Script for Supercell thunderstorm demonstration

ATM419/563 Fall 2025

This demo runs the WRF idealized splitting supercell storm case

* ------------- setup [slide 3] -- *

* move to your lab space

```
$ lab
```

* make a directory in your lab space called SUPERCELL, and move into it

```
$ mkdir SUPERCELL
$ cd SUPERCELL
```

* copy this SETUP.TAR file to your SUPERCELL directory [the space and dot are important]

```
$ cp $LAB/SUPERCELL/SETUP.TAR .
```

* unpack the tar file.

```
$ tar -xvf SETUP.TAR
```

* this unpacks these files into your directory: make_all_links.sh, namelist.input, input_sounding, read_wrfinput.py, submit_wrf, plot_SUPERCELL.ipynb

* ------------- initialize and run [slide 11] --- *

* this script sets up the model environment

```
$ sh make_all_links.sh
```

* typing ‘trsl’ displays the contents of the file rsl.out.0000 as ideal.exe runs, or the tail of the file if execution has completed. Type CTRL-c to break out.

```
$ trsl
```

* inspect the model vertical coordinate. ‘dopython’ invokes a python install. The read_wrfinput.py script reads wrfinput_d01 and displays model coordinate. See slide 11

```
$ dopython
$ python read_wrfinput.py wrfinput_d01
```

* submit the WRF job to the derecho queue system

```
$ qsub submit_wrf
```

* check on your job

```
$ myjobs
```

* typing ‘trsl’ displays the contents of the file rsl.out.0000 as ideal.exe runs, or the tail of the file if execution has completed. Look for SUCCESS COMPLETE WRF.

Type CTRL-c to break out.

```
$ trsl
```

* ------------- visualize output [slide 34+] -- *

* from your web browser, go to this link:
https://jupyterhub.hpc.ucar.edu

- choose casper login and npl-2024b for the nodes and kernel.

* you may start in your home directory. If so,
  - click the LAB link
  - click on your SUPERCELL folder
  - launch plot_SUPERCELL.ipynb

- remember to go to File menu and select “Close and Shut Down” to finish demo. In addition, go to the NCAR menu and select “My Servers” and click “stop”.