# How to run the automation

The automation is a suite of 3 python scripts which run sequentially:

clia\_run\_daemon.py

clia\_analysis\_daemon.py

clia\_trovabase\_uploader\_daemon.py

All 3 scripts require no arguments. Therefore to run simply: python script\_name

The trovaemon account has a cron job for this which calls the script: trovapipe\_wrapper.sh

* A bash script which calls each of the 3 modules sequentially.
* bash /mnt/data/Bioinformatics/trovapipe/trovapipe\_wrapper.sh

# How to add a repository:

Add the path to /mnt/data/Bioinformatics/trovapipe /Utilities/repositories.xml

The change will be reflected the next time the automation runs.

# How to add an email address:

Add the address to /mnt/data/Bioinformatics/trovapipe/Utilities/email.xml

The change will be reflected the next time the automation runs.

* You’ll see priority 1-4 which are based on error level.
  + 1: Warning
  + 4: The entire wrapper is crashing
* We’ll be adding all CLIA persons who run sequencers to these lists at Paul’s request.
* In a future version it may make sense to break these into error types:
  + Wrapper Error
  + Analysis Tool Error
  + Trovabase Error
  + Uniflow Error

# How to Manually Get the Status of Any Run

trovaemon@flash:/mnt/data/Bioinformatics/trovapipe$ python /mnt/data/Bioinformatics/trovapipe/getRunStatus.py flowcell\_ID

# How to Manually Set the Status of Any Run

trovaemon@flash:/mnt/data/Bioinformatics/trovapipe$ python /mnt/data/Bioinformatics/trovapipe/setRunStatus.py flowcell\_ID STATUS

For a list of statuses see:

/mnt/data/Bioinformatics/trovapipe/Keys/Keys.py

# How to Re-Queue an Analysis

1. Ensure the run folder is within one of the repositories described above.
2. Reset the status to NGS\_RUN\_PENDING.
3. The automation should take it up soon after.

trovaemon@flash:/mnt/data/Bioinformatics/trovapipe$ python /mnt/data/Bioinformatics/trovapipe/setRunStatus.py flowcell\_ID NGS\_RUN\_PENDING

# PASSWORDS

Currently the passwords trovaemon uses to access the UniFlow API are stored in 3 files:

1. /mnt/data/Bioinformatics/trovapipe/Utilities/TrovapipeUtils.py
   1. All 3 automation modules use this library to access the Uniflow API.
2. /mnt/data/Bioinformatics/trovapipe/getRunStatus.py
   1. For manual tasks
3. /mnt/data/Bioinformatics/trovapipe/setRunStatus.py
   1. For manual tasks

Note: Passwords expire every three months and must be updated via the web-browser:

https://trovagene.uniconnect.com/uniflow

I’ve requested that expiry be turned off (Eric from onuage) and left it in Mariko and Wilson’s domain as to whether or not this happens.

# How to Copy the Run from MiSeq

1. Go to Windows Explorer on the MiSeq
   1. Go to D://Illumina/MiSeqAnalysis/
   2. Find your run
2. Open up another Windows Explorer window
   1. Go to C://Ilumina/copy\_run.bat
   2. Open in Notepad or just right click and Edit
   3. If you’re MiSeq user, then copy the top path
   4. If you’re SBSUser, then copy the bottom path
3. Copy your run into the correct path
4. Then Wilfred’s automation will copy it to the CLIA runs folder from these two folders where the CLS can look at it
5. The TrovaWrapper will then take one hour to pick it up and push to the LIMS
6. Check IsisError and IsisLog after analysis is complete
7. To get the status of a run: type in
   1. python getstatusrun.py [put in the flow-cell id]

# How to Remove Hot Samples from SampleSheet and Run Analysis

1. Go to the specific run folder
2. Save the raw file as OldSheet and save it in an OldSheets folder
3. Take out hot samples based on what the CLS says
   1. For specific assay as well
4. Renumber the numbers on the first column
5. Go Into Data / Intensity / Basecalls and then delete all the Alignment folders (New Alignment folder will be created when we run MSR)
6. Run PowerShell
   1. Run ./Isis.exe blahblahblah
7. Check IsisError and IsisLog for any errors
8. Run python setRunStatus.py flowcellID NGS\_RUN\_COMPLETE
   1. Assuming the RunQC file already exists because clia\_run\_daemon.py already ran once

# How to Manual Upload Results to Uniflow

1. Sign on to flash, then go to /mnt/data/Bioinformatics/trovapipe/; execute the following command,

Make sure in LIMS the already uploaded analysis result was deleted and the run status should be NGS\_ANALYSIS\_DELETED,

Use getRunStatus.py to check the status.

python getRunStatus.py flowcellID

1. Identify the run result folder location, then go in to ManualUniflowUploader sub-folder: /mnt/data/Bioinformatics/trovapipe/ManualUniflowUploader;

Execute the following command:

python manualLimsUpload.py //anyfolders/…./xxxxx\_analysis\_results.csv flowcellID

1. Go up one folder level to /mnt/data/Bioinformatics/trovapipe/ and run the following command to check Run status, should be “NGS\_ANALYSIS\_CLIA\_REVIEW”

python getRunStatus.py flowcellID

([

{"flowcellID":"000000000-AU6LL",

"status":"NGS\_ANALYSIS\_CLIA\_REVIEW",

"eventDate":"2016-06-23 17:50:09"}

])

1. Wait for CLIA to review the uploaded result and accept it. Check for run status again., should be “NGS\_ANALYSIS\_COMPLETE”

python getRunStatus.py flowcellID

([

{"flowcellID":"000000000-AU6LL",

"status":"NGS\_ANALYSIS\_COMPLETE",

"eventDate":"2016-06-23 17:50:09"}

])

1. Perform TrovaBase Manual Upload if needed.

# How to Manual Upload Results to TROVABASE

1. Sign on to flash, then go to /mnt/data/Bioinformatics/trovapipe/ManualTrovabaseUploader/v13 (or the latest version #); execute the following command,

*sample\_sheet='/mnt/prd/MiSeq[#]/runID/Trovapipe\_Results/SampleSheet\_flowcellID.csv'*

*result\_sheet='/mnt/prd/MiSeq[#]/runID/Trovapipe\_Results/xxx\_flowcellID\_analysis\_results\_upload.csv'*

*stat\_sheet='/mnt/prd/MiSeq[#]/runID/Trovapipe\_Results/ xxx\_flowcellID \_analysis\_statistics.csv'*

*qc\_sheet='/mnt/prd/MiSeq[#]/runID/Trovapipe\_Results/RunQuality\_floecellID.csv'*

*java -jar upload.jar -database trovabase -group CLIA -s $sample\_sheet -r $result\_sheet -stat $stat\_sheet -q $qc\_sheet*

1. Set Run Status to NGS\_UPLOADED\_TO\_TROVABASE if the TrovaBase upload completed without error messages.

*python setRunStatus.py flowcellID NGS\_UPLOADED\_TO\_TROVABASE*

1. Move the run folder in to archive.