DOCUMENTATION

latest : 2.0

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1. Installation

i] Docker

You can find all the information about installing the docker image on your PC on https://hub.docker.com/repository/docker/sithamfr/growthdata.

Load the docker image
Only tested on Linux systems

- Install docker on your system
- Enter "[sudo] docker pull sithamfr/growthdata:(version)" in a shell
- Verify the image is in your images with "[sudo] docker images"

* [...] : depend on your installation of docker, try first without the sudo

* (version) : currently "1.0", "2.0" or "latest" without the quotes. "2.0" and "latest" are the same version.

Versions : *The differencies between all the versions is only on the color analysis part. For depth sequences, you just have to import your original sequence.*

- **latest/2.0** : You should import your sequence with your objects of interest already segmented to analyse them.
- **1.0** : You should import your original sequence with objects of interest corresponding to green leaves. The segmentation part is inside the app but the quality depends on the similarity with the training dataset.

ii] Source code

To install the source code, be sure you have R installed on your machine. You will also need the following libraries : shiny, shinydasboard, shinyWidgets, shinycssloaders, ijtiff, raster, imager, ggplot2, hrbrthemes, plotly, scales and data.table. To well support those R libraries, you will finally need some Linux libraries. Those required Linux libraries are indicated in the CRAN page of each R package.

2. Getting started

i] Docker

You can find all the information about installing the docker image on your PC on https://hub.docker.com/repository/docker/sithamfr/growthdata.

Load the docker image
Only tested on Linux systems

- Launch the app with "[sudo] docker run --rm -p 3838:3838 sithamfr/growthdata:(version)"

- Open your browser and go on "localhost:3838" or just click on the link gaved in the shell.

* [...] : depend on your installation of docker, try first without the sudo

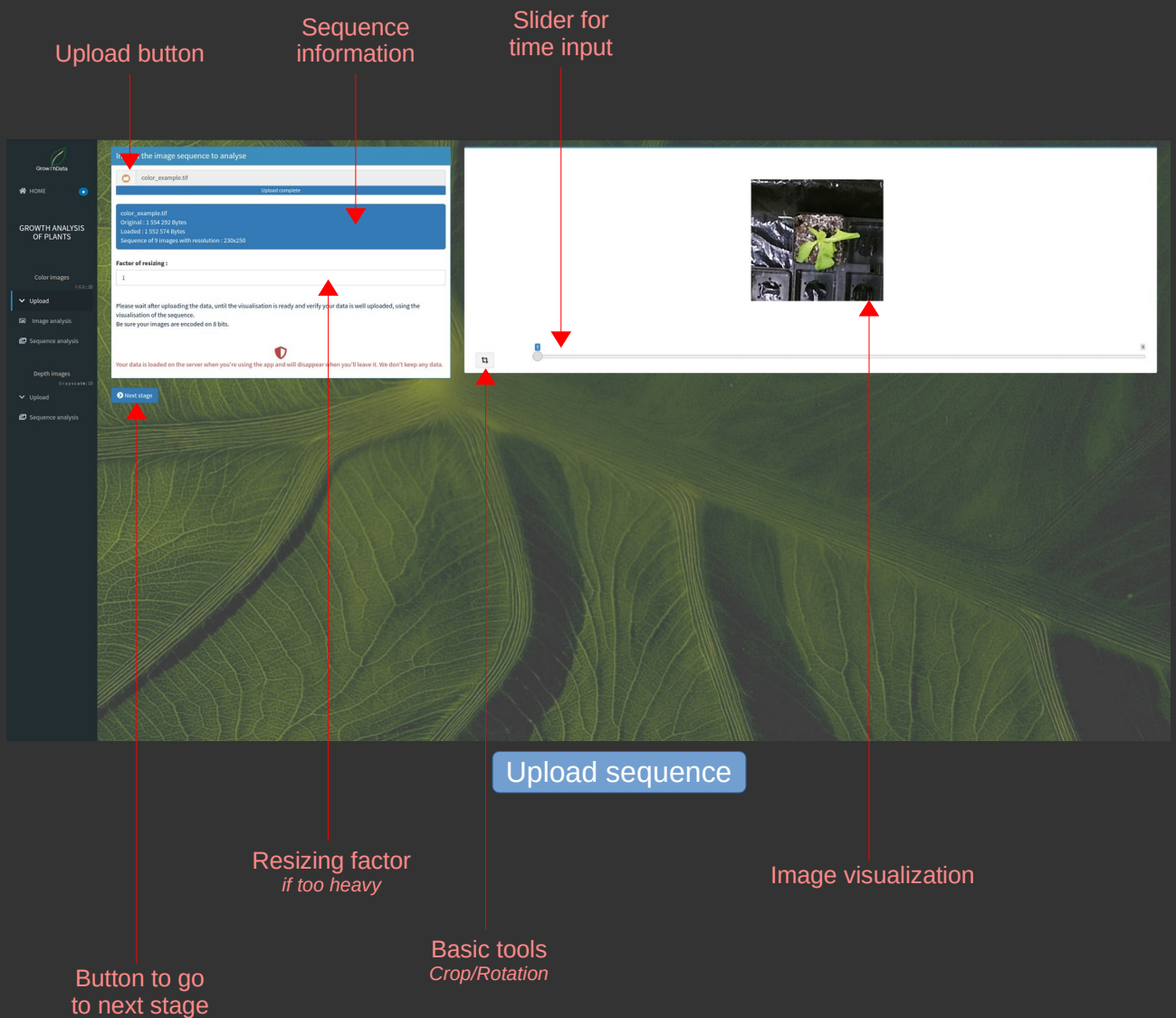
* (version) : currently "1.0", "2.0" or "latest" without the quotes. "2.0" and "latest" are the same version.

ii] Source code

To launch the app, you should type *Rscript .launcher* in your shell located in the *app.R* folder. After a short loading time, the software should be launched in your browser. If not, you should have a link given in the shell : click on it and you will be redirected to the software in your browser.

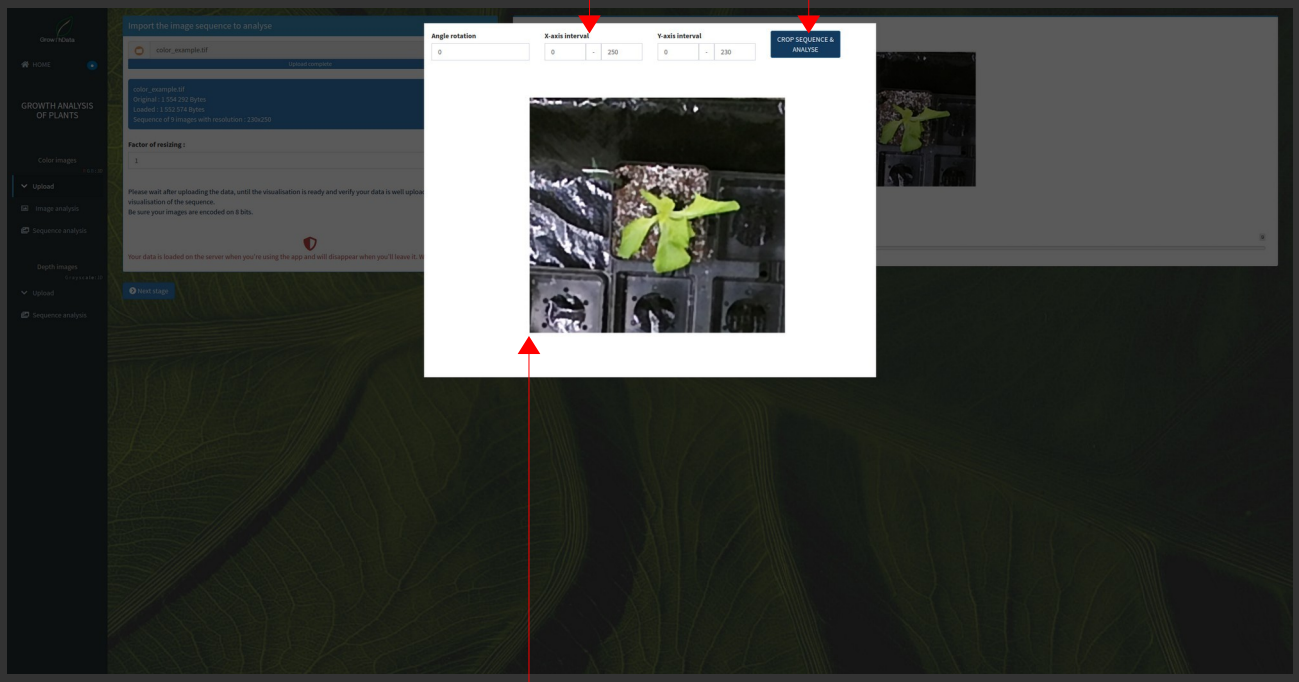
3. Software tools

i] Color sequences



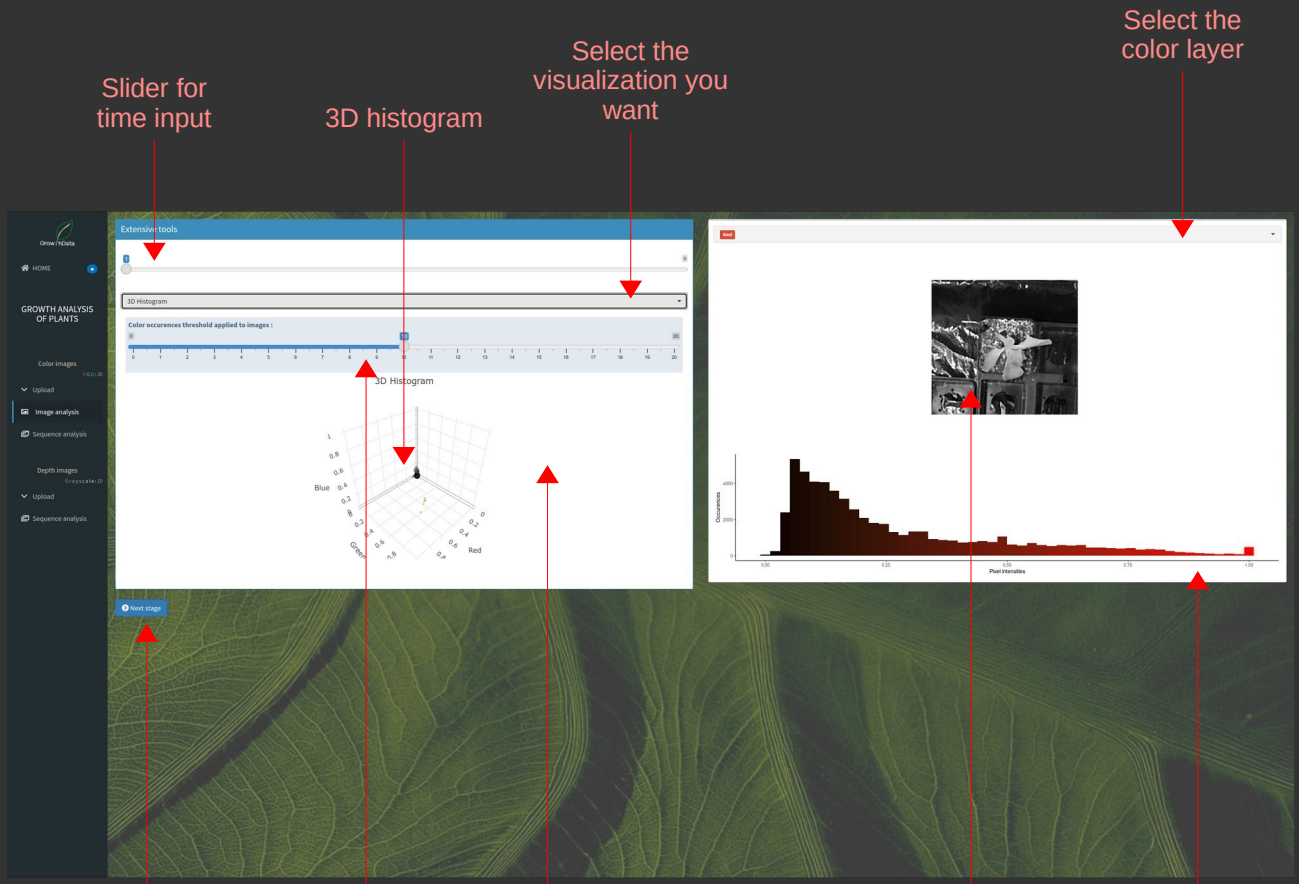
Validate modifications

Modification parameters



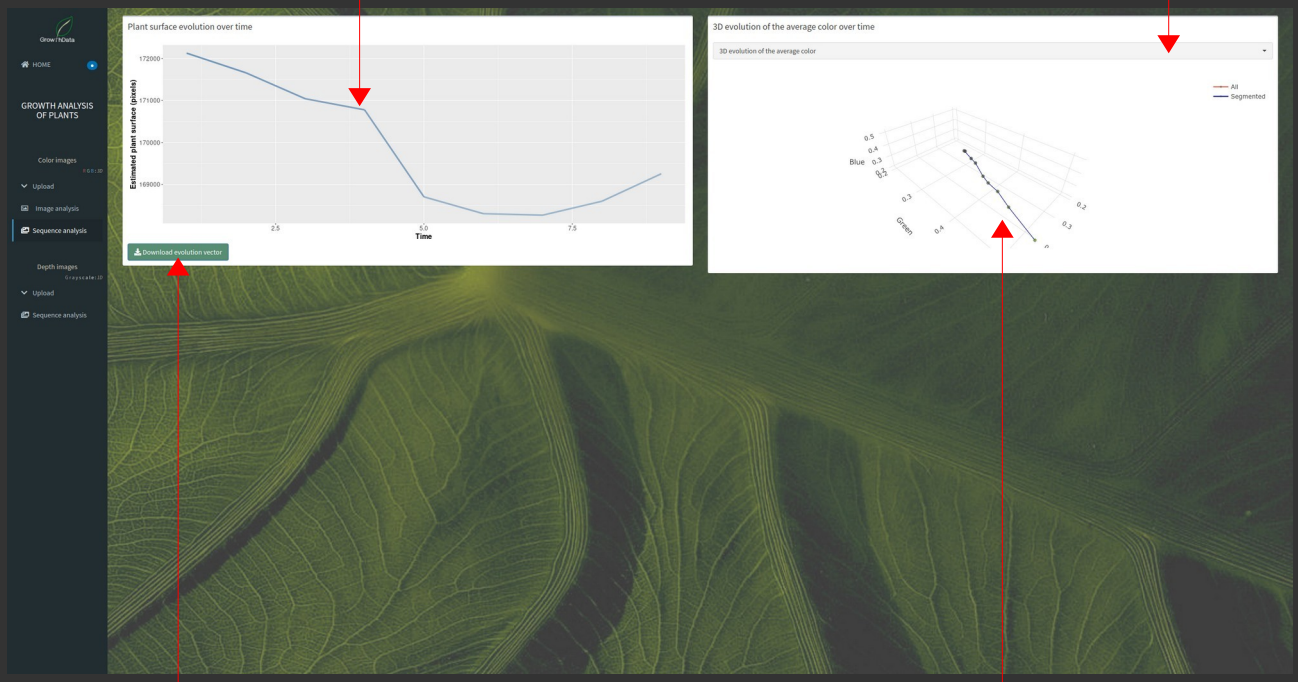
Basic tools

Image visualization


Slider for time input
3D histogram
Select the visualization you want
Select the color layer
Extensive tools
3D Histogram
Color occurences threshold applied to images :
3D Histogram
Blue
Green
Red
Next stage
Image analysis
Slider to select the threshold for 3D histogram
Basic tools
Crop/Rotation
Layer visualization
Layer histogram
Button to go to next stage

Select the visualization tool :
- 3D evolution of the average color
- Difference between two times

Plant surface evolution over time

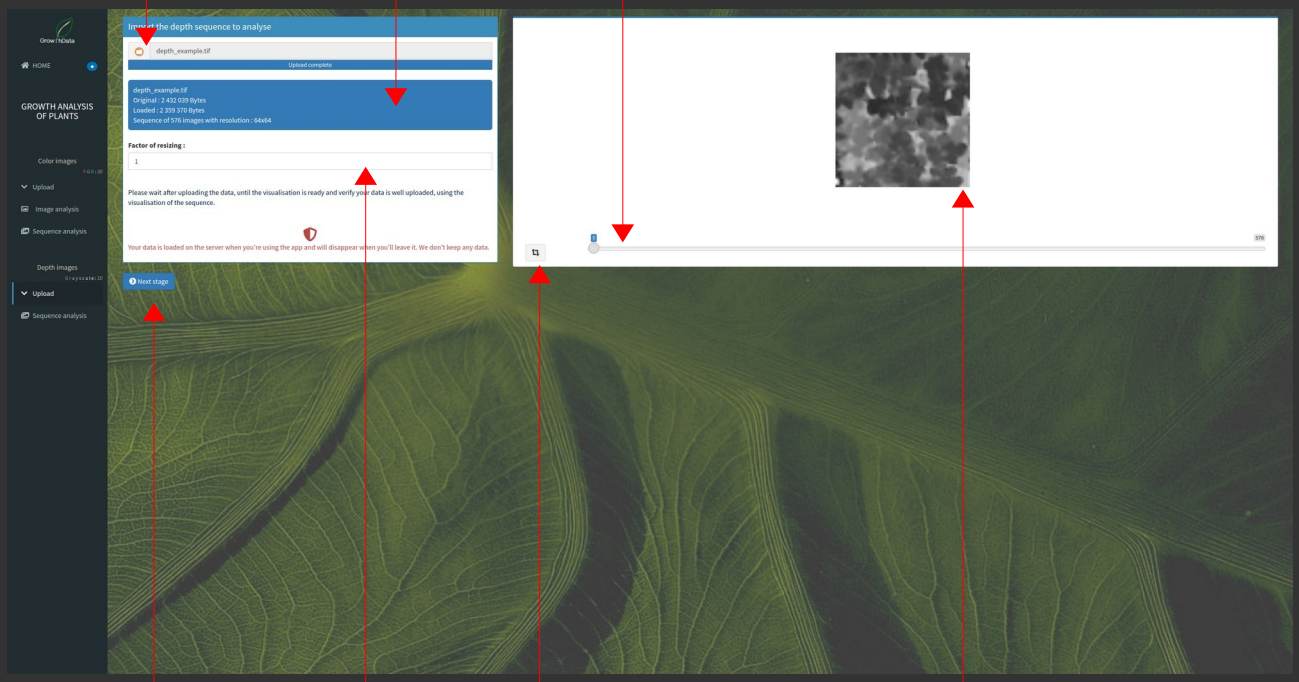


Sequence analysis

Button to download the series of surface

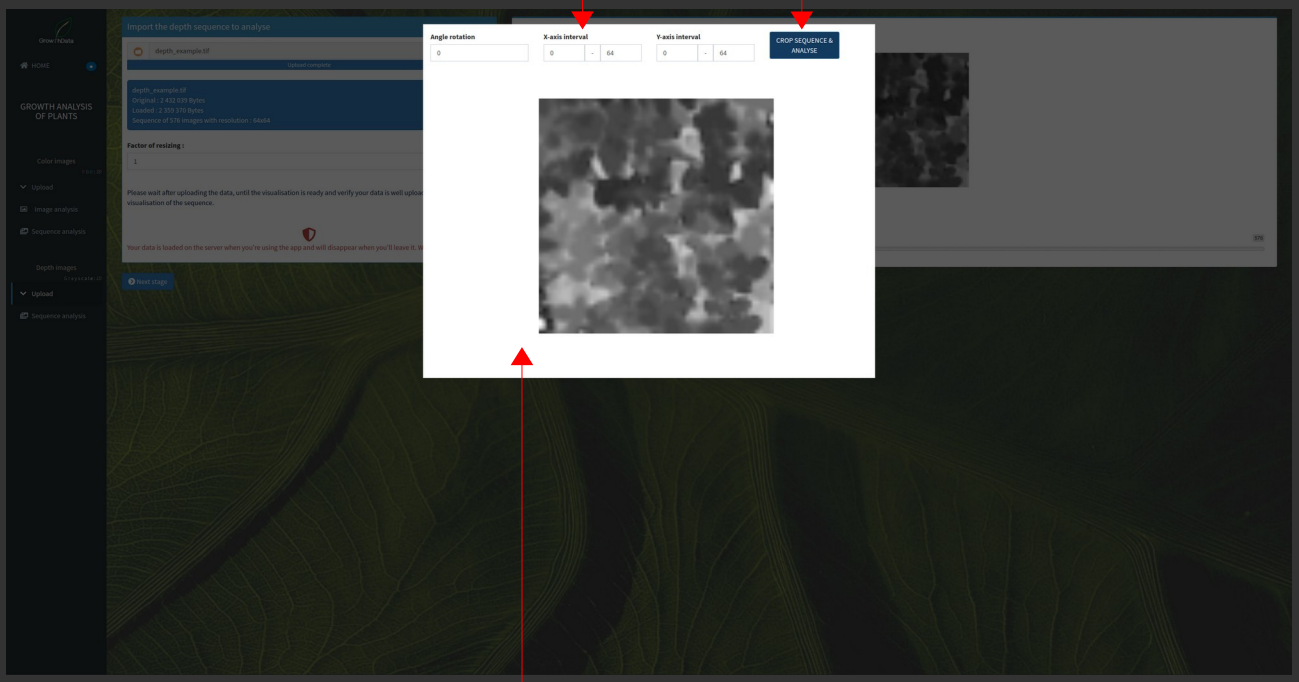
3D evolution of the average color on segmented objects

ii] Depth sequences



Validate modifications

Modification parameters

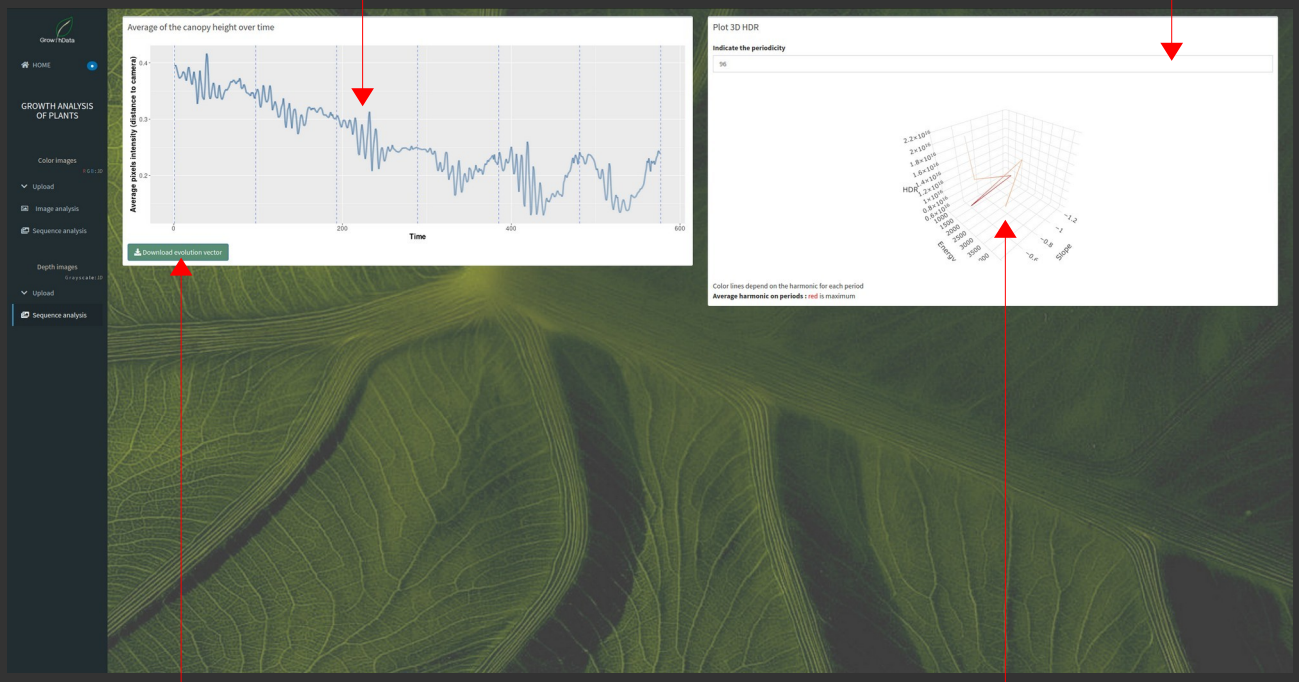


Basic tools

Image visualization

Select the daily
number of acquisitions

Plant distance
evolution over time



Sequence analysis

Button to download
the series of distance

3D evolution of the
frequential features