

Rxnat - Download full subject data

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Download a full set of data for a specific subject from the NITRC XNAT repository

The following tutorial will provide a fully functional example on how to download a full set of images for a specific subject, using the Rxnat package functionality.

Install the Rxnat package

You can install Rxnat from Neuroconductor with:

```
source("https://neuroconductor.org/neurocLite.R")
neuro_install('Rxnat')
```

Setting up system environment variables

To use system environment variables we need to add them to the `.Renviron` file located in the user's home folder. Use `Sys.getenv("HOME")` to get the path (for unix/osx users the location can be easily accessed with `~`, eg. `vi ~/.Renviron`). The Rxnat package will be able to automatically read / use a system environment variable provided the following format is used: `XXXX_RXNAT_USER` and `XXXX_RXNAT_PASS`. `XXXX` is provided as an argument when an XNAT connection is initiated.

As an example NITRC is used as argument and the system environment variables names should be `NITRC_RXNAT_USER`, and `NITRC_RXNAT_PASS`.

```
library(Rxnat)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

nitrc <- xnat_connect('https://nitrc.org/ir', xnat_name='NITRC')

## NITRC_RXNAT_USER is being used for user
## NITRC_RXNAT_PASS is being used for password
```

Retrieve list of subjects

To retrieve the full list of subjects for the `nitrc` XNAT connection, we will use the `nitrc$subjects()` function.

```
nitrc_subjects <- nitrc$subjects()
head(nitrc_subjects)

## # A tibble: 6 x 11
##   project ID    label gender handedness yob  education ses  group race
##   <chr>   <chr> <chr> <chr>   <chr>   <lg1> <lg1>   <lg1> <chr> <chr>
## 1 ABIDE  NITR~ Calt~ M      R      NA    NA      NA    Auti~ ""
## 2 ABIDE  NITR~ Calt~ M      A      NA    NA      NA    Auti~ ""
## 3 ABIDE  NITR~ Calt~ M      R      NA    NA      NA    Auti~ ""
## 4 ABIDE  NITR~ Calt~ M      R      NA    NA      NA    Auti~ ""
## 5 ABIDE  NITR~ Calt~ F      A      NA    NA      NA    Auti~ ""
## 6 ABIDE  NITR~ Calt~ M      R      NA    NA      NA    Auti~ ""
## # ... with 1 more variable: ethnicity <chr>
```

Retrieve list of experiments

To retrieve the full list of experiments for the `nitrc` XNAT connection, we will use the `nitrc$experiments()` function.

```
nitrc_experiments <- nitrc$experiments()
head(nitrc_experiments)

## # A tibble: 6 x 6
##   project subject      ID          type          label          age
##   <chr>   <chr>      <chr>      <chr>      <chr>      <int>
## 1 ABIDE  Caltech_51456 NITRC_IR_E00990 xnat:mrSessionData Caltech_51456 55
## 2 ABIDE  Caltech_51457 NITRC_IR_E00991 xnat:mrSessionData Caltech_51457 22
## 3 ABIDE  Caltech_51458 NITRC_IR_E00992 xnat:mrSessionData Caltech_51458 39
## 4 ABIDE  Caltech_51459 NITRC_IR_E00993 xnat:mrSessionData Caltech_51459 22
## 5 ABIDE  Caltech_51460 NITRC_IR_E00994 xnat:mrSessionData Caltech_51460 34
## 6 ABIDE  Caltech_51461 NITRC_IR_E00995 xnat:mrSessionData Caltech_51461 37
```

Get list of all experiments associated with a subject

For the purpose of this example, we would like to identify a subject that has more than one experiments associated with his id. In order to figure out a good subject ID example, we will filter and select all subjects with more than 1 experiment associated.

```
multi_session = nitrc_experiments %>%
  group_by(subject) %>%
  mutate(n_sessions = n()) %>%
  filter(n_sessions > 1)
head(multi_session)

## # A tibble: 6 x 7
## # Groups:   subject [6]
##   project subject      ID          type          label          age n_sessions
##   <chr>   <chr>      <chr>      <chr>      <chr>      <int>     <int>
## 1 ABIDE  UCLA_51209 NITRC_IR_E01699 xnat:mrSessionD~ UCLA_512~         9         4
## 2 ABIDE  UCLA_51215 NITRC_IR_E01705 xnat:mrSessionD~ UCLA_512~        11         5
```

```
## 3 ABIDE    UCLA_51231 NITRC_IR_E01721 xnat:mrSessionD~ UCLA_512~    10      5
## 4 ABIDE    UCLA_51234 NITRC_IR_E01724 xnat:mrSessionD~ UCLA_512~    10      4
## 5 ABIDE    UCLA_51235 NITRC_IR_E01725 xnat:mrSessionD~ UCLA_512~    10      4
## 6 ABIDE    UCLA_51236 NITRC_IR_E01726 xnat:mrSessionD~ UCLA_512~    12      4
```

We will select the first subject ID (UCLA_51209) to continue our example.

```
subject_id <- "UCLA_51209"
subject_experiments = nitrc_experiments[ nitrc_experiments$subject %in% subject_id, ]
head(subject_experiments)
```

```
## # A tibble: 4 x 6
##   project subject    ID          type          label          age
##   <chr>    <chr>    <chr>        <chr>        <chr>        <int>
## 1 ABIDE    UCLA_51209 NITRC_IR_E01~ xnat:mrSessionD~ UCLA_51209          9
## 2 ABIDE_II UCLA_51209 XNAT_E14819  xnat:mrSessionD~ UCLA_51209_baseline_~ 10
## 3 ABIDE_II UCLA_51209 XNAT_E14820  xnat:mrSessionD~ UCLA_51209_baseline_~  9
## 4 ABIDE_II UCLA_51209 XNAT_E14821  xnat:mrSessionD~ UCLA_51209_followup   13
```

Download all resources

We will use the `download_dir()` function to download of all resources associated with the selected subject ID.

```
download_data = lapply(subject_experiments$ID, function(r) {
  nitrc$download_dir(experiment_ID = r, extract = TRUE)
})
```

```
## https://nitrc.org/ir/data/experiments/NITRC_IR_E01699/scans/ALL/files?format=zip
## /var/folders/wb/l7jtkdy14f761vm4xr9zxjj80000gn/T//RtmpS3zg49/NITRC_IR_E01699.zip
## https://nitrc.org/ir/data/experiments/XNAT_E14819/scans/ALL/files?format=zip
## /var/folders/wb/l7jtkdy14f761vm4xr9zxjj80000gn/T//RtmpS3zg49/XNAT_E14819.zip
## https://nitrc.org/ir/data/experiments/XNAT_E14820/scans/ALL/files?format=zip
## /var/folders/wb/l7jtkdy14f761vm4xr9zxjj80000gn/T//RtmpS3zg49/XNAT_E14820.zip
## https://nitrc.org/ir/data/experiments/XNAT_E14821/scans/ALL/files?format=zip
## /var/folders/wb/l7jtkdy14f761vm4xr9zxjj80000gn/T//RtmpS3zg49/XNAT_E14821.zip
```