

Image Analysis with IAP

Example Workflow for the Analysis of the Provided Maize Dataset

Image Analysis Group - Leibniz Institute of Plant Genetics and Crop Plant Research IPK, Corrensstr. 3, 06466 Gatersleben

Christian Klukas and Jean-Michel Pape

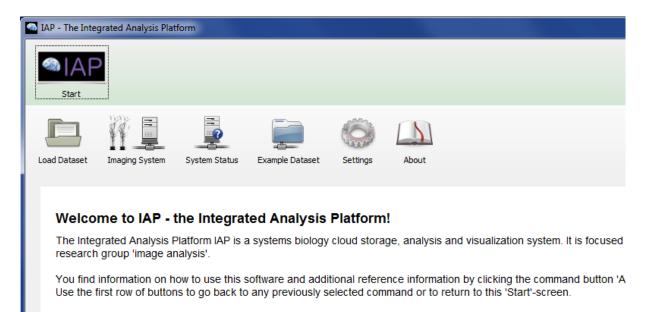
Rev 2 for IAP version 1.1, November 2013

Analysis of the example data set

Load data set

Remark: the provided example data set contains compressed JPG images, the uncompressed PNG data set is available upon request.

At first download and start the IAP. You can find the link to the example data set on the starting screen as shown below (take in mind, this is the link to the compressed data set, it is saved on our webserver, the following steps show how it is used).



To navigate to the data click "Example Data Set" > "Maize (1)" > "Ba (1)" > "1107BA_Corn"

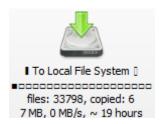


Data set overview

Now you are on the data set overview page. Here you can find some information about the data set also you can view the images by clicking on the Icon "View/Export Data".

IAP - The Integrate	d Analysis Platform
MIAP Start	Example Dataset Maize (1) BA (1) 1107BA_Corn updated 1 week ago
View/Export Data	PDF Report Copy Tools Add to Clipboard Put data in 'Experiments' tab
▼ Experiment 110	7BA_Corn
Name ID Import by Origin Database Coordinator Access Group Experiment-Type Start-Time End-Time Sequence/Stress Remark Outliers Connected Files Numeric Values Storage Time History	1107BA_Corn web-example:index\1373358075551_0_Christian Klukas_1107BA_Corn.iap.index.csv Christian Klukas It:CGH_11:1107BA_Corn CGH_11 BA Imaging System (CGH) Maize 02.03.2011 04.05.2011 1 33,798 (0 KB) 37,766 09.07.13 10:21 -
Analysis Settings	(not assigned) Cancel Save Changes

However for performing the analysis you have to download the data set by clicking on the "Copy" button, here choose the button "To Local File System" and select your target folder. When the coping starts you should see a progress bar as shown below.

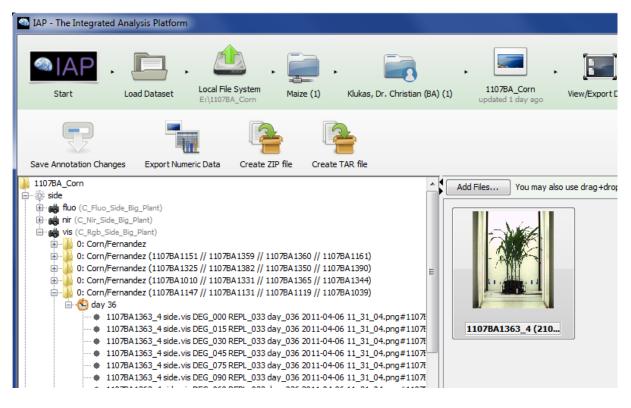


After coping, go to the IAP start screen by clicking on the "Start" icon. Now it is time to load the downloaded data set by clicking on "Load or Create Dataset" > "Load IAP Dataset(s) from File System", choose your target folder, where you saved the data set before. Then navigate further to the data set overview screen. This should look like this:

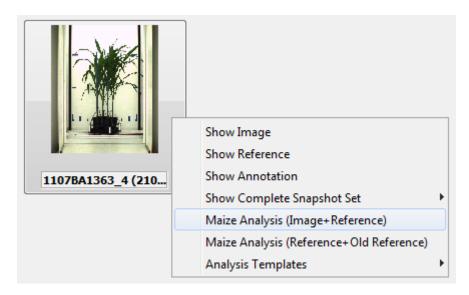
IAP - The Integrate	d Analysis Pl	atform					
IAP Start	Load Data	aset Local File E:\1107B		ize (1) Klu	ukas, Dr. Christian (BA)	(1) 1107BA_Corn updated 1 day ago	
View/Export Data	Analysis	PDF Report	Сору	Tools	Add to Clipboard	Put data in 'Experiments' tab	
				1005			
Experiment 110	/BA_Corn						
Name	1107BA_Co	rn					
ID	user.dir.137	4071238086:index	\1373904160184_(_pape_1107BA	_Corn.iap.index.csv		
Import by	pape						
Origin		107BA_Corn					
Database	CGH_11						
Coordinator	Klukas, Dr.	Christian (BA)					
Access Group	Imaging Sys	stem (CGH)					
Experiment-Type	Maize						•
Start-Time	02.03.2011						
End-Time	04.05.2011						
Sequence/Stress	07.03.2011	•					
Remark	data transf	er errors: 0					
Outliers							
Connected Files	33,798 (114 GB)						
Numeric Values	37,766						
Storage Time	15.07.13 18	3:02					
History	-						
Analysis Settings	Maize Analy	sis (121 lines)					
			Cancel	Save Chang	jes		

Perform Analysis

Now you can see a button "Analysis", click this and then click "Select Analysis Template" to choose the template which fits best to your data set, in our case the "Maize Analysis". Then you can go back and start the analysis with the default settings, but it is recommend to perform some test analysis to convince that the system works properly and maybe to change some settings. Therefore click on "View/Export Data" and select some images by navigating in the tree view as shown below.



Now you can perform a test analysis by clicking right on the image as you can see below.



If the analysis is finished a new window appears. You can scroll through the result of each analysis block step by step. The analysis settings can be changed by clicking on "change analysis settings" as marked in the picture below.

Re-run Analysis (debug Change analysis settings	

After that you can perform an analysis, go back to the data set overview page and select "Analysis" -> "Perform Maize Analysis". After clicking a progress bar should appear. When the analysis is finished the result is automatically displayed.

Numeric Data Export

The numeric results can be exported by navigating "View/Export Data" > "Export Numeric Data" and then choose your preferred data-format.

Create Spreadsheet (XLSX)	Create Spreadsheet (XLSX)	Create Spreadsheet (XLSX)	Create Spreadsheet (XLSX)	Create CSV File
(complete, high mem requ.)	(no histogram, no sections)	(histograms)	(sections)	

Analysis Steps of the Maize Analysis Pipeline

For getting a better understanding of the pipeline construction, we divided the analysis into 5 Steps. The images on the right show the output for each step. The pipeline is defined in the file <u>MaizePipeline.java</u>.

Data-Aquisition

At first the image data will be loaded.

Class Name	Descriptio n	Section Result
BILoadImages	images of all imaging domains loaded	
BICreateDummyReferenceIfNeede d	masks of all imaging domains loaded	

Data-Preprocessing

To get reliable results it is necessary to reduce influences caused by the imaging system. Therefore we perform an image normalisation and to aquire some calibration values.

Class Name	Description	Section Result
BIRotate	align rotation	
BIAlign	align orientation	
BlColourBalanceVerticalVis	apply vertical Colour Balancing on visible image	X X X
BIColourBalanceVerticalFluo	apply vertical Colour Balancing on fluorescence image	

Class Name	Description	Section Result
BlColourBalanceVerticalNir	apply vertical Colour Balancing on near-infrared image	
BIColorBalanceCircularVisNi	apply circular r Colour Balancing	
BIDetectBlueMarkers	detect and delete blue markers	
BICutFromSide	clear images	

Segmentation

The segmentation step is used to separate the foreground (plant) and background (imaging chamber, carrier system).

Class Name	Description	Section Result
BIRemoveBackground	clear background by reference image	
BIIntensityCalculationFluo	create intensity images	
BIKMeansVis	use K- means color segmentatio n to detect fore- and background	
BlAutoAdaptiveThresholdNir	apply adaptive thresholding on near- infrared image	

Class Name	Description	Section Result
BIClosing	apply closing operation	
BIMedianFilterFluo	apply median filter	
BIAdaptiveRemoveSmallObjectsVis Fluo	remove artefacts	
BIAdaptiveUseFluoMaskToClearOth er	remove artefacts by image compare	

Feature-Extraction

In this step the plant traits will be extracted.

Class Name	Description	Section Result
BISkeletonizeVisFluo	calculate the skeleton by thinning	You can find a complete
BISkeletonizeNir	↑ see above	overview about the calculated traits in the documentation, in
BICalcWidthAndHeight	get maximal height and width	the appendix (<u>User</u> <u>Documentation</u>).
BICalcMainAxis	calculate the main axis rotation	
BICalcColorHistograms	calculates overall properties (#pixels, intensities, NDVI)	
BICalcConvexHull	calculates convex hull based shape parameters	
BICalcAreas	calculates plant area based on segmentation result	
BICalcVolumes	calculates plant volumes (biomass)	

Postprocessing

At last, all the data will be collected and saved in a result data set. Also some results will be highlighted in the result images.

Class Name	Description	Section Result
BIRunPostProcessors	draw analysis results of feature extraction blocks	
BIDrawSkeleton	draw skeleton in result images	
BIMoveMasksToImageSet	copy images in result image set	
BlHighlightNullResults	mark errors and outliers in result image set	