



Batch Analysis
via the Acapella CLI

Overview

This guide outlines a basic workflow describing how to submit Batch Analysis jobs via the Acapella command line interface (CLI).

Note that jobs which are submitted via the Acapella CLI are processed outside of the Columbus application framework, and as such job submissions will not be recorded via the Columbus Job Status page, nor will the Results output be available within the Columbus user interface.

Prerequisites

- The data being analysed must be in a native IDX/TIF format
- The data being analysed must be accessible via the Columbus server filesystem
- The analysis script being used must be accessible via the Columbus server filesystem
- All data must be readable by the 'columbus' Linux user account

Preparing a data set

Acapella expects the data to be in a native structure. One way of ensuring the data is in the correct format would be to use a data set which has been exported from Columbus. Via the Export page of the Columbus UI it's possible to export the data directly to the local filesystem of the Columbus server, by specifying an absolute path when choosing the Export Folder, e.g. /tmp, /home/user, etc. Only the Image Data and the Analysis scripts need to be exported, using the export formats "SinglePlane TIF" and "Script" respectively. See example shown below.



Select Data

Method: Columbus

Selected Measurements: 1

Added data.

Select Export Options

Method: Export to Disk

Export Folder: /tmp

Image Data: SinglePlane TIF

Results: Excel (txt)

Analysis: Script

Assay Definition: Native XML

Annotations: Default

Start Export

Ready for export.

Submitting a Batch Analysis job

Connect to the Columbus server back-end via an SSH client such as PuTTY/Terminal as the 'columbus' user. Jobs can now be executed via the Acapella CLI.

Syntax:

```
acapella -s datafilename="/path/to/ImageIndex.xml" \  
-s resultfilename="/path/to/ResultsOutput.dat" \  
-s scriptfilename="/path/to/AnalysisScript.aas" \  
'<AcapellaAssayLanguage|BBBatchPlayer.script>'
```

Parameters:

- datafilename Path to the ImageIndex xml file which describes the data structure. The ImageIndex.ColumbusIDX.xml is located within the same directory as the tiff files of a Columbus exported data set.
- resultfilename Path to the output file used to store the analysis results. The output path/filename is arbitrary.
- scriptfilename Path to the .aas script file that should be used during the analysis. The .aas files are found in the measurement level folder of a Columbus exported data set.

Example:

Given a data set with the following directory structure/content on the local filesystem:

```
/Screen[01]  
├─ Plate[01]  
│   └─ Measurement[01]  
│       ├── AnalysisScript.aas  
│       ├── Images[01]  
│       │   ├── 001001-1-001001001.tif  
│       │   ├── 001001-1-001001002.tif  
│       │   ├── 001001-2-001001001.tif  
│       │   ├── 001001-2-001001002.tif  
│       │   └─ ImageIndex.ColumbusIDX.xml  
│       └─ MeasurementIndex.ColumbusIDX.xml
```

And assuming the Results output should be directed to the Measurement level directory, the following command would be correct:

```
acapella -s datafilename="/Screen[01]/Plate[01]/Measurement[01]/Images[01]/ImageIndex.ColumbusIDX.xml" -s resultfilename="/Screen[01]/Plate[01]/Measurement[01]/Results.dat" -s scriptfilename="/Screen[01]/Plate[01]/Measurement[01]/AnalysisScript.aas" '<AcapellaAssayLanguage|BBBatchPlayer.script>'
```