

CARE Lab - Environment Setup

Learning Objectives

- ❑ How to set up CARE to be used within a conda environment on LINUX.
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Preamble: We assume conda is installed (if not, we suggest to install and use 'miniconda' because it comes with all you need). Then follow the instructions below to set up the environment we'll need for this lab.

Step-by-step Installation Instructions

1. Open a browser, navigate to <http://csbdeep.bioimagecomputing.com>
 - This is the main page of CSBDeep, a collection of open software tools, currently mostly CARE. Click on the python logo, this will bring you to the GitHub repo we need to clone.
2. Clone the GIT repo.
 - Open a terminal.
 - Go to a folder of your choice.
 - Clone the repo within the folder you chose by executing:
`$ git clone https://github.com/CSBDeep/CSBDeep.git`
 - A new folder `<some_folder>/CSBDeep` should now exist.
3. Create a new conda environment for CARE.
 - In the terminal, execute
`$ conda create --name care python=3.5`
 - Then activate the newly created environment via
`$ conda activate care`
4. Install required dependencies.
 - Be sure you activated the conda environment 'care' (see above).
 - `$ conda install tensorflow-gpu keras jupyter`
This will install a bunch of dependencies, like cuDNN, which are otherwise a pain to be installed. But note: despite being convenient, it does not allow you to pick any version of those libraries you might want or need. Still, for CARE the default versions conda will install are just fine!
 - `$ pip install csbdeep`
This installs a bunch of dependencies and convenience methods we will later learn to use (in parts at least). The reason for us to provide this extra layer is to enable non-expert users to use CARE as well.