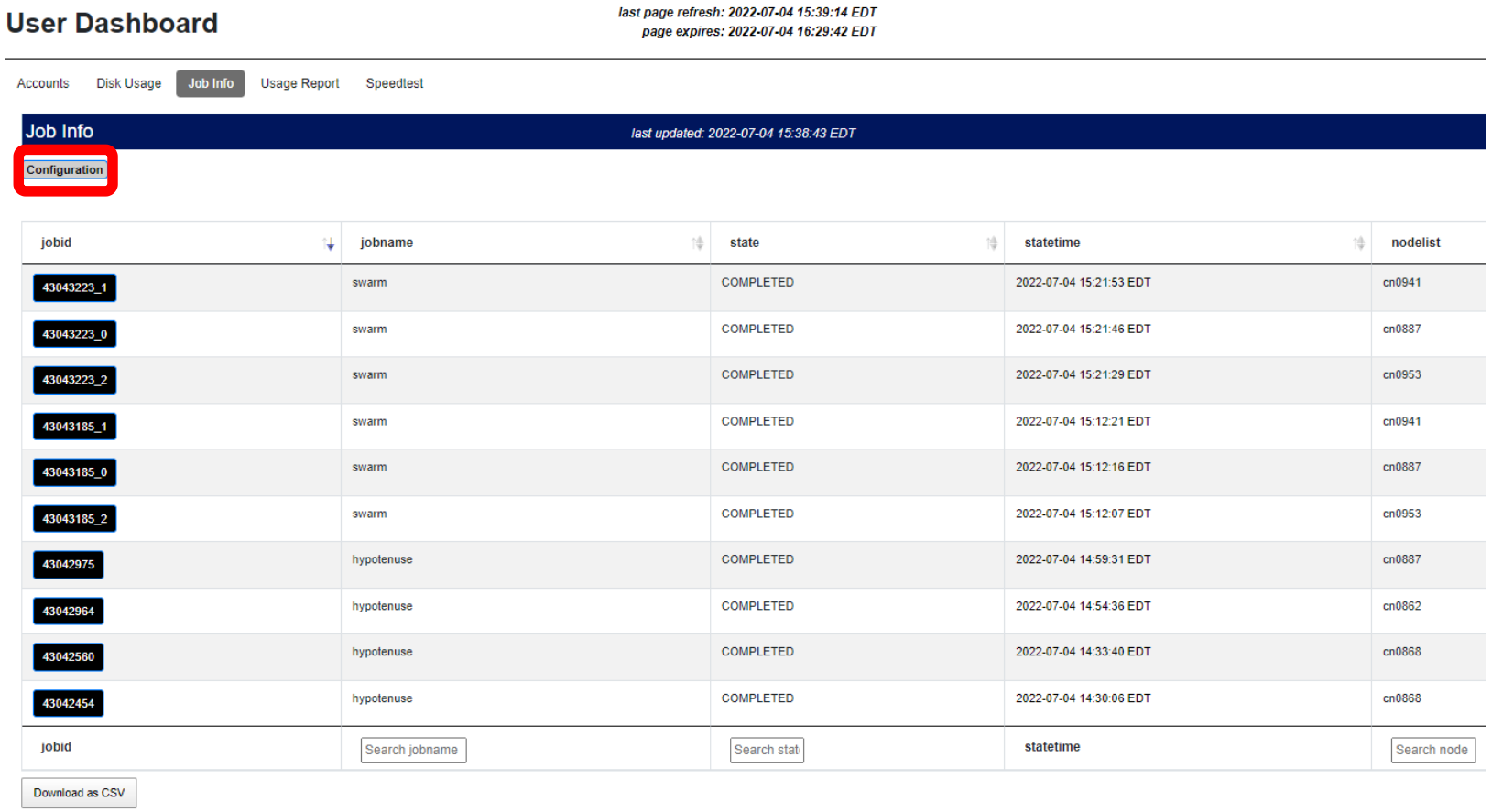

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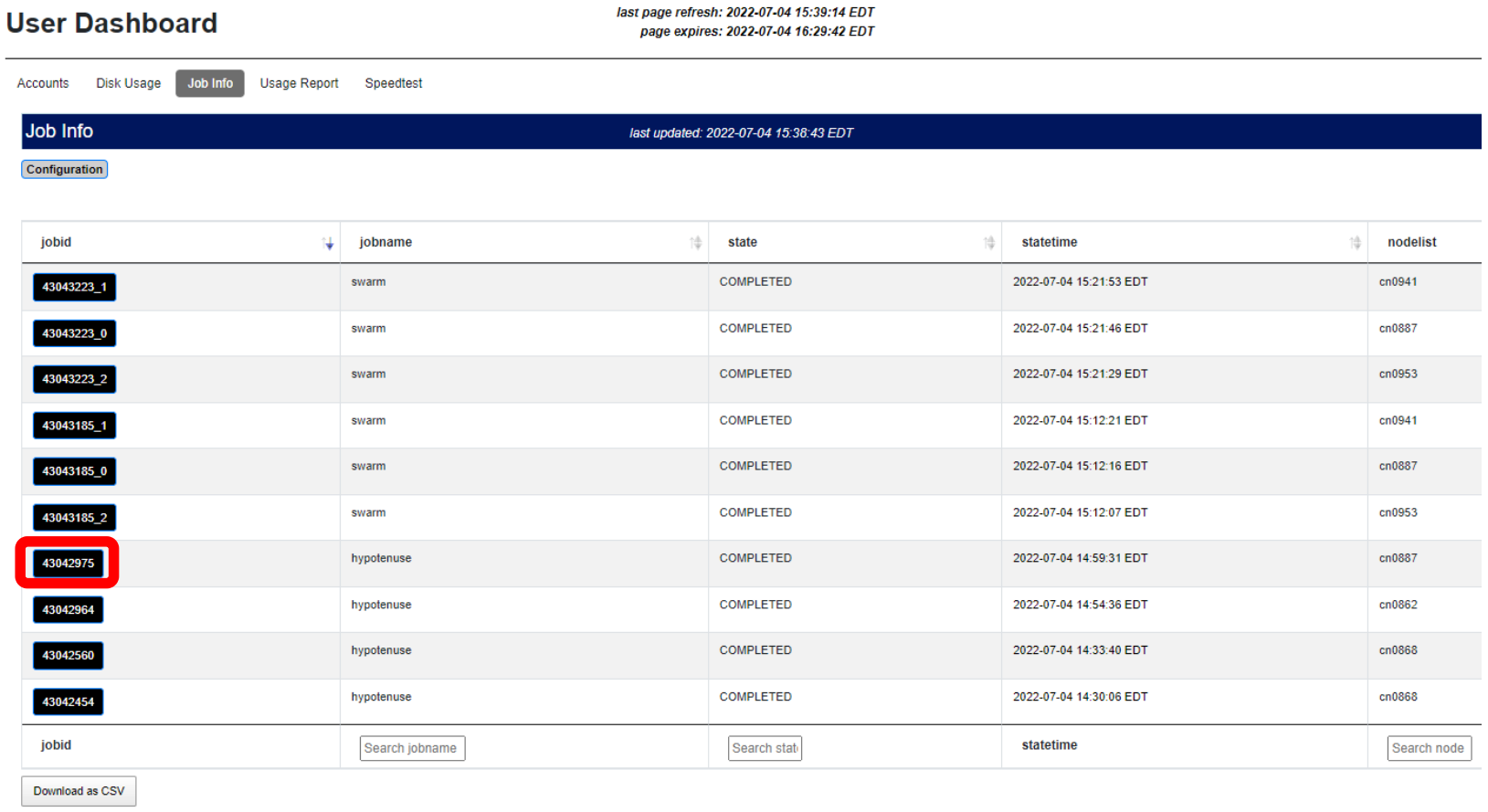

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- Try to run jobs with walltime > 15 minutes
- Read your NIH email in case Biowulf staff needs to contact you regarding your running jobs

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- Know how to run Matlab both in an interactive session and as a batch job
- Know how to avoid common pitfalls while running Matlab batch jobs

Biowulf staff


Steve Bailey


Susan Chacko, Ph.D.


Gennady Denisov, Ph.D.

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Afif Elghraoui


Ali Erfani


Andrew Fant, Ph.D.


Jonathan Goodson, Ph.D.


David Hoover, Ph.D.


Patsy Jones

Picture unavailable

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Tim Miller


Nitish Narula, M.S.


Charlene Osborn


David O'Brien


Mark Patkus


Wolfgang Resch, Ph.D.


Antonio Ulloa, Ph.D.


Qi Yu, Ph.D.

Source: hpc.nih.gov/about

Questions? Comments?

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