DNAnexus Command Line Interface

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Contents

Chapter 1

Setup

First we have to load the DNAnexus command line interface utility. Both CCAD and Biowulf have it installed as a module.

```
#CCAD:
module load dx
#BIOWULF:
#module load DNAnexus
```

Next we have to login, select a project, and

```
#Log in (only have to do this the first time)
#dx login

#See what projects you have access to:
dx find projects

#Select the project you want from the above list:
dx select project-FbvPXyQOpgP1PQbkJG1vfQpz
```

```
## project-FbvPXyQOpgP1PQbkJG1vfQpz : Steve@NCI (ADMINISTER)
## project-FXfKVQj99yPxP6YqB7ykfBZ8 : AzureWest_Project (CONTRIBUTE)
## project-Ff54zy09462pQB99BpVZv7kG : steveTestProject (ADMINISTER)
## project-FYf1F7j9BppKqvGPK5GvqBzz : Genetic Susceptibility to Subsequent Neoplasms (CONTRIBUTE)
## Selected project project-FbvPXyQOpgP1PQbkJG1vfQpz
```

Once dx is loaded and a project is selected, you can use many standard linux commands on the project by prefacing the command with "dx"

```
dx ls
dx cd test
dx cd ..

dx mkdir test2
dx rmdir test2
```

```
## test/
## findNi
```

For a full list of available commands:

```
dx help all
```

```
## dx all: All commands
##
## Commands:
```

```
##
##   add                Add one or more items to a list
##   add developers     Add developers for an app
##   add member         Grant a user membership to an org
##   add stage          Add a stage to a workflow
##   add users          Add authorized users for an app
##   add_types          Add types to a data object
##   api                Call an API method
##   build              Upload and build a new applet/app, or a workflow
##   build_asset        Build an asset bundle
##   cat                Print file(s) to stdout
##   cd                 Change the current working directory
##   clearenv           Clears all environment variables set by dx
##   close              Close data object(s)
##   cp                 Copy objects and/or folders between different projects
##   describe           Describe a remote object
##   download           Download file(s)
##   env                Print all environment variables in use
##   exit               Exit out of the interactive shell
##   find               Search functionality over various DNAnexus entities
##   find analyses      List analyses in the current project
##   find apps          List available apps
##   find data          List data objects in the current project
##   find executions    List executions (jobs and analyses) in the current project
##   find globalworkflowsList available global workflows
##   find jobs          List jobs in the current project
##   find org           List entities within a specific org.        "dx find org
##                      members" lists members in the
##                      specified org        "dx find org
##                      projects" lists projects billed to the
##                      specified org        "dx find org
##                      apps" lists apps billed to the
##                      specified org  Please execute "dx find
##                      org -h" for more information.
##   find org apps      List apps billed to the specified org
##   find org members   List members in the specified org
##   find org projects  List projects billed to the specified org
##   find orgs          List orgs
##   find projects      List projects
##   generate_batch_inputsGenerate a batch plan (one or more TSV files) for batch
##                      execution
##   get                Download records, apps, applets, workflows, and files
##   get_details        Get details of a data object
##   head               Print part of a file
##   help               Display help messages and dx commands by category
##   install            Install an app
##   invite             Invite another user to a project or make it public
##   list               Print the members of a list
##   list database      List entities associated with a specific database. For
##                      example,           "dx list database
##                      files" lists database files associated
##                      with a specific database.
##                      Please execute "dx list database -h"
##                      for more information.
##   list database filesList files associated with a specific database
##   list developers    List developers for an app
##   list stages        List the stages in a workflow
```

```
##    list users        List authorized users for an app
##    login             Log in (interactively or with an existing API token)
##    logout            Log out and remove credentials
##    ls                List folders and/or objects in a folder
##    make_download_url Create a file download link for sharing
##    mkdir             Create a new folder
##    mv                Move or rename objects and/or folders inside a project
##    new               Create a new project or data object
##    new org           Create new org
##    new project       Create a new project
##    new record        Create a new record
##    new user          Create a new user account
##    new workflow      Create a new workflow
##    publish           Publish an app or a global workflow
##    pwd               Print current working directory
##    remove            Remove one or more items to a list
##    remove developers Remove developers for an app
##    remove member     Revoke the org membership of a user
##    remove stage      Remove a stage from a workflow
##    remove users      Remove authorized users for an app
##    remove_types      Remove types from a data object
##    rename            Rename a project or data object
##    rm                Remove data objects and folders
##    rmdir             Remove a folder
##    rmproject         Delete a project
##    run               Run an applet, app, or workflow
##    select            List and select a project to switch to
##    set_details       Set details on a data object
##    set_properties    Set properties of a project, data object, or execution
##    set_visibility    Set visibility on a data object
##    setenv            Sets environment variables for the session
##    ssh               Connect to a running job via SSH
##    ssh_config        Configure SSH keys for your DNAnexus account
##    tag               Tag a project, data object, or execution
##    terminate         Terminate jobs or analyses
##    tree              List folders and objects in a tree
##    uninstall         Uninstall an app
##    uninvite          Revoke others' permissions on a project you administer
##    unset_properties  Unset properties of a project, data object, or execution
##    untag             Untag a project, data object, or execution
##    update            Update certain types of metadata
##    update member     Update the membership of a user in an org
##    update org        Update information about an org
##    update project    Updates a specified project with the specified options
##    update stage      Update the metadata for a stage in a workflow
##    update workflow   Update the metadata for a workflow
##    upgrade           Upgrade dx-toolkit (the DNAnexus SDK and this program)
##    upload            Upload file(s) or directory
##    wait              Wait for data object(s) to close or job(s) to finish
##    watch             Watch logs of a job and its subjobs
##    whoami            Print the username of the current user
```

Chapter 2

A Simple Example:

We are going to do a very simple example in which we upload some data, run a program on it, and then download the result.

Say we want to extract all the dictionary words that begin with "ni".

Chapter 3

The App Builder Wizard:

The first step is to create a new App. You can generate the files from a template, write them yourself, or you can use the dx app creation wizard. For your first project, I recommend the last option.

Since the wizard is interactive, I have already performed this step and the example directory contains a copy of the output:

```
cp -R ../examples/findNi_original ./ex/findNi
```

Chapter 4

Modifying the App:

The app produced by the wizard is very minimal, it doesn't actually DO anything.

```
ls ./ex/findNi/
```

```
## dxapp.json
## findNi_original
## Readme.developer.md
## Readme.md
## resources
## src
## test
```

```
ls ./ex/findNi/src
```

```
## findNi.sh
```

The main files that you will need to modify are the dxapp.json file:

```
cat ./ex/findNi/dxapp.json
```

```
## {
##    "name": "findNi",
##    "title": "Find Ni",
##    "summary": "Finds words that begin with ni",
##    "dxapi": "1.0.0",
##    "version": "0.0.1",
##    "inputSpec": [
##      {
##        "name": "wordsFile",
##        "label": "File of all words",
##        "class": "file",
##        "optional": false,
##        "patterns": [
##          "*"
##        ],
##        "help": ""
##      }
##    ],
##    "outputSpec": [
##      {
##        "name": "outfile",
##        "label": "Output file of words",
##        "class": "file",
##        "patterns": [
```

```
##          "*"
##        ],
##          "help": ""
##      }
##    ],
##    "runSpec": {
##      "timeoutPolicy": {
##        "*": {
##          "hours": 48
##        }
##      },
##      "interpreter": "bash",
##      "release": "16.04",
##      "distribution": "Ubuntu",
##      "file": "src/findNi.sh",
##      "execDepends": [
##          {"name": "openjdk-8-jre-headless",
##           "package_manager": "apt"},
##
##          {"name": "tabix",
##           "package_manager": "apt"}
##      ]
##    },
##    "regionalOptions": {
##      "aws:us-east-1": {
##        "systemRequirements": {
##          "*": {
##            "instanceType": "mem1_ssd1_x4"
##          }
##        }
##      }
##    }
##  }
## }
```

and also the bash script in the src directory:

```
cat ./ex/findNi/src/findNi.sh
```

```
## #!/bin/bash
## # helloWorldTestApp 0.0.2
##
## main() {
##
##     #First, let's print out the input file, to make sure the inputs
##     # got set properly:
##     echo "Value of wordsFile: '$wordsFile'"
##     echo "Value of wordsFile_name: $wordsFile_name"
##
##     #Next let's download the words file from the cloud and into
##     # our virtual machine.
##     dx download "$wordsFile" -o $wordsFile_name
##
##     #This part is the program itself. It takes the input and grabs
##     # all the words that begin with Ni
##     cat $wordsFile_name | grep "^ni" > words.that.begin.with.ni.txt
##
##     #This part uploads the resultant file to the cloud
##     # If you don't do this, then all the files you made will be
```

```
##      # deleted when the virtual machine gets shut down.
##      #Note: dx upload --brief returns a file code that
##      # the next tool needs in order to register the output.
##      outfile_dx_code=$(dx upload words.that.begin.with.ni.txt --brief)
##
##      #Finally: this part registers the output and connects it to this job
##      # That way the output will be accessable from the job screen.
##      dx-jobutil-add-output outfile "$outfile_dx_code" --class=file
##
##
## }
```

I have already generated new versions of these files.

For the json file, I just added some dependencies just to show how one would do that. In this case I told the VM to install tabix and openJDK. Note: I don't actually need them in this example.

```
cp ../examples/files/dxapp.v2.json ./ex/findNi/dxapp.json
cat ./ex/findNi/dxapp.json
```

```
## {
##     "name": "findNi",
##     "title": "Find Ni",
##     "summary": "Finds words that begin with ni",
##     "dxapi": "1.0.0",
##     "version": "0.0.1",
##     "inputSpec": [
##       {
##         "name": "wordsFile",
##         "label": "File of all words",
##         "class": "file",
##         "optional": false,
##         "patterns": [
##           "*"
##         ],
##         "help": ""
##       }
##     ],
##     "outputSpec": [
##       {
##         "name": "outfile",
##         "label": "Output file of words",
##         "class": "file",
##         "patterns": [
##           "*"
##         ],
##         "help": ""
##       }
##     ],
##     "runSpec": {
##       "timeoutPolicy": {
##         "*": {
##           "hours": 48
##         }
##       },
##       "interpreter": "bash",
##       "release": "16.04",
##       "distribution": "Ubuntu",
##       "file": "src/findNi.sh",
```

```
##       "execDepends": [
##           {"name": "openjdk-8-jre-headless",
##            "package_manager": "apt"},
##
##           {"name": "tabix",
##            "package_manager": "apt"}
##       ]
##     },
##     "regionalOptions": {
##       "aws:us-east-1": {
##         "systemRequirements": {
##           "*": {
##             "instanceType": "mem1_ssd1_x4"
##           }
##         }
##       }
##     }
## }
```

Next we write the script itself. The main function gets executed once the virtual machine is spun up and everything is installed and prepped. Note that it sets a bunch of environment variables that link to the input files.

The program below runs through the provided words file and returns a file containing all the words that begin with "ni".

```
cp ../examples/files/findNi.v2.bash ./ex/findNi/src/findNi.sh
cat ./ex/findNi/src/findNi.sh
```

```
## #!/bin/bash
## # helloWorldTestApp 0.0.2
##
## main() {
##
##     #First, let's print out the input file, to make sure the inputs
##     # got set properly:
##     echo "Value of wordsFile: '$wordsFile'"
##     echo "Value of wordsFile_name: $wordsFile_name"
##
##     #Next let's download the words file from the cloud and into
##     # our virtual machine.
##     dx download "$wordsFile" -o $wordsFile_name
##
##     #This part is the program itself. It takes the input and grabs
##     # all the words that begin with Ni
##     cat $wordsFile_name | grep "^ni" > words.that.begin.with.ni.txt
##
##     #This part uploads the resultant file to the cloud
##     # If you don't do this, then all the files you made will be
##     # deleted when the virtual machine gets shut down.
##     #Note: dx upload --brief returns a file code that
##     # the next tool needs in order to register the output.
##     outfile_dx_code=$(dx upload words.that.begin.with.ni.txt --brief)
##
##     #Finally: this part registers the output and connects it to this job
##     # That way the output will be accessible from the job screen.
##     dx-jobutil-add-output outfile "$outfile_dx_code" --class=file
##
##
## }
```

Chapter 5

Building the App:

Now we have to "build" the app, which packages up the app and uploads it to your current project

```
cd ./ex/
dx build -f findNi
```

```
## WARNING:dxpy:name "findNi" should be all lowercase
## INFO:dxpy:Deleting applet(s) applet-FgG0938OpgP9P23bOYf68q17
## {"id": "applet-FgG097Q0pgP48jZG4Py695pb"}
```

Chapter 6

Uploading Input Files

Before we can run our new app, first we need to upload an input file. For this we use the upload command:

```
dx upload ../examples/indata/linux.words.txt --brief --path /test/linux.words.txt
```

```
## file-FgG097j0pgP50503941gB926
```

Chapter 7

Running the software

Before we can run our new app, first we need to upload an input file. For this we use the upload command:

```
dx run findNi -i wordsFile=/test/linux.words.txt --destination /test/
```

Chapter 8

Downloading results

We can now download the results using the dx download command:

```
dx download /test/words.that.begin.with.ni.txt
#Let's see the first 50 words:
cat words.that.begin.with.ni.txt | head -n50
```

```
## Error: path "/mnt/nfs/gigantor/ifs/Shared/hartleys/docs/DnaNexusTutorial/build
## /words.that.begin.with.ni.txt" already exists but -f/--overwrite was not set
## ni
## niacin
## niacinamide
## niacins
## niagara
## niagra
## niais
## niaiserie
## nialamide
## niata
## nib
## nibbana
## nibbed
## nibber
## nibbing
## nibble
## nibbled
## nibbler
## nibblers
## nibbles
## nibbling
## nibblingly
## nibby
## nibby-jibby
## nibelung
## niblic
## niblick
## niblicks
## niblike
## nibong
## nibs
## nibsome
## nibung
```

```
## nicad
## nicads
## nicaean
## nicaragua
## nicaraguan
## nicaraguans
## niccolic
## niccoliferous
## niccolite
## niccolo
## niccolous
## nice
## niceish
## niceling
## nicely
## nicene
## nice-Nellie
```

Chapter 9

Other useful commands:

You can use cat to quickly preview files:

```
dx cat /test/words.that.begin.with.ni.txt | head -n10
```

```
## ni
## niacin
## niacinamide
## niacins
## niagara
## niagra
## niais
## niaiserie
## nialamide
## niata
```

```
dx describe /test/words.that.begin.with.ni.txt
```

```
## Result 1:
## ID                   file-Ff75Y1802Kz9BfkxGQX1zjG4
## Class                file
## Project              project-FbvPXyQ0pgP1PQbkJG1vfQpz
## Folder               /test
## Name                 words.that.begin.with.ni.txt
## State                closed
## Visibility           visible
## Types                -
## Properties           -
## Tags                 -
## Outgoing links       -
## Created              Fri Sep 27 14:48:37 2019
## Created by           hartleys
##  via the job         job-Ff75XgQ0pgP61V589qpvGG8G
## Last modified        Fri Sep 27 14:48:39 2019
## archivalState        "live"
## Media type           text/plain
## Size                 10.33 KB
```

```
set -x
dx describe /test/words.that.begin.with.ni.txt
```

```
## + dx describe /test/words.that.begin.with.ni.txt
## Result 1:
## ID                   file-Ff75Y1802Kz9BfkxGQX1zjG4
```

```
## Class            file
## Project          project-FbvPXyQ0pgP1PQbkJG1vfQpz
## Folder           /test
## Name             words.that.begin.with.ni.txt
## State            closed
## Visibility       visible
## Types            -
## Properties       -
## Tags             -
## Outgoing links   -
## Created          Fri Sep 27 14:48:37 2019
## Created by       hartleys
##  via the job     job-Ff75XgQ0pgP61V589qpvGG8G
## Last modified    Fri Sep 27 14:48:39 2019
## archivalState    "live"
## Media type       text/plain
## Size             10.33 KB

dx watch <jobid>
```

Chapter 10

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