

How to Create an R Kernel for Jupyter Lab

Course: DS 5100
Module: 11 R Programming II
Topc: R Kernel
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Motivation

You want to run R in a Jupyter notebook. This means having available an R kernel in the list of kernels you see in the Launcher window (in Jupyter Lab).

1. Create and activate an R environment with Conda

From the command line in Rivanna, create and activate an R environment.

First, create one with the essentials and base packages for R using this command:

```
conda create -n r_env r-essentials r-base
```

Then activate the environment with this command:

```
conda activate r_env
```

You are now in an environment that runs R.

2. Run the R shell

Now, run R from the command line like so:

```
R
```

3. Register the kernel

Once in the R interactive shell, register the kernel with the following commands:

```
install.packages("IRkernel") # Not really needed since included in r-essentials
IRkernel::installspec(name = 'r_env', displayname = 'R Environment')
quit()
```

4. Deactivate the environment

Once you are done with this, you can deactivate the environment like so:

```
conda deactivate
```

5. Run Jupyter Lab

Now start Jupyter Lab from the OpenOnDemand webpage.

If you already have a session running, close it down and restart it.

You should see a kernel tile like the following in the launcher window:



6. Going Forward

If everything worked, you can close down the command line terminal and work in Jupyter Lab.

Note that you can add more packages to your R environment by issuing the command from within the R environment:

```
conda install -c r <r-package>
```

<r-package> can be anything from the following list:

- <https://repo.anaconda.com/pkg/r/>

Or, if you are not in the R environment, you can specify the target environment with the argument `-n`:

```
conda install -n r_env -c r <r-package>
```