

# *Presentation of iRODS : basic usages and easicmd tools*

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## Summary

- 1 Presentation of iRODS
- 2 Introduction to iRODS
- 3 easycmd a tool to rule them all

## What is iRODS ?

- iRODS : integrated Rule Oriented Data System
- A data management middleware software (open source)
- Developed since 1995
- Use by CC-IN2P3, NOAO , NCDC etc...



## Why using iRODS ?

- **Virtualisation**, which provides an uniform interface for all data regardless of the heterogeneity of storage infrastructure.
- **Workflow Automation** through rules and microservices
- Secure **Collaboration** and data sharing between collaborating or distributed teams.
- Data Discovery through the use of descriptive **metadata**

## iRODS-zone

- A Zone is a iRODS deployment with a single set of management policies and a single metadata catalog.
- iRODS Zones are independent administrative units. Several zones **can be federated** (world-wide)

example of zone : lbbeZone, ccin2p3

## i-object

There is three kind of i-object in irods :

- file —> **dataObject (-d)**
- folder —> **Collection (-C)**
- user —> user (-u)

```
/lbbeZone/home/gdebaecker:  
C- /lbbeZone/home/gdebaecker/article  
/lbbeZone/home/gdebaecker/article:  
C- /lbbeZone/home/gdebaecker/easycmd  
/lbbeZone/home/gdebaecker/easycmd:  
C- /lbbeZone/home/gdebaecker/example  
/lbbeZone/home/gdebaecker/example:  
C- /lbbeZone/home/gdebaecker/fast5_asellus <-- Collection  
/lbbeZone/home/gdebaecker/fast5_asellus:  
FAL56006_29db37dd_250.fast5  
FAL56006_29db37dd_251.fast5  
FAL56006_29db37dd_252.fast5  
FAL56006_29db37dd_253.fast5  
FAL56006_29db37dd_25.fast5  
C- /lbbeZone/home/gdebaecker/integrity  
/lbbeZone/home/gdebaecker/integrity:  
C- /lbbeZone/home/gdebaecker/NeGa  
/lbbeZone/home/gdebaecker/NeGa:
```

} dataObject

## Metadata : Enrichment of your data

- No limit of number for one object

```
AVUs defined for dataObj /lbbeZone/home/g
attribute: technology          <--- A
value: nanopore_long_reads    <--- V
units: minion                  <--- U
----
attribute: Species            <--- A
value: Proasellus_coiffiati    <--- V
units:                          <--- U
----
attribute: Person_in_charge   <--- A
value: George                  <--- V
units: team_E3S                <--- U
----
attribute: Date_sequencing    <--- A
value: 25_09_21                <--- V
units: run2                     <--- U
----
attribute: Date_prelevement    <--- A
value: 23_09_21                <--- V
units:                          <--- U
```

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- Can be associated with dataObject, Collection or User

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- *Mkdir ~/.irods*
- Copy/create and edit the `irods_environment.json`
  - *cp /etc/irods/irods\_environment.json ~/.irods*
  - `"irods_zone_name" : "lbbeZone",`
  - `"irods_user_name" : "user_name",`
  - `"irods_host" : "lbbe-irods-local",`
  - `"irods_port" : 1247`

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- *Mkdir ~/.irods*
- Copy/create and edit the `irods_environment.json`
  - *cp /etc/irods/irods\_environment.json ~/.irods*
  - `"irods_zone_name" : "lbbeZone",`
  - `"irods_user_name" : "user_name",`
  - `"irods_host" : "lbbe-irods-local",`
  - `"irods_port" : 1247`
- *iinit* → use your password



## First step in iRODS : i-comands

- Give users a command-line interface to operate on data in iRODS

Linux	iRODS
ls	ils
cd	icd
pwd	ipwd
rsync	irsync
mkdir	imkdir
cp	icp
etc	ietc

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- Are Linux style shell commands
- Some of them need the type of object your work with (-d/-C/-u)
- list of icommand

<https://docs.irods.org/4.2.10/icommands/user/>

Linux	iRODS
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cd	icd
pwd	ipwd
rsync	irsync
mkdir	imkdir
cp	icp
etc	ietc

## Example : put data on iRODS

iput

ex : `iput -rPKVf my_folder [path/in/iRODS]`

irsync

ex : `irsync -rKV my_folder i:[path/in/irods/my_folder]`

If no iRODS path given folder is put in  
"/zone/home/user"

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■ `-r` -> recursive

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- `-K` -> calculate and verify the checksum on the data, client-side and server-side, and store it in the icat

If no iRODS path given folder is put in  
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ex : `irsync -rKV my_folder i:[path/in/irods/my_folder]`



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- `-f` → force (overwrite)

If no iRODS path given folder is put in  
"/zone/home/user"

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ex : `irsync -rKV my_folder i:[path/in/irods/my_folder]`

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### iput

ex : `iput -rPKVf my_folder [path/in/iRODS]`

- `-r` -> recursive
- `-P` -> progress
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- `-V` -> verbose mode
- `-f` -> force (overwrite)

If no iRODS path given folder is put in  
"/zone/home/user"

### irsync

ex : `irsync -rKV my_folder i:[path/in/irods/my_folder]`

- `i` : -> "from iRODS"
- **Caution!** not as unix rsync :  
`irsync my_folder == irsync my_folder/`  
put the name of the folder in path if you want to create it
- if no iRODS path given (`i :`) -> create the folder in  
"/zone/home/user"

## Example : get data from iRODS

iget

ex : `iget -rPK path/in/iRODS local/path/`

irsync

ex : `irsync -rKV i :[path/in/irods/my_folder] local/path/`

## Example : get data from iRODS

# iget

ex : `iget -rPK path/in/iRODS local/path/`

- `-r` → recursive
- `-P` → progress
- `-K` → calculate and verify the checksum on the data, client-side and server-side, and store it in the icat

# irsync

ex : `irsync -rKV i:[path/in/irods/my_folder] local/path/`

## Example : add metadata

```
imeta add -iobject_type path/to/iobject attribute value unit
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- **-iobject\_type** → file/dataObject = -d , folder/Collection = -C and user = -u

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- **path/to/object** -> path to your object in iRODS

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- **attribute** -> work as a key

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- **path/to/object** -> path to your object in iRODS
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- **value** -> value associated with attribute

## Example : add metadata

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- **imeta** -> command to work on metadata
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- **-iobject\_type** -> file/dataObject = -d , folder/Collection = -C and user = -u
- **path/to/object** -> path to your object in iRODS
- **attribute** -> work as a key
- **value** -> value associated with attribute
- **unit** -> can be null

## Example : add metadata

**imeta add -iobject\_type path/to/iobject attribute value unit**

```
$ imeta add -d /NeGA/Aselidae/sequencing/long-read/ONT/fast5/FAL56006_29db37dd_250.fast5 /  
seqkit LSK-110
```

```
$ imeta add -d /NeGA/Aselidae/sequencing/long-read/ONT/fast5/FAL56006_29db37dd_250.fast5 /  
flowcell R10_40
```

```
$ imeta add -d /NeGA/Aselidae/sequencing/long-read/ONT/fast5/FAL56006_29db37dd_250.fast5 /  
date 10_04_21 3_days
```

```
$ imeta add -d /NeGA/Aselidae/sequencing/long-read/ONT/fast5/FAL56006_29db37dd_250.fast5 /  
author Debaecker Gautier
```

## Example : find a data

Find an object based on metadata :

**imeta** **qu** **-iobject\_type** **attribute** **OPERATION** **value**

- **imeta** **qu** **-d** **flowcell** **=** **R10\_40**
- **imeta** **qu** **-d** **date** **like** **%04\_21**

Find an object based on name (only for file) :

**ilocate** **name**

- **ilocate** **FAL56006\_29db37dd\_250.fast5**
- **ilocate** **%fast5**

## A step-forward : i-rules

- Execution on server side
- Allow automatising of task
- iRODS rule language (C-like structure)



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## EASy-Irods-CoMmanDs

A python script to :

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- Add the **auto-completion** for some irods i-commands

## EASy-Irods-CoMmanDs

A python script to :

- **"Wrap"** the principal IRODS i-commands
- **Facilitate/automate** the use of irods for new users
- Add the **auto-completion** for some irods i-commands

Link to the git :

git clone [https://github.com/sigau/easy\\_irods\\_commands](https://github.com/sigau/easy_irods_commands)

[illegible]

## PUSH : PUT LOCAL DATA ON IRODS AND ADD METADATA

### ARGUMENT :

easicmpd.py **push** **path/to/local\_object**

### EXAMPLE :

```
### PUT THE LOCAL FOLDER "PROJECT_1" IN THE IRODS FOLDER "MY_PROJECT" AND ADD METADATA
$ ./easicmpd.py push PROJECT_1
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/MY_PROJECT
                                     /lbbeZone/home/gdebaecker/irods_test
                                     /lbbeZone/home/gdebaecker/irods_test/raw_data
                                     /lbbeZone/home/gdebaecker/irods_test/raw_data/fast5
                                     /lbbeZone/home/gdebaecker/MY_PROJECT
                                     /lbbeZone/home/gdebaecker/NeGa

Running recursive pre-scan... pre-scan complete... transferring data...
C- /lbbeZone/home/gdebaecker/MY_PROJECT/PROJECT_1:
0/2 - 0.00% of files done 0.000/0.000 MB - 0.00% of file sizes done
Processing file.fastq - 0.000 MB 2021-11-03.17:06:50
    file.fastq 0.000 MB | 0.047 sec | 0 thr | 0.000 MB/s
1/2 - 50.00% of files done 0.000/0.000 MB - 0.00% of file sizes done
Processing file.fasta - 0.000 MB 2021-11-03.17:06:50
    file.fasta 0.000 MB | 0.041 sec | 0 thr | 0.000 MB/s

add metadata ?(y/n): y
attribut (empty to stop) : client
value : MISTER_X
unit : Top_Secret

$ ils -r MY_PROJECT
/lbbeZone/home/gdebaecker/MY_PROJECT:
C- /lbbeZone/home/gdebaecker/MY_PROJECT/PROJECT_1
/lbbeZone/home/gdebaecker/MY_PROJECT/PROJECT_1:
file.fasta
file.fastq
```

## PULL : GET BACK DATA FROM IRODS

### ARGUMENT :

easycmd.pwd **pull** **iobject\_type** [path/to/local]

### EXAMPLE :

```
### PUT THE IRODS FOLDER "PROJECT_2" IN THE LOCAL FOLDER "MY_LOCAL_PROJECT"
$ ./easycmd.py pull -C MY_LOCAL_PROJECT/
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/MY_PROJECT/PROJECT_2
/lbbeZone/home/gdebaecker/irods_test
/lbbeZone/home/gdebaecker/irods_test/raw_data
/lbbeZone/home/gdebaecker/irods_test/raw_data/fast5
/lbbeZone/home/gdebaecker/MY_PROJECT
/lbbeZone/home/gdebaecker/MY_PROJECT/PROJECT_2
/lbbeZone/home/gdebaecker/Ne6a

0/3 - 0.00% of files done 0.000/0.000 MB - 0.00% of file sizes done
Processing file_bis.r - 0.000 MB 2021-11-03.17:35:48
file_bis.r 0.000 MB | 0.036 sec | 0 thr | 0.000 MB/s
1/3 - 33.33% of files done 0.000/0.000 MB - 0.00% of file sizes done
Processing file.fasta - 0.000 MB 2021-11-03.17:35:48
file.fasta 0.000 MB | 0.029 sec | 0 thr | 0.000 MB/s
2/3 - 66.67% of files done 0.000/0.000 MB - 0.00% of file sizes done
Processing file.fastq - 0.000 MB 2021-11-03.17:35:48
file.fastq 0.000 MB | 0.027 sec | 0 thr | 0.000 MB/s

$ls MY_LOCAL_PROJECT
PROJECT_2/
```

```
### PUT THE CONTAIN OF IRODS FOLDER "PROJECT_2" IN THE LOCAL FOLDER "MY_LOCAL_PROJECT"
$ ./easycmd.py pull -C MY_LOCAL_PROJECT/
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/MY_PROJECT/PROJECT_2
irods file (tap tab) : %
file_bis.r 0.000 MB | 0.037 sec | 0 thr | 0.000 MB/s
file.fasta 0.000 MB | 0.030 sec | 0 thr | 0.000 MB/s
file.fastq 0.000 MB | 0.035 sec | 0 thr | 0.000 MB/s

$ls MY_LOCAL_PROJECT
file_bis.r file.fasta file.fastq

### DOWNLOAD ONE SPECIFIC FAST5 IRODS FILE IN MY CURRENT LOCAL FOLDER
$ ./easycmd.py pull -f
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/irods_test/raw_data/fast5
irods file (tap tab) : FAL56086_29db37dd_251.fast5
0/1 - 0.00% of files done 0.000/181.788 MB - 0.00% of file sizes done
Processing FAL56086_29db37dd_251.fast5 - 181.788 MB 2021-11-03.17:42:38
From server: NumThreads=40, addr:/lbbe-irods-local, port:20089, cookie=449953456
FAL56086_29db37dd_251.fast5 - 160.932/181.788 MB - 93.48% done 2021-11-03.17:42:38
FAL56086_29db37dd_251.fast5 - 181.788/181.788 MB - 100.00% done 2021-11-03.17:42:38
FAL56086_29db37dd_251.fas 181.788 MB | 1.769 sec | 46 thr | 186.344 MB/s

$ls FAL56086_29db37dd_251.fast5
FAL56086_29db37dd_251.fast5
```



## SYNCHRO : SYNCHRONIZE MODIFIED DATA FROM A LOCAL FOLDER WITH IRODS

### ARGUMENT :

The folder is not yet in iRODS :

**easycmd.py** **synchro** **path/to/local** **path/in/irods**

The folder already exist in irods (or has to be put in "/zone/home/user") :

**easycmd.py** **synchro** **path/to/local**

### EXAMPLE :

```
## SYNCHRONISE THE LOCAL FOLDER "Nanoplot" in irods folder "PROJECT_ASSELU/ONT_READS"

$ ll
/1bbeZone/home/gdebaecker:
C- /1bbeZone/home/gdebaecker/MeGa
C- /1bbeZone/home/gdebaecker/PROJECT_ASSELU

$ ls Nanoplot/
full_report.pdf QC_porechop

$ ./easycmd.py synchro /beegfs/home/gdebaecker/1rule/Nanoplot /1bbeZone/home/gdebaecker/PROJECT_ASS

$ ll -s /PROJECT_ASSELU/ONT_READS/Nanoplot/
/1bbeZone/home/gdebaecker/PROJECT_ASSELU/ONT_READS/Nanoplot:
full_report.pdf
C- /1bbeZone/home/gdebaecker/PROJECT_ASSELU/ONT_READS/Nanoplot/QC
```

```
## SYNCHRONISE THE LOCAL FOLDER "Nanoplot" in irods folder "PROJECT_ASSELU/ONT_READS"

$ ll
/1bbeZone/home/gdebaecker:
C- /1bbeZone/home/gdebaecker/MeGa
C- /1bbeZone/home/gdebaecker/PROJECT_ASSELU

$ ls Nanoplot/
full_report.pdf QC_porechop

$ ./easycmd.py synchro /beegfs/home/gdebaecker/1rule/Nanoplot /1bbeZone/home/gdebaecker/PROJECT_ASS

$ ll -s /PROJECT_ASSELU/ONT_READS/Nanoplot/
/1bbeZone/home/gdebaecker/PROJECT_ASSELU/ONT_READS/Nanoplot:
full_report.pdf
C- /1bbeZone/home/gdebaecker/PROJECT_ASSELU/ONT_READS/Nanoplot/QC
```

# IMKDIR : CREATE AN IRODS WITHOUT KNOWING THE FULL TREE VIEW

ARGUMENT :

easycmd.py **imkdir**

EXAMPLE :

```
$ ilrs -r

C- /lbbeZone/home/gdebaecker/irods_test
/lbbeZone/home/gdebaecker/irods_test:
  final_summary_FAL56006_29db37dd.txt
C- /lbbeZone/home/gdebaecker/NeGa
C- /lbbeZone/home/gdebaecker/sr_aselus

$ ./easycmd.py imkdir
create : /lbbeZone/home/gdebaecker/irods_test/test_C-test/raw_test/raw_test2/new_folder

$ ilrs /lbbeZone/home/gdebaecker/irods_test/test_C-test/raw_test/raw_test2/
/lbbeZone/home/gdebaecker/irods_test/test_C-test/raw_test/raw_test2:
  C- /lbbeZone/home/gdebaecker/irods_test/test_C-test/raw_test/raw_test2/new_folder
```

## IRM : REMOVE DATA FROM IRODS

ARGUMENT :

easycmd.py **irm** **iobject\_type**

EXAMPLE :

```
## REMOVE ALL THE ".r" file from the "MY_PROJECT" irods folder
$ ils ./MY_PROJECT/
/lbzeZone/home/gdebaecker/MY_PROJECT:
file_bis_2.r
file_bis_3.r
file_bis_4.r
file_bis_5.r
file_bis.r
file.fasta
file.fastq
C- /lbzeZone/home/gdebaecker/MY_PROJECT/PROJECT_2

$ ./easycmd.py irm -f
you can use * as wildcard
ifolder (empty = /zone/home/user ): /lbzeZone/home/gdebaecker/MY_PROJECT
irods file (tap tab) : ".r"

$ ils ./MY_PROJECT/
/lbzeZone/home/gdebaecker/MY_PROJECT:
file.fasta
file.fastq
C- /lbzeZone/home/gdebaecker/MY_PROJECT/PROJECT_2
```

```
REMOVE THE "MY_PROJECT" irods folder
$ ils
/lbzeZone/home/gdebaecker:
C- /lbzeZone/home/gdebaecker/irods_test
C- /lbzeZone/home/gdebaecker/MY_PROJECT
C- /lbzeZone/home/gdebaecker/NeGa
C- /lbzeZone/home/gdebaecker/sr_aselus

$ ./easycmd.py irm -C
you can use * as wildcard
ifolder (empty = /zone/home/user ): /lbzeZone/home/gdebaecker/MY_PROJECT

$ ils
/lbzeZone/home/gdebaecker:
C- /lbzeZone/home/gdebaecker/irods_test
C- /lbzeZone/home/gdebaecker/NeGa
C- /lbzeZone/home/gdebaecker/sr_aselus
```

## ADD\_META : ADD METADATA ASSOCIATED WITH AN OBJECT

ARGUMENT :

easycmd.py **add\_meta** **iobject\_type**

EXAMPLE :

```
## ADD METADATA TO IRODS FOLDER "sr_aselus"
$ ./easycmd.py add_meta
add metadata to folder (C) or file (f) : C
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/sr_aselus
attribut (empty to stop) : technology
value : illumina
unit : 150pb
imeta add -C /lbbeZone/home/gdebaecker/sr_aselus technology illumina 150pb
attribut (empty to stop) : Species
value : Proasellus_coiffaiti
unit :
imeta add -C /lbbeZone/home/gdebaecker/sr_aselus Species Proasellus_coiffaiti
attribut (empty to stop) : Coverage
value : 200X
unit :
imeta add -C /lbbeZone/home/gdebaecker/sr_aselus Coverage 200X
attribut (empty to stop) :
```

```
$ imeta ls -C sr_aselus/
AVUs defined for collection /lbbeZone/home/gdebaecker/sr_aselus:
attribute: Species
value: Proasellus_coiffaiti
units:
----
attribute: technology
value: illumina
units: 150pb
----
attribute: Coverage
value: 200X
units:
```

# RM\_META : REMOVING METADATA ASSOCIATED WITH AN OBJECT

## ARGUMENT :

easycmd.py **rm\_meta** **ibobject\_type**

## EXAMPLE :

```
## REMOVE METADATA FROM iRODS FOLDER "sr_aselus"
## REMOVE THE "species" METADATA
$ imeta ls -C sr_aselus/
AVUs defined for collection /lbbeZone/home/gdebaecker/sr_aselus:
attribute: Species
value: Prosellus coiffaiti
units:
...
attribute: technology
value: illumina
units: 150pb
...
attribute: Coverage
value: 200X
units:
$ ./easycmd.py rm_meta
remove metadata from folder (C) or file (f) : C
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/sr_aselus
attribut (empty for all): Species
```

```
$ imeta ls -C sr_aselus/
AVUs defined for collection /lbbeZone/home/gdebaecker/sr_aselus:
attribute: technology
value: illumina
units: 150pb
...
attribute: Coverage
value: 200X
units:
$ ./easycmd.py rm_meta
remove metadata from folder (C) or file (f) : C
ifolder (empty = /zone/home/user) : /lbbeZone/home/gdebaecker/sr_aselus
attribut (empty for all):
$ imeta ls -C sr_aselus/
AVUs defined for collection /lbbeZone/home/gdebaecker/sr_aselus:
None
```

## SHOW\_META : SHOW THE METADATA ASSOCIATED WITH AN OBJECT

ARGUMENT :

easycmd.py **show\_meta** **iobject\_type**

EXAMPLE :

```
$ ./easycmd.py show_meta -C
ifolder (empty = /zone/home/user ): /lbbeZone/home/gdebaecker/sr_aselus
AVUs defined for collection /lbbeZone/home/gdebaecker/sr_aselus:
attribute: technology
value: illumina
units: 150pb
----
attribute: Species
value: Proassellus_coifaiti
units:
```

## SEARCH\_BY\_META : SEARCH FOR IRODS OBJECTS (FOLDER/FILE) BASED ON THE METADATA

ARGUMENT :

easycmd.py **search\_by\_meta** **iobject\_type**

EXAMPLE :

```
###SEARCH ALL THE IRODS FOLDER THAT HAVE THE ATTRIBUTE "technology"
./easycmd.py search_by_meta -C
attribute: technology
          auteur
          technology
          Species
value (% as *): %
               illumina
               Nanopore

collection: /lbbeZone/home/gdebaecker/irods_test/raw_data/fast5
----
collection: /lbbeZone/home/gdebaecker/sr_aselus
```

## SEARCH\_NAME : SEARCH FOR IRODS OBJECT BASED ON (PARTS) OF THE OBJECT NAME

ARGUMENT :

easycmd.py **search\_name** **iobject\_type**

EXAMPLE :

```
### FIND ALL THE ".fast5" FILES ON IRODS
$ ./easycmd.py search_name -f
your query(% as *) : %.fast5
/lbbeZone/home/gdebaecker/irods_test/raw_data/FAL56006_29db37dd_253.fast5
/lbbeZone/home/gdebaecker/irods_test/raw_data/fast5/FAL56006_29db37dd_250.fast5
/lbbeZone/home/gdebaecker/irods_test/raw_data/fast5/FAL56006_29db37dd_251.fast5
/lbbeZone/home/gdebaecker/irods_test/raw_data/fast5/FAL56006_29db37dd_252.fast5
/lbbeZone/home/gdebaecker/irods_test/raw_data/fast5/FAL56006_29db37dd_253.fast5
/lbbeZone/home/gdebaecker/irods_test/raw_data/fast5/FAL56006_29db37dd_25.fast5
/lbbeZone/home/gdebaecker/irods_test/test_C-test/raw_test/raw_test3/FAL56006_29db37dd_253.fast5

###FIND ALL THE "fastQ" FOLDER IN IRODS
$ ./easycmd.py search_name -C
your query (you can use *) : *fastQ
/lbbeZone/home/gdebaecker/irods_test/raw_data/UNICORN_AND_DRAGON/fastQ
/lbbeZone/home/gdebaecker/NeGa/MY_2nd_PROJECT/TIGER/fastQ
/lbbeZone/home/gdebaecker/NeGa/MY_PROJECT/Proasellus/fastQ
```



## IDUSH : AN IRODS EQUIVALENT TO `du -sh`

ARGUMENT :

`easycmd.py idush`

EXAMPLE :

```
$ ./easycmd.py idush
ifolder (empty = /zone/home/user ): /lbbeZone/home/gdebaecker/irods_test/raw_data/fast5
                                   /lbbeZone/home/gdebaecker/irods_test
                                   /lbbeZone/home/gdebaecker/irods_test/raw_data
                                   /lbbeZone/home/gdebaecker/irods_test/raw_data/fast5

913.7MiB
```

QUESTION ?



*That's all Folks!*