

Using the R package

An explanation about how to install and use the R package can be found here: [R](#)

In this document we will create an example tutorial to learn how to work with the R client.

```
# Load the R package
library(opencgaR)

# We need to define the host where OpenCGA is installed.
# Users following this tutorial will need to change the host variable to point to their own installation.
con <- initOpencgaR(host = "localhost:8080/opencga/", version = "v1")

# 'con' will be an instance of our OpencgaR class and will need to be passed to any method

# And login passing the main configuration and defining our user credentials
con <- opencgaLogin(opencga = con, userid = "user", passwd = "userPassword")

# First, we will look for the first 10 families containing a particular disorder
families <- familyClient(con, family = NULL, action="search", params=list(study="RD38", limit=10, disorders="
Rod-cone dystrophy", include="id,members.id"))

# families will be a data frame containing all the Family fields we have included
# To see the family ids we will need to
families$id

# To see the list of members of the families for each family, we will need to run something like
for (i in c(1:10)) {
  print (families$id[i])
  print (families$members[[i]]$id)
}

# Next, we will fetch the first 10 variant ids associated to the previous families falling in the 'BMP2' gene
# To do so, we will first create a function to fetch those variants given a familyId
getVariants <- function(familyId, con) {
  variants <- analysisVariantClient(con, action="query", params=list(study="RD38",gene="BMP2",
family=familyId,includeSamples="None",limit=10))
  return (variants$id)
}

# And now, we can get those results by running the following line:
variants <- sapply(families$id, getVariants, con=con)
# This way, we will get a list of familyId -> list of 10 associated variant ids
```