

R for cytometry - cytobank

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Download data from cytobank

```
# load CRAN package
require(CytobankAPI)
# Authenticate via authentication token
cyto_session <- authenticate(site="cellmass",
                             auth_token="xxx")

# specify experiment id
experiment_id <- 12
# specify data directory
data_dir <- "fcs_from_cytobank/"
dir.create(data_dir, recursive = TRUE)
# list fcs files
files <- fcs_files.list(cyto_session,
                        experiment_id = experiment_id)
```

Download data from cytobank

```
# download fcs files
downloaded_zip <- fcs_files.download_zip(
  UserSession = cyto_session,
  experiment_id = experiment_id,
  fcs_files = files[, "id"],
  directory = data_dir,
  timeout = 60*nrow(files))
unzip(downloaded_zip, exdir = data_dir)
```

Change data

```
require(flowCore)
# read fcs file
ff <- read.FCS(paste0(data_dir, file_name))
ff_new <- ff
ff_new@exprs <- cbind(
  ff@exprs,
  cluster = rbinom(nrow(ff@exprs), size = 1, prob = 0.5))
ff_new@parameters@data <- rbind(
  ff@parameters@data,
  data.frame(
    name = "cluster",
    desc = "random_cluster", range = 1,
    minRange = 0, maxRange = 1,
    row.names =
      paste0("$P", nrow(ff@parameters@data) + 1)))
```

A look at the changed data

```
# measured intensities  
dim(ff@exprs)  
dim(ff_new@exprs)  
  
# annotation  
tail(pData(ff@parameters))  
tail(pData(ff_new@parameters))
```

Writing FCS file

```
# write file  
new_file_name <- gsub(".fcs", "_new.fcs", file_name)  
write.FCS(ff_new,  
          filename = paste0(data_dir, new_file_name))
```

```
## [1] "fcs_from_cytobank/Marrow1_01_Basal1_new.fcs"
```

```
# zip output files  
zip_filename <- paste0(data_dir, "clustered_data.zip")  
zip(zip_filename, paste0(data_dir, new_file_name))
```

Uploading files to cytobank

```
# create new experiment
```

```
new_experiment_name <- "test_upload"
```

```
new_experiment <- experiments.new(  
  cyto_session,  
  experiment_name = new_experiment_name,  
  purpose = "testing")
```

```
# upload files
```

```
fcs_files.upload_zip(cyto_session,  
  experiment_id = new_experiment$id,  
  file_path = zip_filename,  
  timeout = 720)
```