

# Downloading data for 10 (or 40) unrelated subjects

Here's a complete [Python](#) script for downloading the R-fMRI, structural, and diffusion packages for a predefined set of subjects. Note that you will need to [install the HCP-customized version of pyxnat](#) to run this.

The script takes two optional command-line arguments:

```
python download-hcp-packages.py [username] [password]
```

If you omit the password or both the username and the password, the script will prompt you to enter them.

As written, the script downloads packages for the 10 unrelated subjects, but it can be modified to download the 40 unrelated subjects instead by substituting `unrelated_40` for `unrelated_10` in line 61. The package selection can similarly be changed by modifying the second argument to the download request in line 61; consult the full [ConnectomeDB-Python tutorial](#) for details.

**download-hcp-packages.py**

```

#!/usr/bin/python
# Download R-fMRI, structural, and diffusion for 10 unrelated subjects
# Requires HCP-customized pyxnat:
#   https://github.com/Human-Connectome-Project/pyxnat/tree/hcp-db
#
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#
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# POSSIBILITY OF SUCH DAMAGE.

import sys, getpass
import pyxnat

one_subject = ['100307']
unrelated_10 = ['100307', '103414', '105115', '110411', '111312',
               '113619', '115320', '117122', '118730', '118932']
unrelated_40 = ['100307', '103414', '105115', '110411', '111312',
               '113619', '115320', '117122', '118730', '118932',
               '123117', '124422', '125525', '128632', '129028',
               '130013', '133928', '135932', '136833', '139637',
               '149337', '149539', '151223', '151627', '156637',
               '161731', '192540', '201111', '209733', '212318',
               '214423', '221319', '298051', '397760', '414229',
               '499566', '528446', '654754', '672756', '792564']

structural = ['3T_Structural_preproc']
diffusion = ['3T_Diffusion_preproc']
r_fmri = ['3T_rfMRI_REST1_preproc', '3T_rfMRI_REST2_preproc']

def main():
    user = sys.argv[1] if 2 <= len(sys.argv) else raw_input('ConnectomeDB user: ')
    password = sys.argv[2] if 3 <= len(sys.argv) else getpass.getpass()

    cdb = pyxnat.Interface('https://db.humanconnectome.org', user, password)

    cdb.packages.download(unrelated_10, structural + diffusion + r_fmri)

if __name__ == '__main__':
    main()

```