Lab09 Appendix: Pillow installation instructions

Some versions of Anaconda appear to come with the Pillow package already operational, and others do not. To check whether Pillow is operational, open a new console in Spyder and at the Python prompt enter (with exactly the same upper and lower case letters):

```python
from PIL import Image
```

If this command generates no output, then Pillow is available. If Python generates an error of the form `ImportError: No module named 'PIL'` then Pillow is not available and you must install it following the procedure described below. This procedure is the same as when you installed Biopython in Lab 07.

To install non-default packages into Anaconda, we use the `conda` command. Note that the `conda` command is not part of Python – you must run it from a command prompt. The details of starting a command prompt depend on your operating system:

- In Windows, run the "Anaconda command prompt" (use the search feature to find this program). It should start in your Anaconda directory.
- In MacOS, start a "Terminal" and go to your Anaconda directory.
- In Linux, start a shell and go to your Anaconda directory.

Once you have a command prompt and are in your Anaconda directory, you should be able to type `conda install pillow`, press enter, and then accept the default choices from that point forward. You must have an Internet connection for this to work, since `conda` needs to download the Pillow package (and possibly some other packages which it wants to update). Assuming that the `conda` command completes successfully, when you restart Spyder you should be able to repeat the import command given above without error.

For your future reference, there is a full list of the packages integrated with Anaconda ([https://docs.continuum.io/anaconda/pkg-docs#python-3-4](https://docs.continuum.io/anaconda/pkg-docs#python-3-4)). Those that are included by default are labelled as "True" in the final column "In Installer"; you should be able to import any of the modules within those packages without any further effort. Those packages that are not included by default (such as Biopython) can be installed using the `conda` command as described above.