PHENOSPEX
Smart Plant Analysis

HORTCONTROL 3.12

Manual

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Disclaimer

Information contained in this manual is intended for explanatory purpose only. Due to the continuous product improvement and development program, the specifications are subject to change without prior notice.

PHENOSPEX B.V. is not liable for any damage, loss of profit, loss of confidential or other information, interruption of business, personal damage, loss of privacy, breach of duty, including duties in good faith or duty of care, property or other damage which may arise or related to the use of this manual or the products described herein. This applies also in cases where PHENOSPEX B.V. has been informed of the possibility of such damage.

IMPORTANT TO KNOW

It is essential to become familiar with the software prior to the first experiment. This will enable you to set up your system in a timely manner and to avoid errors in the result data. The most crucial subjects for the successful setup and results are:

- Experiment Setup
- Visualizing and analyzing experiment data
- Machine learning
- Monitor the status of your system

Another important aspect of HortControl are the concepts around which the software is built around. These are explained in detail in Chapter 3.4.1.

Help button in HortControl

Many pages have a question mark icon in either the top left or right corner. Click this icon if you need help understanding the different steps and tools on the page.

We recommend using this manual as a supplement document in addition to the HortControl training provided directly by Phenospex.

Symbols in this document

Since HortControl multiple sensors can be connected. Some chapters in this manual are marked with a symbol indicating if it is only applicable to a certain sensor.

CONTENT

1. ABOUT THIS MANUAL

1.1. Purpose and target group

This manual describes the use of the PHENOSPEX software HortControl. This software is intended for personnel who will be appointed to operate PHENOSPEX equipment.

If you plan to work with the software, please read this manual carefully before starting.

1.2. Manual location

HortControl documentation can be found within the software, under the information bar.

A copy is also available on demand at info@phenospex.com.

1.3. Manual management

We highly suggest keeping at least one printed copy of this manual easily accessible to those working with the software at all times. It is the responsibility of the operator to ensure that other participating personnel are informed about the whereabouts of this user manual.

It is recommended for the manual to always be stored in a location protected from heat and moisture, close to the server on which the software is installed.

1.4. Supplementary equipment documentation(s)

Please also read the user manual of the respective equipment that you will operate along with HortControl and become familiar with it as well.

IMPORTANT

It is in your best interest to get familiar with this manual, and to set up and simulate various test experiments prior to the designated operations. Incorrect setup and use could result in faulty result data. If something is unclear, or you would like more information, please ask your superior or contact the manufacturer.

2. INTRODUCTION

2.1. Description

HortControl is an operating system for plant data management that comes with a web interface to set up experiments and analyze data acquired by the Phenospex product suite, including PlantEye 600 scanner(s), DroughtSpotter, and Climate data loggers.

With HortControl, you can:

- Graphically create, adjust and save experiments with various parameters
- Display and analyze data
- Download raw .ply files
- Download (aggregated) data
- Create predicting models with the machine learning tool

2.2. Installation

HortControl does not need to be installed on your computer. It is a web-based software, which is Google Chrome compatible. We highly advise you to upgrade to the latest Chrome versions prior to use.

The minimum HortControl requirements:

- Web-server/storage infrastructure (Provided)
- Internet connection (Mandatory)
- Actual software code, which is installed on the web server (Provided)
- Data administration/ software maintenance services

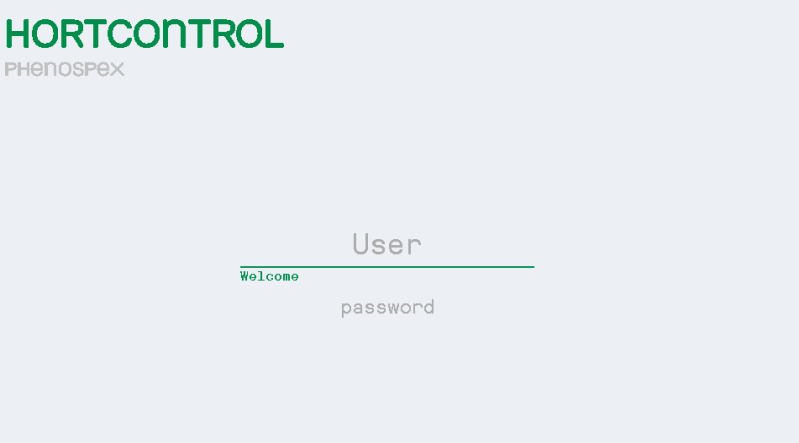
3. WORKING WITH HORTCONTROL

3.1. Access HortControl

If you have a direct Wi-Fi connection with your Phenospex product, you can easily access HortControl by typing “hortcontrol” into your browser. **When you are not connected to Wi-Fi**, but to your local network, you should use the IP address that was assigned to your product by your local IT department.

3.1.1. Login

With the first connection, a login prompt will appear and you will be asked for your credentials (username and password). On successful login, you will be directed to the homepage. After closing your browser, you can still access HortControl without authentication for the next hour from your machine.



3.1.2. Roles & Users

There are two user roles. Each role has a default user and password:

Admin The default admin user is *psx-admin*. This user can access the system board, where new user accounts can be created, passwords changed, and admin rights adjusted. The default password for this user is the username itself – *psx-admin*.

User The default user is *psx-usr*. This user cannot access the system board and has the most limited rights. The default password for this user is the username itself – *psx-usr*.

IMPORTANT

If you forget your password, you should contact your administrator. He can reset your password to become the same as your username. Therefore, if your username is “Dirk”, the administrator can reset your password to “Dirk”. You can then login with these credentials and change your password.

3.1.3. Safe system shutdown

When you need to unplug your device from the power supply to move, please make sure to take the following actions into account for a safe system shutdown:

1. Make sure that the last file you scanned has been processed. Either check if the data is visible in the HortControl data board. Alternatively, wait for at least 5 minutes after the last scan to power down the system, to ensure that all data has been processed.
2. Make sure that all reprocessing jobs are finished. In the HortControl experiment board, check that there are no active reprocessing jobs

When those two checks are done, you can now turn off the system by switching off the power button.

3.2. Navigating through HortControl

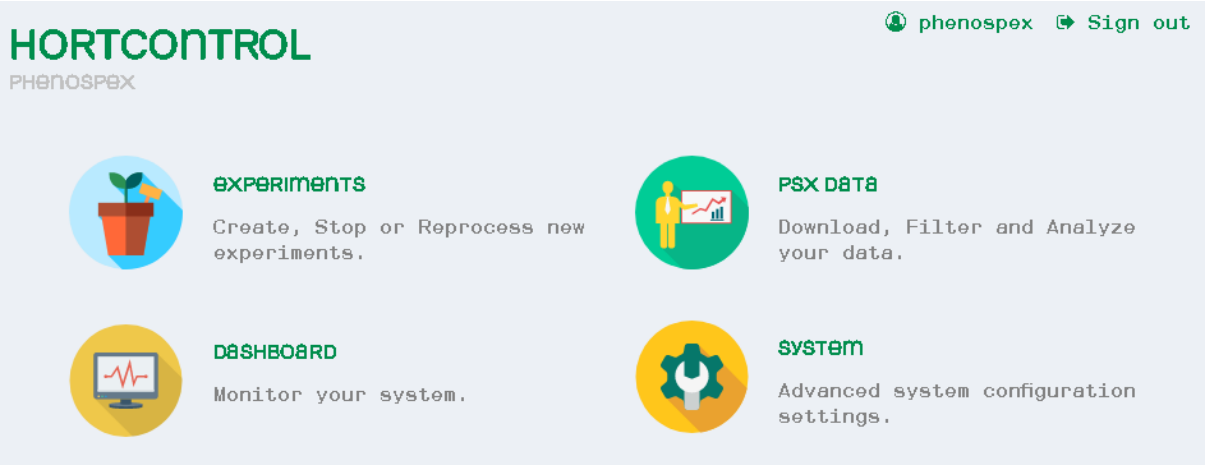
HortControl consists of an initial **Homepage** and multiple **Boards**. In turn, each board combines different functionalities or ***Modules***, which consist of one or more visualization options or *Views*.

The two most important structural concepts to understand are:

- User Interface: Board(s), Module(s) and View(s)
- Experiment setup: Experiment, blocks and splitting

3.2.1. Homepage layout

Once successfully logged in, you will find yourself on the homepage from which you can access any of four boards: **Experiments**, **PSX Data**, **Dashboard** and **System**. Once one of the boards is selected, you can easily switch to another from the HortControl drop-down menu in the upper left corner. You can always go back to the homepage by clicking on **HORTCONTROL** in the upper left corner.



Experiments. In this board you can manage, create or stop your experiments. For more information please refer to section 3.3.

PSX Data. On the **PSX Data** board you can access your experimental data, as well as filter, analyze and visualize it. This is described in detail in section 3.4.

Dashboard. The dashboard acts as the control room of your system. Here you can consult the system's current state. Please refer to 3.5 for additional information.

System. The System board is only accessible by admin users. It has multiple system management functions concerning system layout, database management, user management and advanced PHENA settings. The details about this board can be found in section 3.6.

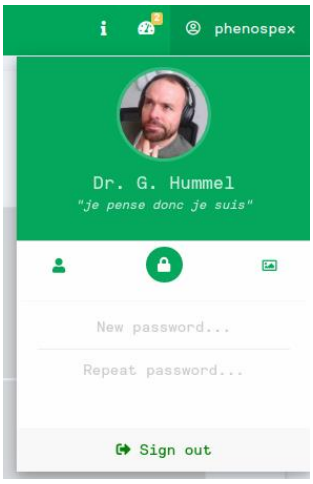
3.2.2. Board(s) layout

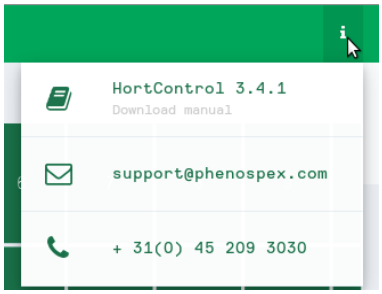
Once selected, each board has the same structural layout and consists of:

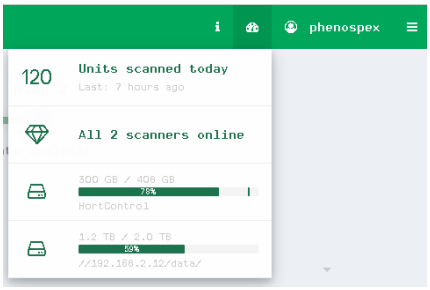
1. Navigator with board drop down (top-left) to easily access the homepage or other boards
2. Module sidebar (left) to easily navigate to the different modules
3. Information bar (top) to adjust user details and to view a summary of the system status
4. Main view (central) to check the core information/functionality of your selected module
5. Settings sidebar (right, optional) to adjust settings of your current module view

In the information bar you can:

- Have a quick glance at the system status
- Adjust your user image, name and password
- Download the manual and find PHENOSPEX support contact details



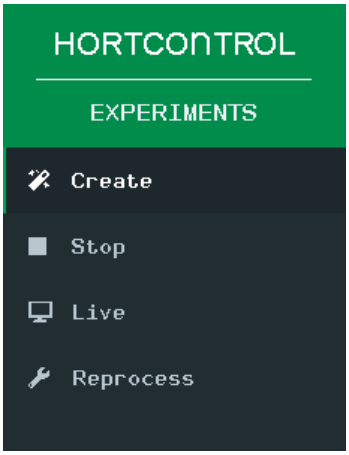




3.3. Experiments Board

In HortControl, there can be one or multiple experiments running on your platform simultaneously, all of which can be managed independently within the **Experiment** board. This board consists of four modules:

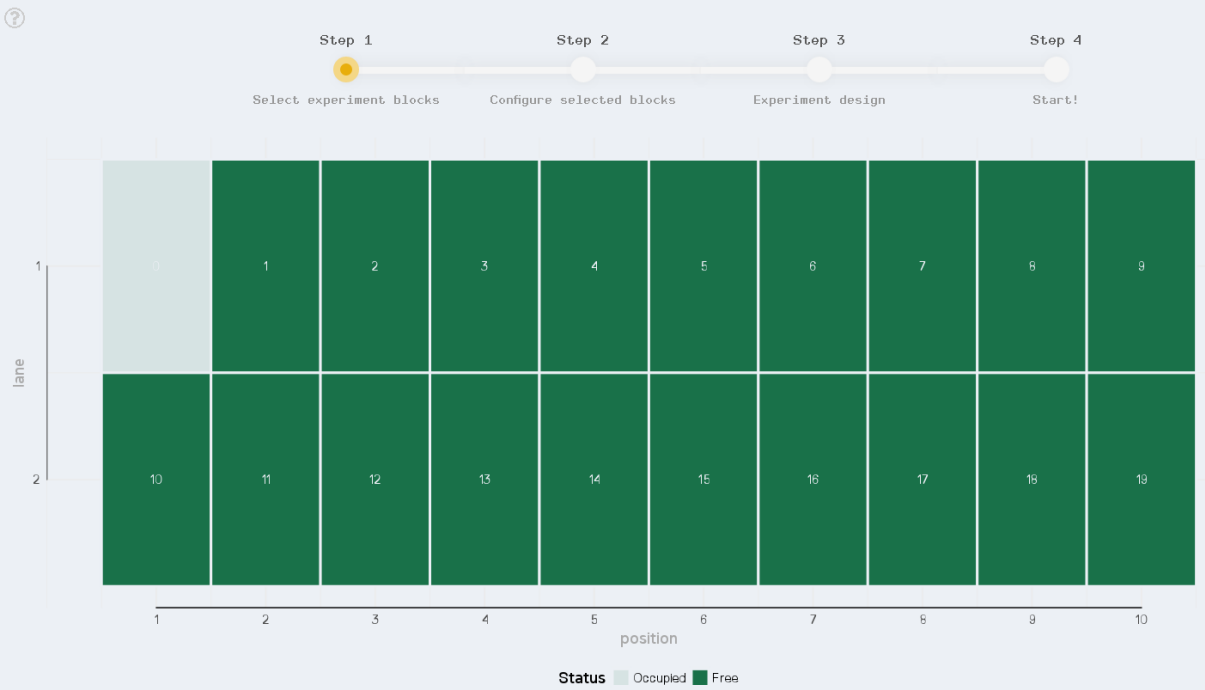
1. **Create**, New experiment setup
2. **Stop**, Stop active experiments
3. **Irrigation**, update irrigation schedules for DroughtSpotter
4. **Live**, Select block for next PlantEye scan
5. **Reprocess**, Adjust PHENA settings and reprocess PlantEye scans



3.3.1. Create Module

Creating a new experiment involves telling your devices how to interpret your physical platform, and allocating plants (with their respective genotype and treatment information) to specific locations on your platform.

The main view of the ***Create*** module (image below) shows your system layout, with available blocks (colored green), and occupied by active experiments blocks (colored gray).



Setting up an experiment involves several steps (please note them on the top of the main window in the image above). The numbers for each step can differ when more than one sensor is linked to your system:

Block reservation - Step 1

1. **Select experiment blocks,** Reserve blocks for the experiment by selecting free (green) blocks

Product & Experiment configuration -Step 2 & 3 or Step 2,3 & 4

2. **DroughtSpotter irrigation** (*DroughtSpotter*), setup the scales & watering regimes
3. **Block splitting** (*TraitFinder, MicroScan, FieldScan*), split blocks into units
4. **Experiment Design**, Add genotype and treatment information, meta data, to the units

Finish setup – Step 4 or 5

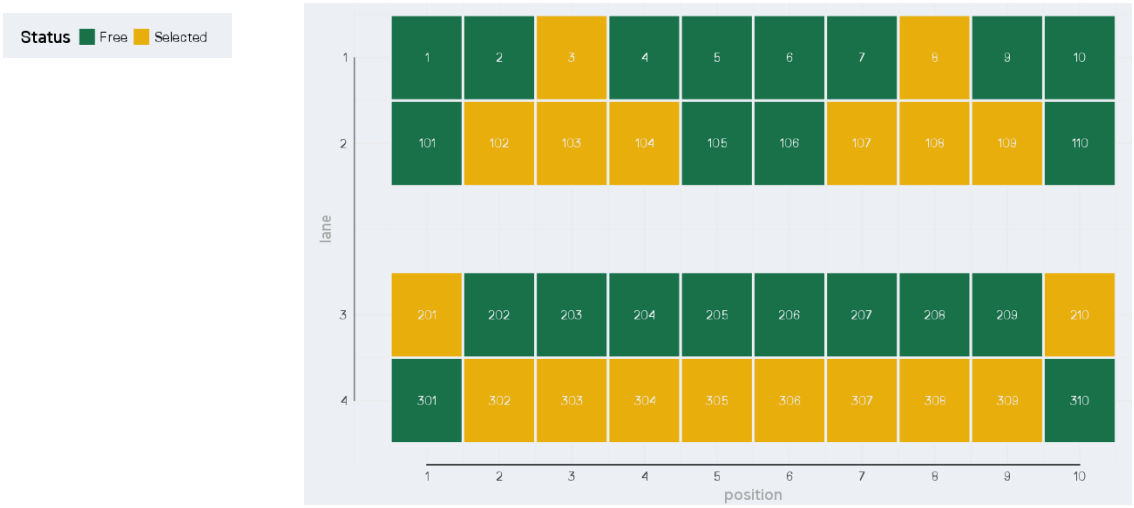
5. **Start** Check & Upload your experiment and start it

When each step is completed, the step circle will change its color from yellow to green. Only then, you can proceed to the next step. An available, but unfinished step highlighted in gray. A product configuration step can also be skipped when the selected blocks are not linked to a product of the corresponding step. The step will become inactive, and is not selectable.

3.3.1.1. Select experiment blocks

In the first step, you reserve blocks for your new experiment. Once you click on any green/available rectangle it will switch its color to yellow. This block is now reserved for your experiment. If you want to add blocks to this selection you hold the “Ctrl” button while dragging or clicking on the other blocks. If you want to remove

blocks from your selection you hold Shift, while dragging (releasing Shift first) or clicking the other blocks. Double clicking will clear your complete selection.

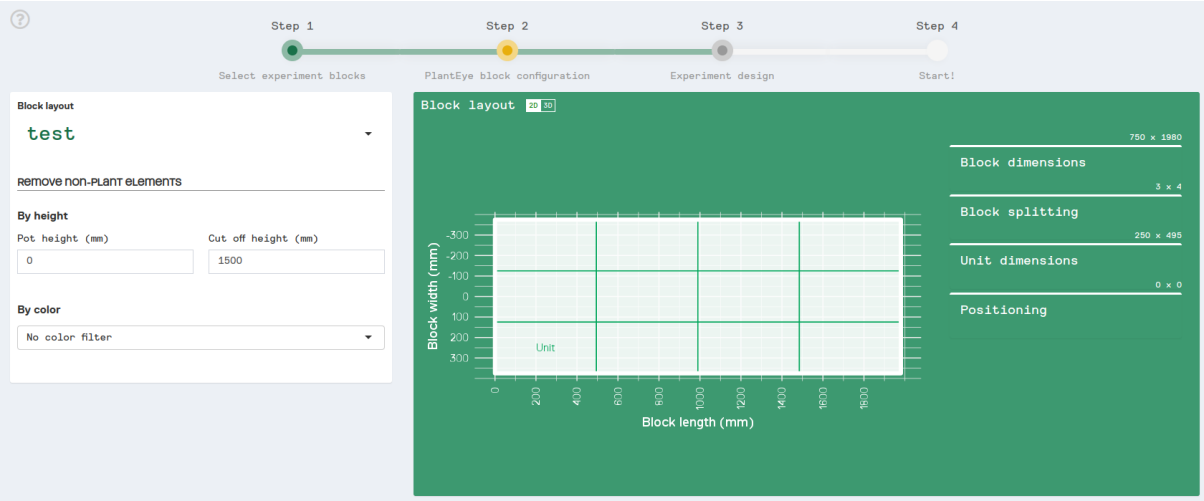


Now that the blocks are selected, the first product configuration step becomes available, depending on your system it can be **PlantEye block splitting**, **DroughtSpotter irrigation** or both.

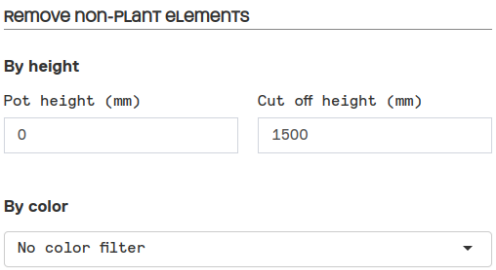
3.3.1.2. PlantEye block configuration

In this step you can tell HortControl how the PlantEye scans that will be created in your new experiment need to be converted to separate digital plants on which HortControl can calculate digital plant parameters. Therefore this step allows you to define (1) how the background needs to be segmented from your plants and (2) how to separate different plants in one scan.

Once you select/reserve a block in Step 1, and go to the step: **Configure selected blocks**, you will be prompted to the next window (shown below).



Separate plants from background



First, HortControl allows you to define how plants need to be separated from background material like soil, supporting structures, pots, table, floor,... in future scans. There are two major options that are offered under the “Remove non-plant elements” section. The first is to use the power of 3D, i.e. the height to tell between which height boundaries (pot height and cut off height) you expect the plants to be. To finetune the background separation further, there are two more tools that use the power of color to help you remove background that could not be filtered away with height, i.e. manual color filter and a training-based color filter. The selected separation options for height and color will be combined to segment plants from background. You can always look at the effect in the 3D view (see image below).

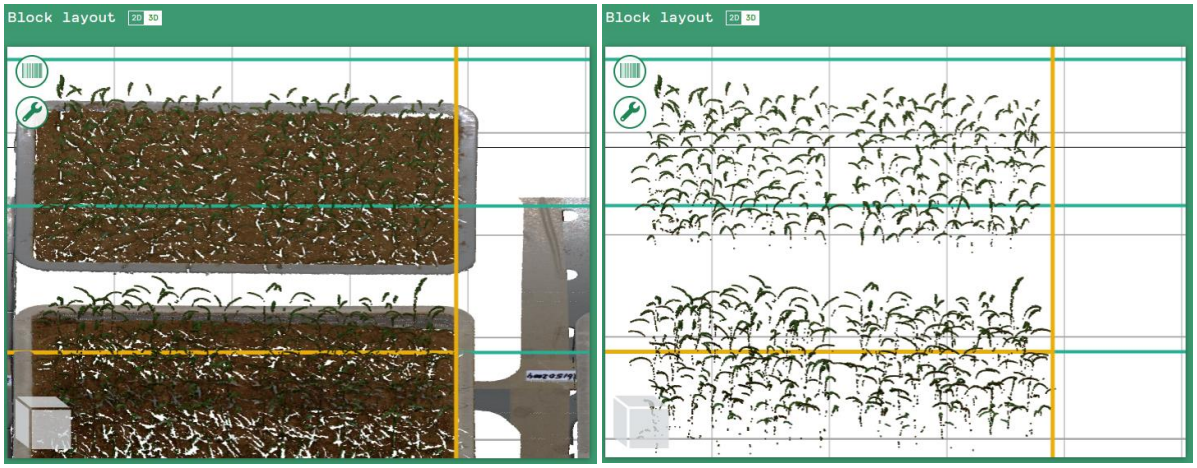
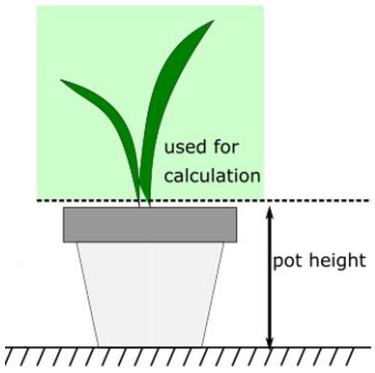


Figure: 3D view to see what effect the height and color options have on the separation of plants from background. Left: pot height:0mm without color filter. Right: pot-height:84mm with training-based color filter.

Separate plants from background by height

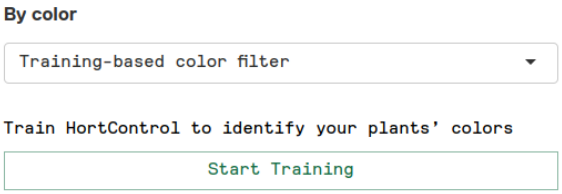
Define pot height. The pot height (in mm) is the height at which the plant starts. Everything below will be ignored during processing of the 3D file. Measure your pot with a ruler, and set the pot height 3 to 5 mm above the measured height. This way you will ensure that the rim of the pot is extracted from the image. When the top of your pots are not always well aligned horizontally then use it in combination with the training-based color filter to make sure the rim of your pots is always removed if it extends above the pot height.



Define cut off height. The cut off height (in mm) is the maximum height at which the analysis of plant data should end. Everything above will be ignored during processing of the 3D file. The combination of pot height and cut off height is interesting when you want to focus your analysis to a specific region of your plant. If you do not want to focus to an upper threshold then set the cut off height to a high value, e.g. 2000mm.

Separate plants from background by color

Training-based color-filter. When you have defined the pot height it can still be that there are parts you want to remove, like pot rims or supporting structures. For that HortControl offers a tool where you can train the software what background and plant material is. For that purpose, click the training-based color filter from the “By color” drop-down. Clicking start training will guide you through training and creation of the filter. HortControl will ask you to select a scan to train and ask you to mark a few plant and background points. With that input it will propose a separation and ask you to validate if it is good or not. You can always add more points during the training process. When you are not satisfied with the separation HortControl proposes you can always cancel and select “no filter” again. When you are satisfied you can accept and the filter is selected and can be reviewed for the rest of the selected blocks in the 3D view.



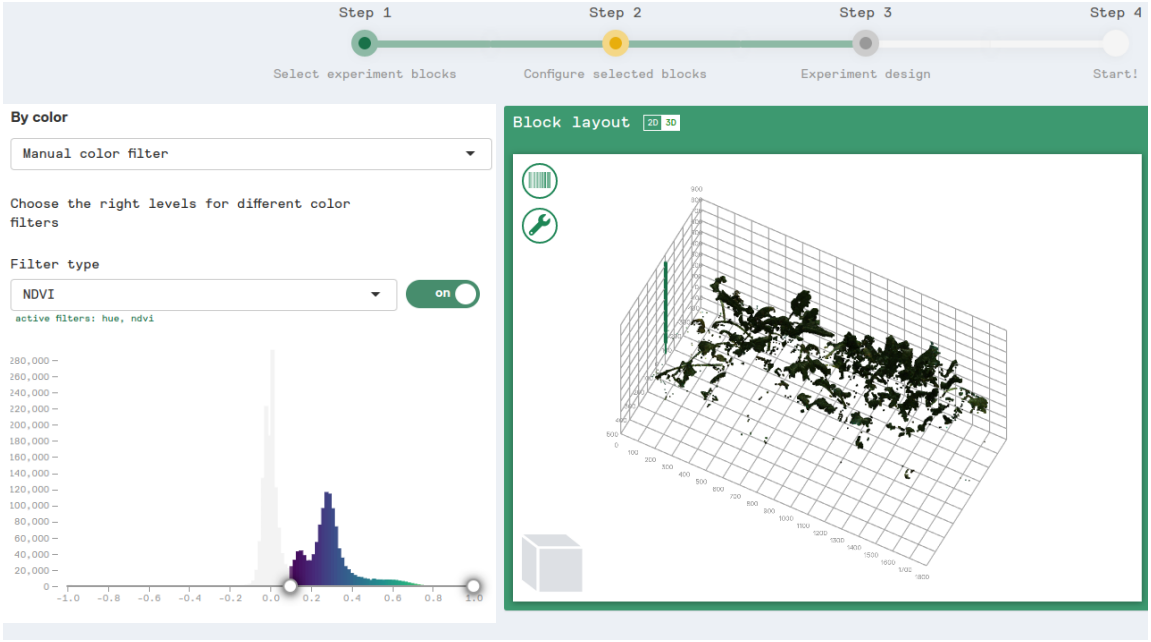
IMPORTANT

The training-based filter will show you the full image without taking into account the pot height and cut off height settings. Therefore always focus on the remaining background you want to filter away, and do not pay attention to the background that is under your pot height or above your cut off height as this will be filtered anyway.

Manual color filter. Optionally, you can also add a manual color segmentation processing step. While the training-based color filter uses and combines all the spectral data, you might want to keep it simple and manually create a color filter based on the supported spectral indices. With this step you can choose which parts of the different color indices you want to keep for calculating plant parameters. For example (image below), you can choose to only include parts of the plant that have an NDVI color range of 0.2 - 0.8, thus, filtering out all other color ranges before calculating the plant parameters. You can choose from a selection of color indices, and further utilize a histogram to select the desired range. For an optimal color segmentation, you can use multiple color indices filters simultaneously.

1. From the dropdown list select on which color parameter you want to filter
2. press the button “off” next to it to enable the filter for this experiment
3. Click and hold the slider on the bottom of the histogram (the small circles) to select the values you want to keep. The 3D file on the right will update accordingly.
4. Optionally you can enable multiple color filters to optimize

Currently, color segmentation tool works only in Google Chrome browser.

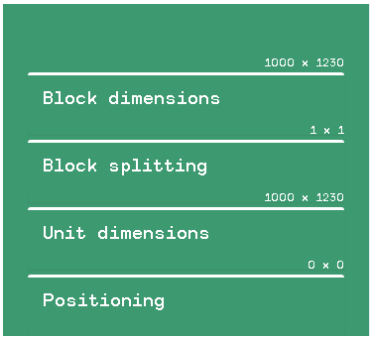


Once you have named your block layout and entered your pot height, it is time to adjust the block layout by changing values for block splitting, unit dimensions and positioning. These can be found on the right side of your “Block layout” window (shown on the right).

Separate plants from each other

After defining how to split background from plants, we can define how to separate plants in a scan.

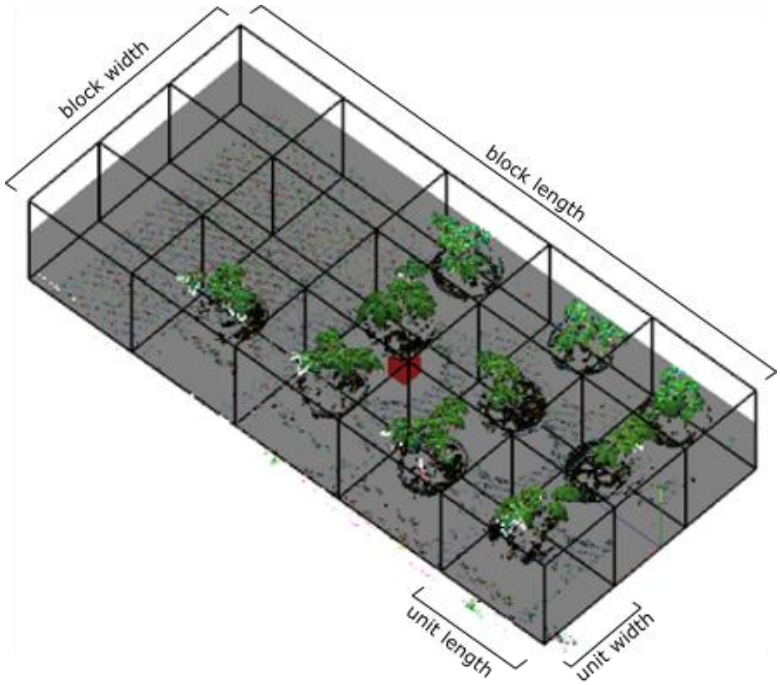
For that , you define a block layout name first and save it. The saved block layouts can be reused in later experiments. To create a new block layout, you enter a new name first, e.g. *NL Tomato*. Click on the area under “Block layout” on the left side, type in the name and press “Enter”.



IMPORTANT

When dealing with a large system (multiple lines, hundreds of plants and/or multiple barcodes) it is advised to include barcode numbers associated with this block within your block layout name.

Block dimensions. It is advised to only change this setting if you are comfortable with the system. In most cases the block dimensions have been pre configured by Phenospex, and you do not need to change them. This setting defines the scan area from the origin along the block length and block width (see image below).



Block splitting. Here you can define how many units you want to create, i.e. how many unit rows and columns the scan should be split into. As an example, in the image on the left, there are 3 rows and 5 columns, therefore, your block splitting in this case will be 3x5. The “auto-split” button will calculate the maximum number of unit rows and columns that can fit in the scan area with the given unit dimensions and positioning.

Unit dimensions. Defines the size (length and width) of each unit (see image on the left for example). The “auto-size” button will maximize the unit size for the given number of units and positioning inside the scan area.

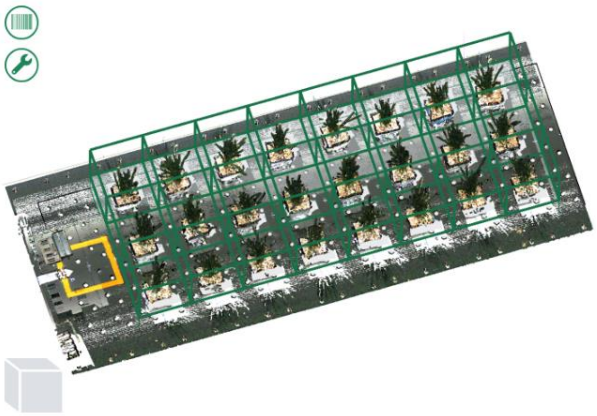
Positioning. This is a starting point for scanning as defined on your visual block. It is defined as the distance between the first unit and the top left corner. You can use the “center” button to automatically adjust to the center of your scan area.

When you are satisfied with your settings you can click the “create” button and the layout will be saved and ready for use immediately and in the future.

To help you figure out how to get the right settings as quickly as possible, we present two common use cases.

3D splitting tool

Incorporating the 3D layout tool will enable you to check the validity of your settings more accurately than with 2D (used in the 2 examples above). Here, the last scan to create a visible aid for setting up the blocks (image below).



Select the barcode for which you want to adjust the block setting. The last 3D scan file for that barcode is then loaded. In the bottom left there is a gray cube with 3 planes visible. You can click any of the planes to move to the respective view (side, front, top).

Apart from the block splitting settings explained above, there are a few other settings to optimize the view for splitting. These settings can be found by clicking the icons in the top left corner (image below).

Time aggregation

x Block
Select the block of which you want to see the latest scan.

x Boundary
Toggle to display the 3D points that fall outside the splitting area.

x Resolution
Sets the resolution of the requested scan. A high resolution will demand more graphical power from your machine and will be slower as the file has to be downloaded from the server.

x Color
Selects a color map.
Color. Will display the color as measured by the scanner
Height. Will color the 3D points by height. Different color maps can be selected to optimize the visual cue.
Position. Will color the 3D points based on the unit they belong to. The colors assigned to a unit follow a 2x2 checkerboard pattern.

3.3.1.3. DroughtSpotter irrigation

Before each experiment starts, it is important to check if the scales are empty, cleaned, **set to zero** and **flushed**.

This product configuration step is available after selecting system blocks in step 1 and allows you to design the DroughtSpotter irrigation schedule for every selected unit in your new experiment. This step allows you to download an irrigation schedule template file based on your currently selected units and upload one or more irrigation schedule files. An irrigation schedule file contains a set of instructions that DroughtSpotter understands to build the irrigation schedule for the selected units.

In the next pages we will give detailed explanations about:

1. Irrigation schedule template
2. Setting the Header
3. Constructing an Irrigation program
4. Visualizing the irrigation program

How does DroughtSpotter irrigation work?

DroughtSpotter supports 5 different irrigation modes which you can chain in hourly mode blocks to create a flexible irrigation schedule for your plants. Each mode performs a specific irrigation task that is different from the other modes.

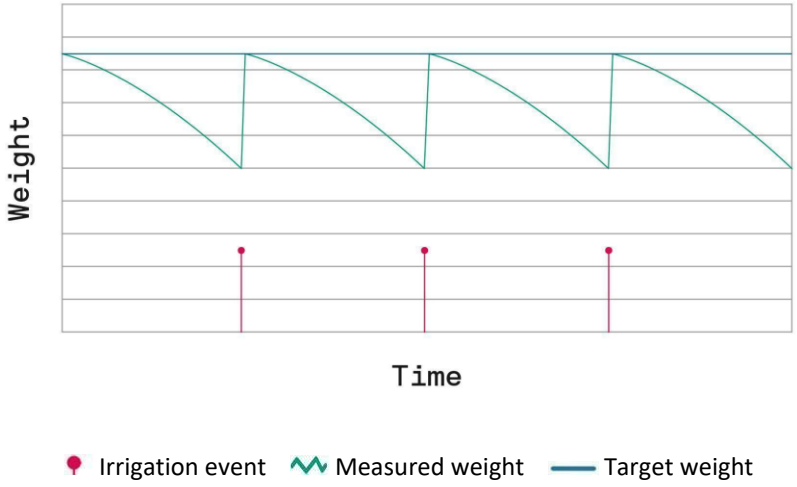
The five irrigation modes are:

1. **Hold mode** – Target weight is maintained by watering at pre-defined time points
2. **Fixed mode** – Fixed water amounts are given at pre-defined time points
3. **Deviation mode** – Target weight is maintained by watering when lower threshold is reached
4. **Copy mode –** Link irrigation of many plants to the weight of one master plant.
5. **No irrigation mode**

- ***Hold mode***

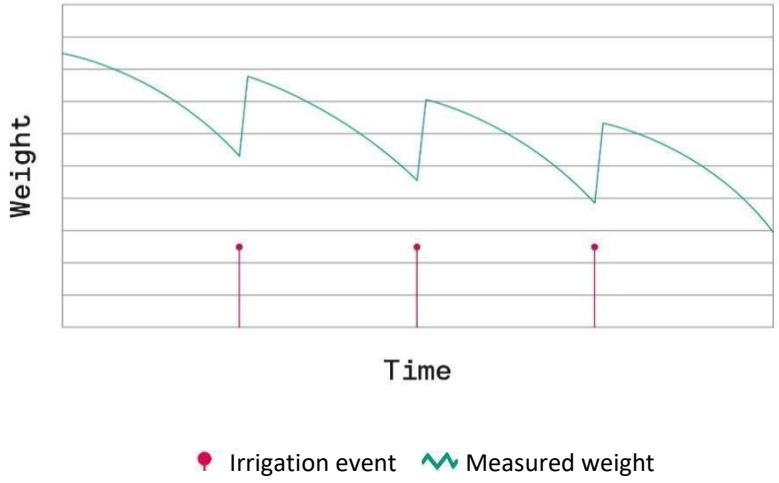
In hold mode a plant is watered at a defined time per day to a certain target weight. The image below illustrates an example for an irrigation in “Hold” mode. The blue line represents the configured target weight for the plant. The green line shows the actual weight of the plant.

There are three watering times defined. During these times the plant is re-watered up to the defined target weight. The amount of water given is equivalent to the difference between target weight and weight before the watering event.



- ***Fixed mode***

In “Fixed” mode a plant is watered at defined times per day with a defined amount of water. The image below illustrates an example for an irrigation in “Fixed” mode. There are three watering events defined. During these events the plant is watered with a fixed amount defined in the experiment settings. If the plant transpires more water as it receivers, the overall weight will reduce over time. In “Fixed” mode a maximum weight can be specified to avoid over-flooding.



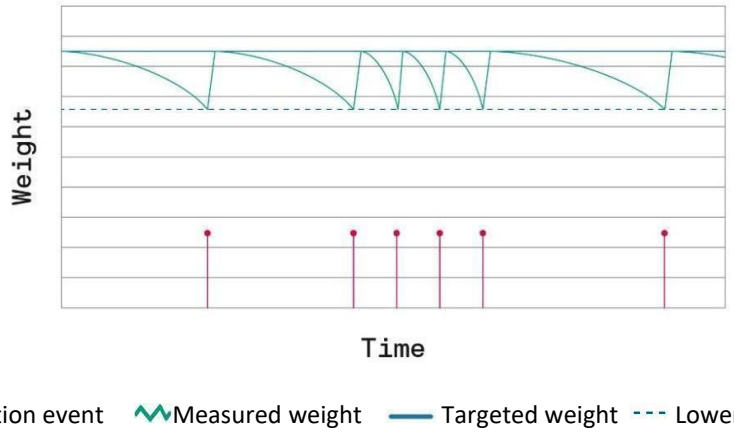
- ***Deviation mode***

One of the most powerful irrigation modes is the “Deviation” mode. The same as in “Hold” mode, the plants will be watered to a target weight. Other than in “Hold” mode, the plant will not be rewatered at a specified time but whenever a threshold is reached. This way the plant can be kept at a very narrow and controlled water level.

The image below is an example for irrigation in “deviation” mode. The blue line represents the set target weight for the plant. The green line shows the actual weight of the plant. The dotted line represents the lower

threshold at which the irrigation needs to be triggered. Whenever the actual plant weight is lower than this threshold it will be rewatered up to the target weight.

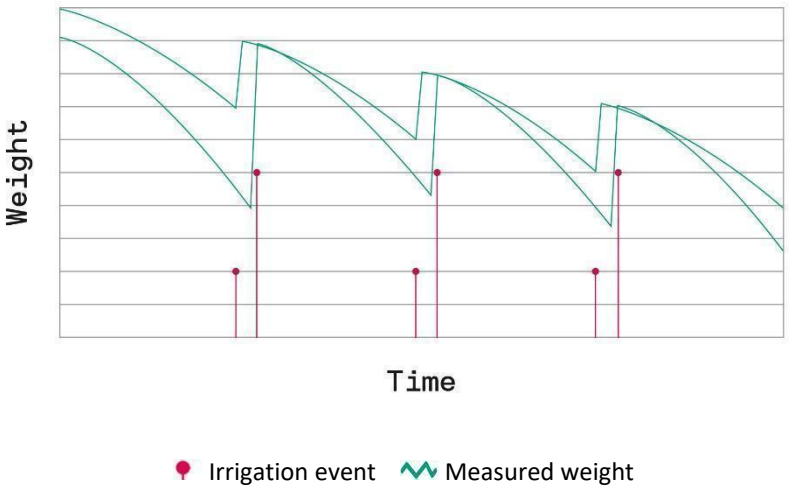
The amount of water given is equivalent to the difference between the target weight and the weight measured before watering.



- ***Copy Mode***

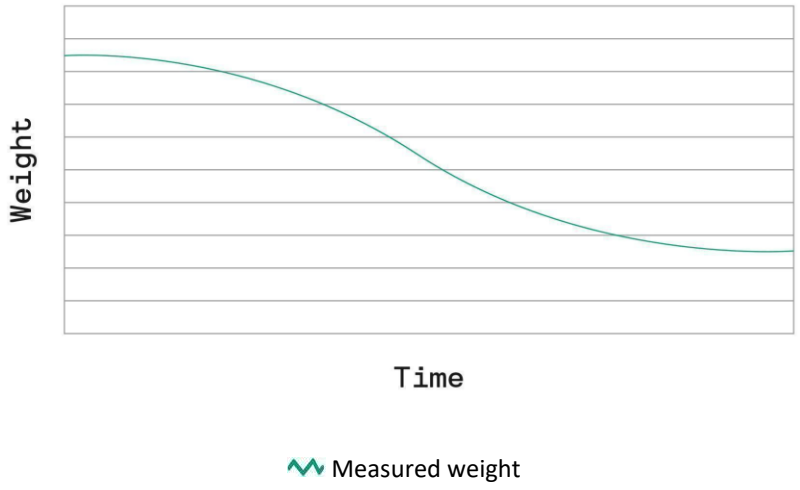
In "Copy" mode there are **pattern** and **copy** plants. Pattern plants behave like in "Fixed" mode. They will receive a defined amount of water at the defined time points. A copy plant is linked to a pattern plant and will follow the weight of this plant.

The image below shows an example of two plants, one as pattern and the other one as copy. The pattern plant uses more water than it receives on "Fixed" mode and slowly loses weight. The copy plant is rewatered at defined time points up to the weight of the pattern plant. If the pattern plant has less weight as the copy plant during the irrigation time, there will be no water added.



- ***No Irrigation Mode***

In “No Irrigation” mode a plant is not watered. The weight data will be recorded regardless of the missing irrigation.



These modes can be combined or alternated to fit your irrigation needs.

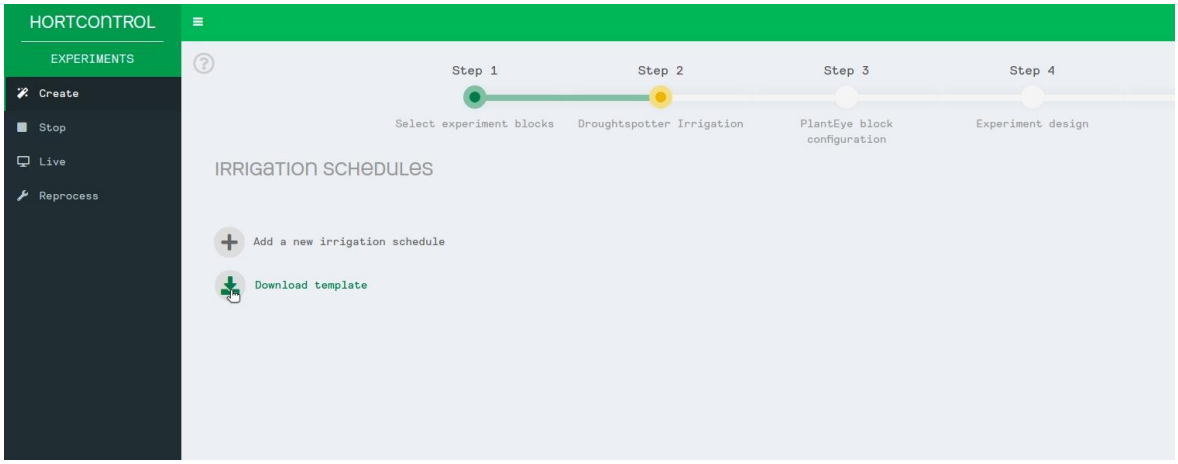
How to design an irrigation schedule?

In order to instruct DroughtSpotter how to irrigate your plants we need to create an irrigation schedule document where we chain the irrigation modes and specify a few other irrigation settings such as irrigation targets and irrigation timing. The document is built up by two major parts:

- A header part for the general irrigation settings
- A program part for specific irrigation instructions and targets per unit

These irrigation schedules can be uploaded in HortControl.

To get started, you can also download an irrigation schedule template in HortControl, click the download button in the DroughtSpotter Irrigation step. The file has CSV format and can therefore be opened in Excel.



- ***The irrigation schedule header***

The "Header" section contains multiple parameters that defines the irrigation behavior in the experiment. *Please note that some of the parameters are only used in certain irrigation modes*. The parameter names are listed in the first column of the spreadsheet, whereas the corresponding values are in the second column. Some parameters can have multiple values. For parameters with multiple values write the first value in column 2, the second value in column 3 and so on. Example: Irrigation_time_hold has values at column 2 & 3 in the table below.

Name	New irrigation scheduled	
Irrigation_times_hold	16:00	21:00
Irrigation_times_fixed	12:00	18:00
Irrigation_interval_fixed (days)	1	2
Irrigation_times_copy	13:00	
Irrigation_interval_copy (days)	1	
Irrigation_at_deviation_from_target (%)	5	
Error_tolerance_for_irrigation (g)	2	
Max_weight_fixed_or_copy (g)	300	
Max_water_per_irrigation_step (g)	200	
Max_irrigation_steps	10	
Interval_irrigation_steps (minutes)	1	
Starting_time_program	2021.04.08 05:00:00	

The following header parameters can be configured for an irrigation schedule:

Name. The name of the irrigation schedule. Each schedule name has to be unique per experiment.

Irrigation_times_hold. The times at which an irrigation should be started for "Hold" mode. The time format is HH:MM (H = hour and M = minute) using the 24-hour clock. One cell with a starting time is needed per "Hold" mode in the program. Setting up this program is defined in the chapter "Irrigation behavior values".

Irrigation_times_fixed. The times at which an irrigation should be started for fixed mode. The time format is HH:MM (H = hour and M = minute) using the 24-hour clock. One per fix mode in the program is needed. One cell with a starting time is needed per fixed mode in the program. Setting up this program is defined in the chapter “Irrigation behavior values”.

Irrigation_times_copy. The times at which an irrigation should be started for copy mode. The time format is HH:MM (H = hour and M = minute) using the 24-hour clock. Multiple values are allowed (one per column).

Irrigation_interval_fixed / Irrigation_interval_copy (days). The number of days between irrigation events. Set the interval if you do not want to apply the water dosage every day. For instance, if you want to apply 200ml every third day you can set this value to 3. If you want to water every day, set the value to 1. A value is needed for each irrigation_times_hold / fixed / copy defined. In the example there are 2 values for the irrigation_times_hold. In the row below there are two interval values, one for every irrigation time defined.

Irrigation_at_deviation_from_target (%). The deviation from the target weight at which plants will be re-watered up to target weight in percentage. I.e. When you define a target weight of 1000g and a deviation of 5% the deviation mode will rewater as soon as the weight value is below 950g (independent of time).

Error_tolerance_for_irrigation (g). The error tolerance for irrigation. This setting is for all irrigation modes. Rule of thumb: Take 0,1% of the total pot & plant weight on the scale. E.g. 10kg pots can have a 10g error tolerance. We advise to not go below 2g. *E.g.*, The irrigation tolerance is set to 2g. The plant weight is 900g and a fixed irrigation with 100ml is applied. The software will show the last irrigation as OK as long as the weight after irrigation is between 1002g and 998g.

Max_weight_fixed_or_copy (g). The maximum weight for fixed and copy irrigation mode. It is used in “Fixed” and “Copy” irrigation to prevent water from accumulating over time and flooding the pot. *I.e.*, a 1L pot is placed on the system for 10 days and receives a fixed dosage of 200ml water per day. If there is no transpiration it will be full after 5 days. If the max weight is set to 1000g the irrigation will be skipped to avoid over flooding.

Max_water_per_irrigation_step (g). This setting sets a limit to the amount of water per irrigation event. The irrigation event is split into several steps if the amount of water needed at this time point exceeds the limit. *E.g.* The soil can only absorb 50ml per 10 minutes but you need to irrigate 100ml. You can set a limit of 50ml here. Then you need to set the interval_irrigation_steps to 10 minutes. This irrigation event then will be split in 2 irrigation steps. Only in hold mode these steps can be configured. The other modes will water the irrigation amount in one step.

Max_irrigation_steps. Specifies the maximum number of steps that can be performed in one irrigation event. Only in hold mode the steps can be configured. The other modes will water the irrigation amount in one step.

Interval_irrigation_steps (minutes). The time in minutes the system should wait before starting the next irrigation step. The time format is MM (M= minute). Please note that the number of steps and the interval between steps define together with the amount of water the total length of one irrigation event. Only in hold mode the steps can be configured. The other modes will water the irrigation amount at once.

Starting_time_program. This setting defines the date and the time at which the experiment program should start to be executed. The format is “YYYY.MM.DD HH:MM”.

- ***The irrigation program section***

The second section in the irrigation file is the program section. It consists of three main parts, colored in the image below.

- The units (green) identified by id
- The irrigation section headers (orange) with irrigation mode and duration in the next columns
- And the irrigation amount settings (purple) per scale and irrigation section

	72	24	48	24	72	Duration_program_section
id	d	f	h	n	c	Irrigation_mode
1:1:1	3000	100	3000	0	100	
1:2:1	3150	110	3150	0	1:1:1	
1:1:2	2500	150	2500	0	1:1:1	
1:2:2	2000	100	2000	0	200	
1:1:3	3000	100	3000	0	1:2:2	
1:2:3	5000	200	5000	0	1:2:2	

Unit ID (Green). The units used in the experiment are specified by the virtual unit id.

Irrigation program sections (Orange). Every purple column with an orange header is an irrigation program "Section". All sections combined is the irrigation program. The program will run one section at a time. When the first section ends the section in the next column starts.

The irrigation mode for each section is specified in the orange column header. You can have as many irrigation modes as you want. Each irrigation section is specified with a duration in hours for that section.

Below the direction you define the irrigation mode with an abbreviation (f FIX; h HOLD; c COPY; d DEVIATION; n NO IRRIGATION). The hours each program section needs to run are on top of the section. The program will run each section after the other.

In the example above it will start with 72 hours of "Deviation" mode, followed by 24 hours of "Fixed" mode, 48 hours of "Hold" mode, 24 hours of "No irrigation" mode and then 72 hours of "Copy" mode. The total length of the program is therefore 240 hours.

Irrigation behavior values (Purple). Define the irrigation behavior for each scale and for every irrigation section. Each different irrigation mode has its own values to define.

> **In FIX (f)** mode the value given represents the fixed amount of water in ml the plant will receive. E.g. 20 will irrigate 20g of water every irrigation event.

In HOLD (h) mode the value represents the target weight for each plant in grams that will be used as a watering target. E.g. If the target weight is set to 300 and the specific row and column is weighed at 260 it will irrigate 40 grams of water in the next irrigation event.

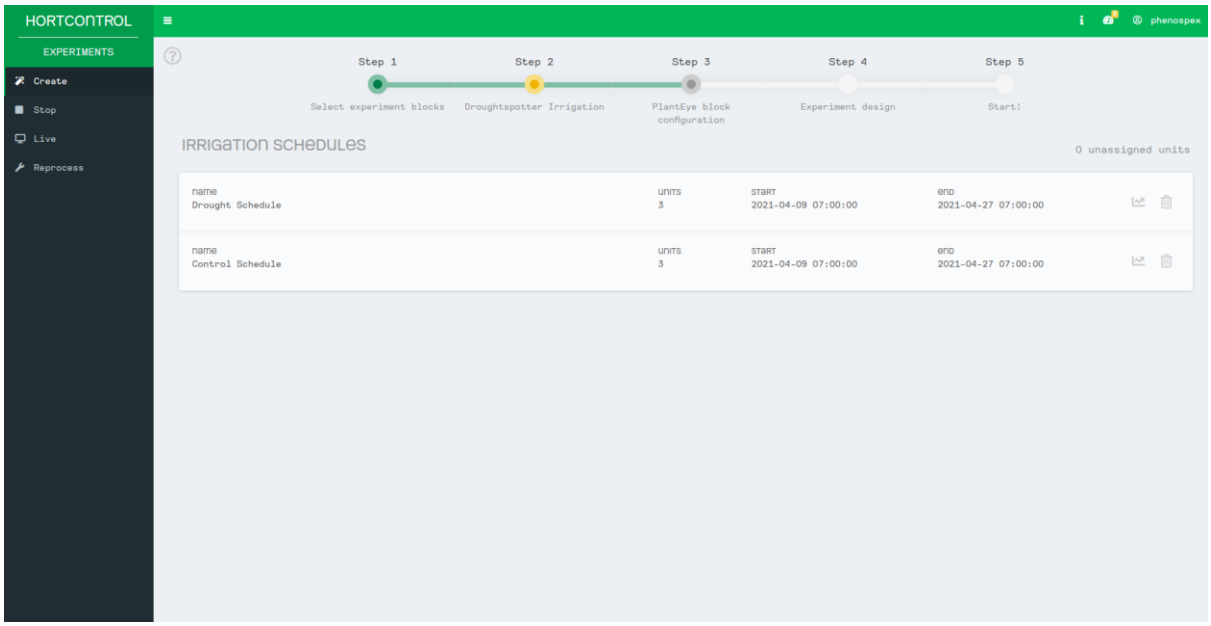
In COPY (c) mode there are two options. For the template plant the values are numeric. 0 means that the plant will not receive water, 100 means the plant will receive 100 grams of water. If the value is the abbreviation of another cell in the experiment (e.g. 1:1:1) this plant will use the weight of 1:1:1 as target weight.

In DEVIATION (d) mode the value represents the target weight for each plant in grams that will be used as a watering target. Other than in "Hold" mode the plant will get re-watered as soon as the threshold is reached

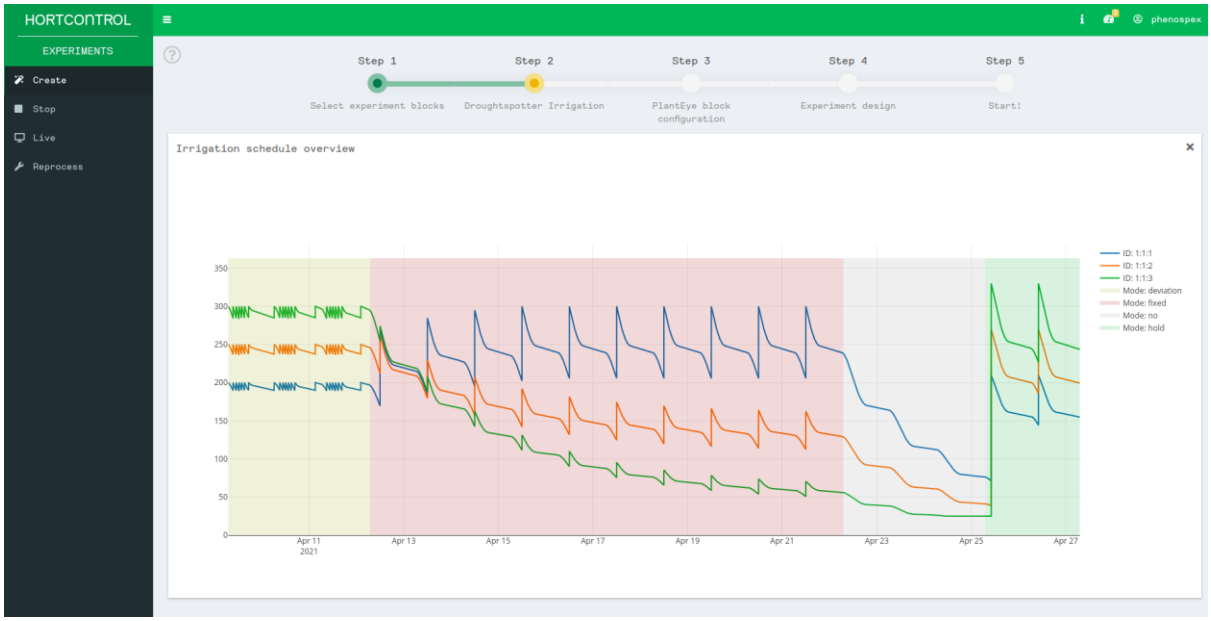
In NO irrigation (n) mode the value has to be set to 0 (same as FIX with 0 irrigation)

Upload and visualize the irrigation schedule

If you are happy with your schedule you can upload it to HortControl. A summary of all schedules will be available. You can remove a schedule by clicking the bin icon.



Click the graph icon on an irrigation schedule overview bar to open an emulation of the irrigation schedule that you uploaded.



3.3.1.4. Experiment design

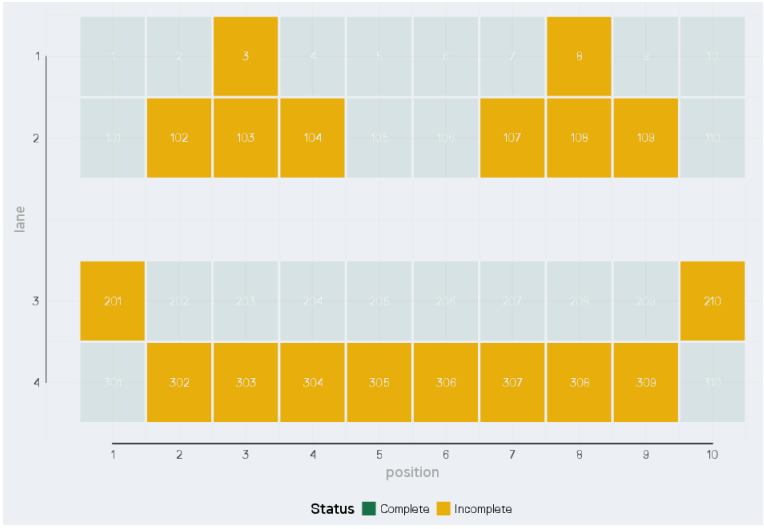
This is a crucial step in which you tell HortControl what plants with what treatment are in each unit of every block. Do this by entering metadata like genotype and treatment.

When visualizing data in the end this allows you to combine and aggregate information and visualize graphs with the correct label. In the data export this meta data is linked with the PlantEye data.

There are two ways to add biological information:

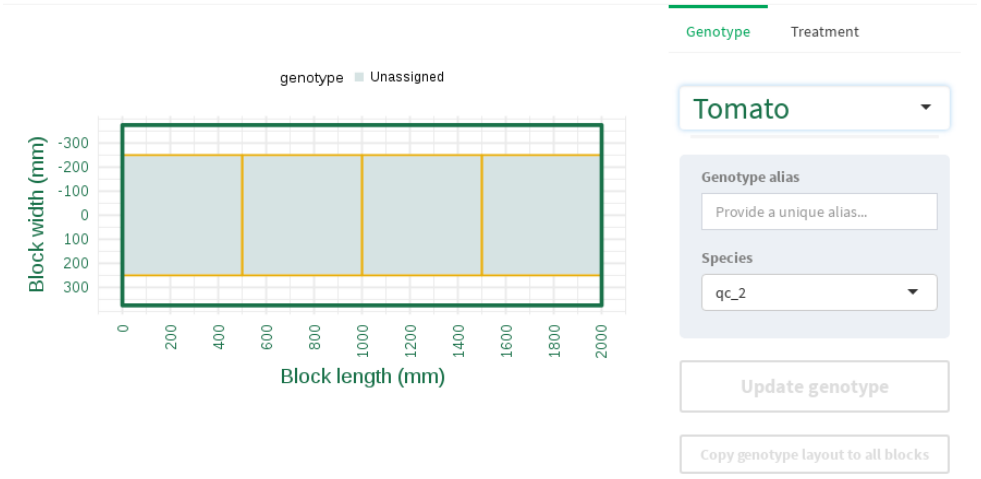
1. adding this information block by block using the system overview
2. batch uploading the biological information using a csv file.

Once the information is assigned / uploaded, the blocks will show up in green.

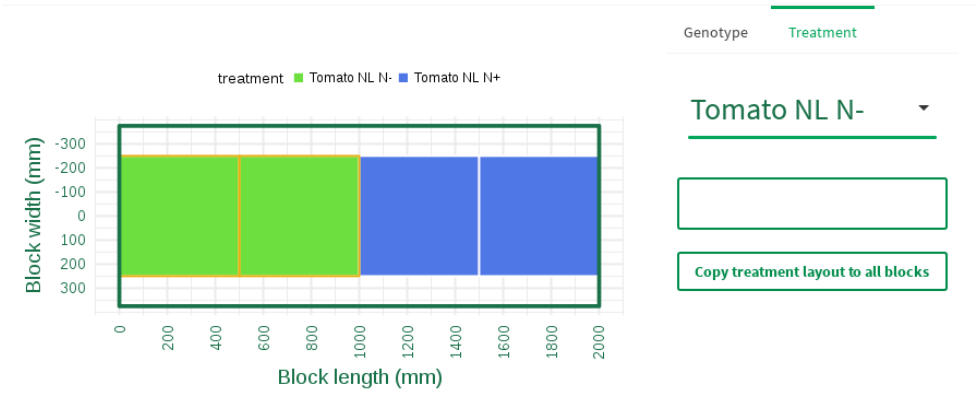


Block by block

This process involves selecting a block in the system overview which will open a modal window (image below). In this window you see the block overview. You can select one or more units by dragging over or clicking on them. The selected units will be highlighted in yellow border. Depending on the tab you selected you can add genotype or treatment information to these selected units.



You can create a new treatment/genotype or choose an existing one from the list. Each genotype needs a unique genotype alias and species information. When you are satisfied with the biological information you have assigned, you can press the “update” button, which will update the selected unit’s information.

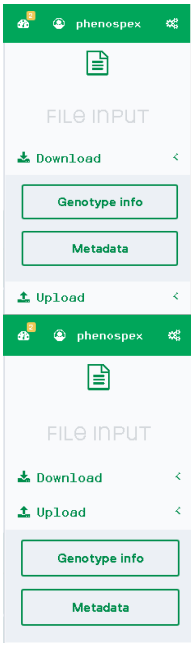


If all your selected experiment blocks need different biological information, you have to update each block separately. However, if the genotype and/or treatment pattern in all your blocks is the same, you have a simple way to copy the current block information to all other selected blocks for your experiment. Simply click on “Copy genotype layout to all blocks” and/or “Copy treatment layout to all blocks” and the information will be applied there too.

Step by step:

1. Select one block by clicking or select multiple with dragging
2. Select an existing genotype from the dropdown list or create a new one. For this click the genotype name currently selected, press backspace and type the new genotype name. Then press enter.
3. Click update genotype
4. If the remaining block all have the same genotype setup in their units you can use the “copy genotype to all blocks” button.
5. Click the treatment button on top and enter treatment information just like you added the genotype information.
6. Close the modal window. If you assigned genotype and treatment information properly the block turned green in the overview.

Batch upload



If you own a large Phenospex system, e.g. a FieldScan, you might not want to add the biological information block by block. For this situation, HortControl provides a batch upload option. To do so, open the settings sidebar by clicking the settings icon in the top right corner. Within the settings sidebar you can choose to download all the genotype information ("Genotype info" button) available in HortControl and a csv file with all the currently created experiment units ("Metadata" button).

These files can be manually updated and uploaded to HortControl repeatedly via the upload section of the sidebar. If you have your own database with biological information, you could create custom scripts to automatically generate the metadata and genotype info files to link your database information to the phenotyping data in HortControl. More information on the required data and format in these files is given below.

Metadata. The metadata file contains three columns that define the position of the plant in system coordinates (barcode, unit column, unit row), and two columns that assign biological information (genotype, treatment) to these positions.

Genotype info. When you want to use a genotype that does not exist in HortControl you have to fill in and upload the genotype info csv. The correct file format can be found by downloading the genotype info. You can remove all the genotypes and start filling in new ones. You will need to provide the genotype name, genotype alias and species.

barcode	unit colum	unit row	genotype	treatment
3	1	1	a	WW
3	1	2	a	WW
3	2	1	a	WW
3	2	2	a	WW
3	3	1	a	WW
3	3	2	a	WW
8	1	1	a	WW
8	1	2	a	WW

IMPORTANT

The genotype and genotype alias should always be a unique combination. Furthermore, the same genotype cannot be assigned to multiple species.

After uploading the genotype info, this genotype name can be used in the metadata file. Once filled in, the metadata file can also be uploaded using the corresponding "upload" button.

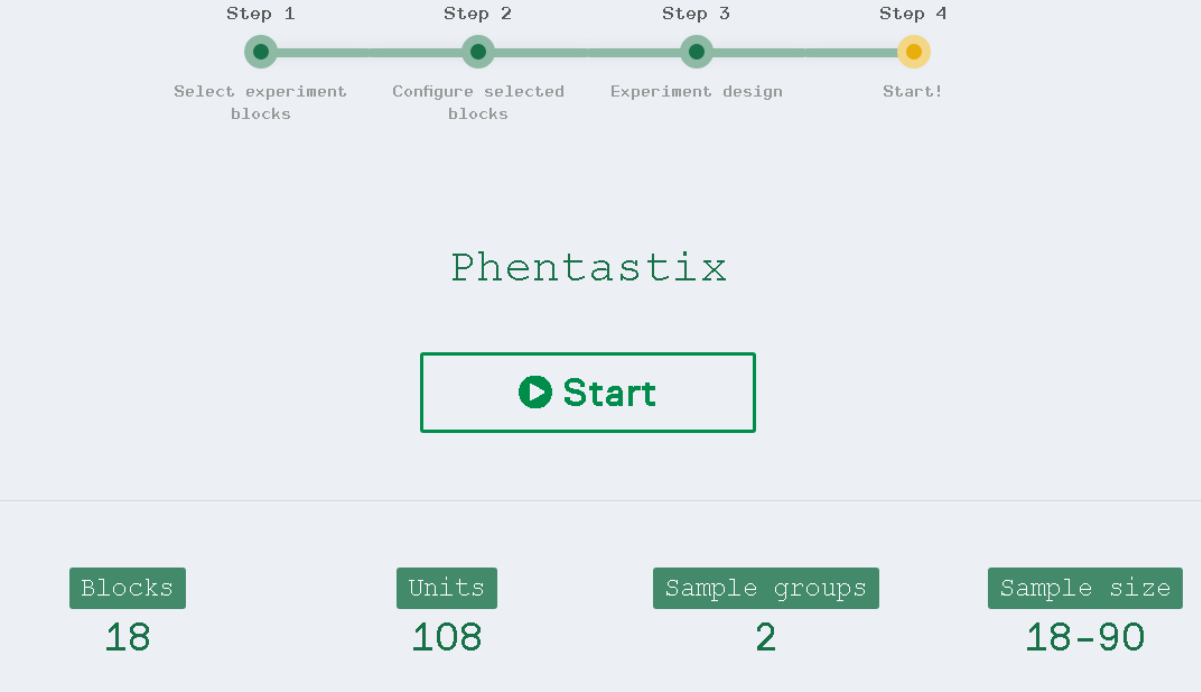
Once a block contains genotype and treatment information for all its units, it will be colored green in the system overview. Following the complete system update, you are ready to move to the final step.

3.3.1.5. Start!

The last step is to come up with a good experiment name and start the experiment. In the window, you will also get an overview of all the blocks, units, sample groups (i.e. unique genotype x treatment groups) and sample size (number of units per sample group). This offers you a chance to examine your experiment setup.

Some common errors in setup:

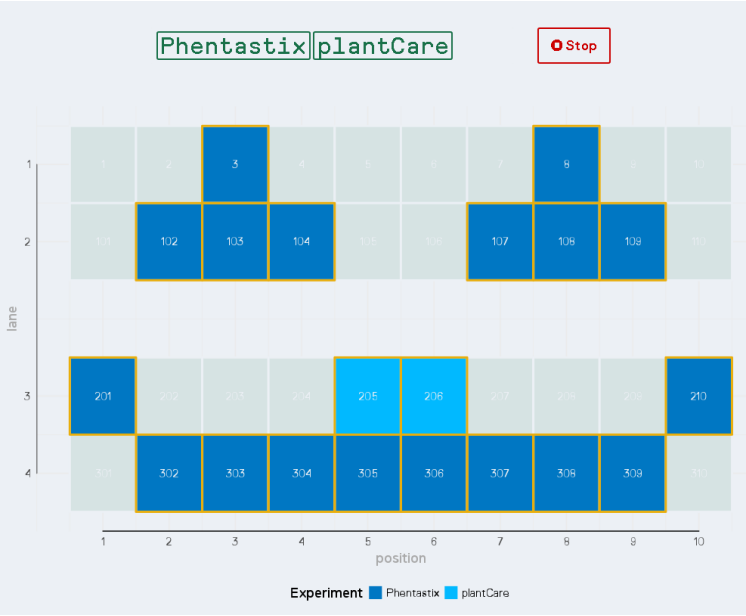
- There are fewer units defined in HortControl compared to the number of plants you wanted to use in your experiment. Therefore, the number of blocks or the block splitting could be wrong.
- The irrigation schedules could not be uploaded to DroughtSpotter.
- You have more sample groups than treatments and genotypes. In this case, the assignment of biological information is wrong.
- There is a large deviation within the sample size, which represents a unique genotype and treatment combinations (as shown in the example below), and/or the incorrect assignment of biological information. These errors can compromise final statistics. For more information about finding the right sample size please refer to Wikipedia: https://en.wikipedia.org/wiki/Sample_size_determination.



Once you have reviewed your setup, the “start” button will be enabled and you can begin your experiment. After the experiment is uploaded to HortControl, you will get a confirmation message. HortControl revert to Step 1 of the experiment creation process, where you will see that the blocks you just used in the experiment are occupied.

3.3.2. Stop Module

The second module in the experiments board is to stop an ongoing experiment. In this module you are presented with a system overview, in which all occupied blocks are colored by the experiment they belong to. You can select the experiment which you want to stop from the drop-down list or drag/click on any of the blocks that belong to the experiment(s) you want to remove. You can also select multiple experiments at once. The “stop” button becomes available after the desired experiment is selected. Once you hit the “stop” button – the experiment is stopped and the blocks become available again. These blocks are now available to be used in another experiment.

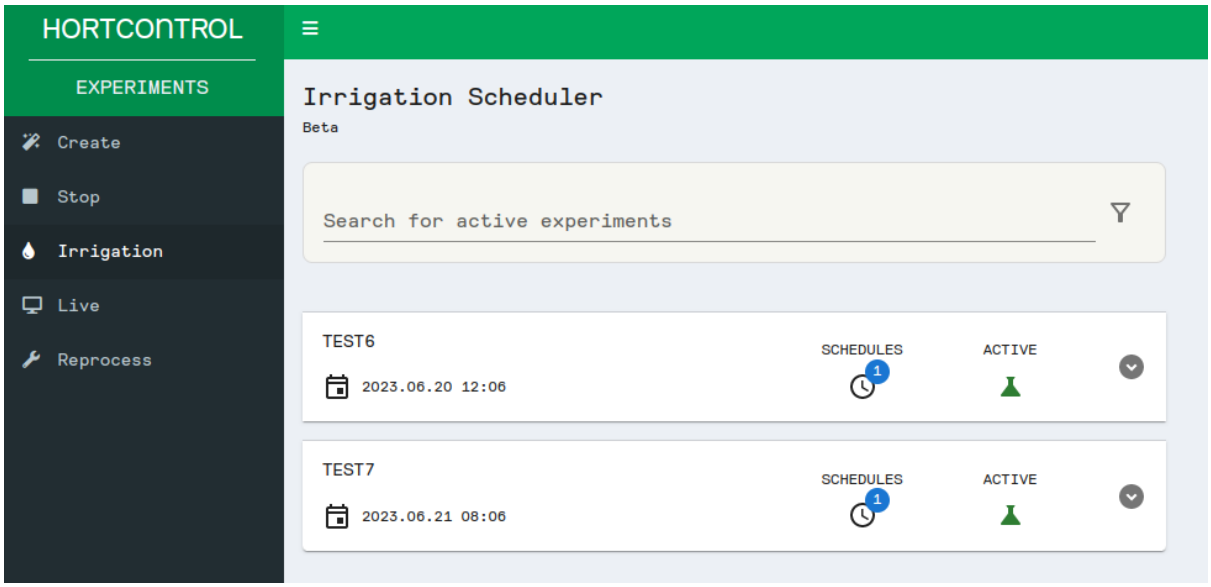


3.3.3. Irrigation Module (beta)

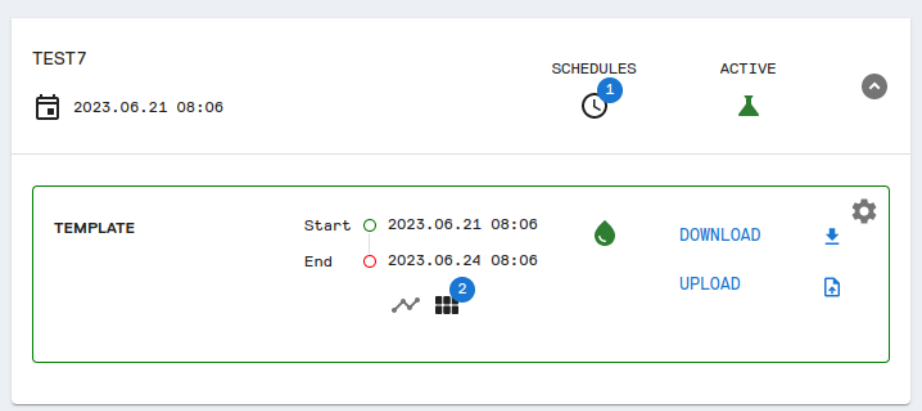
DROUGHTSPOTTER

The module is in beta version, which means we wanted to share the feature with you, but we want to evaluate it thoroughly meaning the usability might still change substantially.

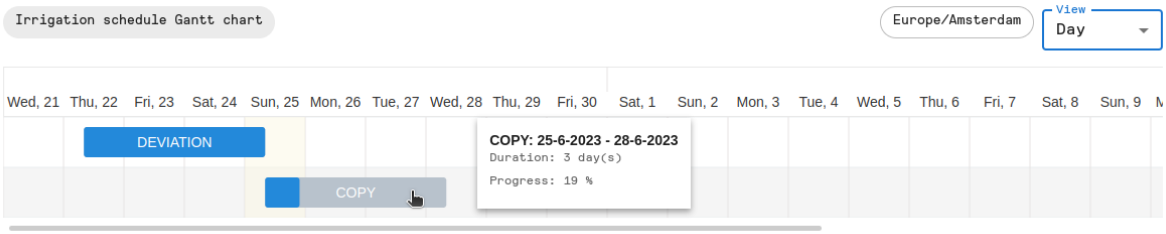
This module can be used when you need to change your irrigation schedule during a running experiment. E.g. when you want to update a target weight or need to change the timing of the irrigation. When you open the module you will see a list of all active experiments.



You can use the filter the list of active experiments on name. Each block represents an experiment and holds key information of the experiment such as the name, start date and number of irrigation schedules that are used in the experiment. Click on an experiment to get more details about the irrigation schedules.



For this experiment we have an irrigation schedule named “TEMPLATE” which is still active, shown by the green drop icon. When the irrigation schedule would be finished the icon would show gray. You can also see other information such as the number of units controlled by the irrigation schedule (2 in this example) and the start time of the schedule and the time it is scheduled to end. If you click the line graph icon you get a time window of the current schedule showing the progress.



To update the schedule, you can press the upload icon and upload the updated schedule as described during the start of an experiment. You can always consult the current schedule by clicking on the download icon. This will give you the schedule that is running, which you can easily update to fit the needs of your experiment. Once that is done you can upload it again.

3.3.4. Live Module

Whenever your scanner mode is set to external block id (3.6.1.4), you can use this live module to set up the next block id. To do so, select the block id you want to scan, and press update. HortControl will inform you when the block id has been updated successfully. The next scan you will make will be assigned to that selected block, the data will be stored in HortControl accordingly.

3.3.5. Reprocess Module

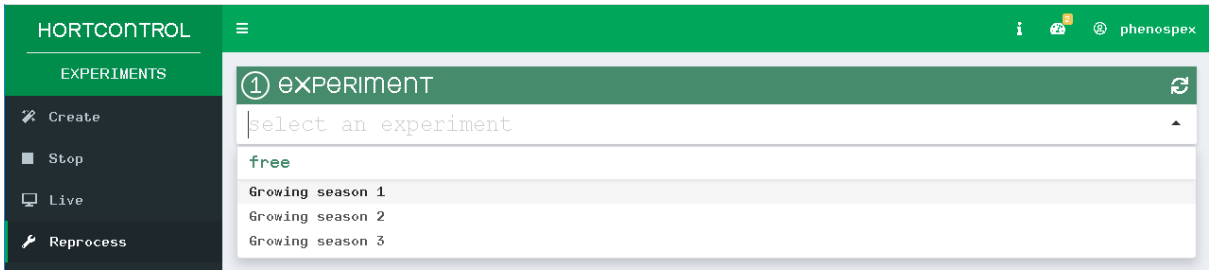
PLANTEYE

In some cases you may find a mistake with your initial setup (e.g. splitting settings) after the experiment has been completed or you would like to adjust parameters (e.g. limits of the hue bins) mid experiment. For these cases there is a reprocessing module. It gives you an option to change splitting settings and/or multispectral bin limits, to reprocess the 3D scans with the new settings, and to update the old dataset. The reprocessing is done in four steps:

1. Select the experiment to reprocess
2. Select an example scan
3. Update settings and compare old data with new data
4. Start the reprocessing job for your whole experiment

3.3.5.1. Select your experiment

In the reprocess module, the first thing you need to do is to select the experiment you want to reprocess.



When selecting from the dropdown menu, you see a list of all experiments grouped by reprocessing status. There are five statuses defined for an experiment reprocess job:

Free. The experiment is available for reprocessing.

Queue. The experiment reprocess job has been registered, but did not start yet as there is currently another experiment being reprocessed.

Active. Files are being reprocessed. You can select the experiment to see its progress.

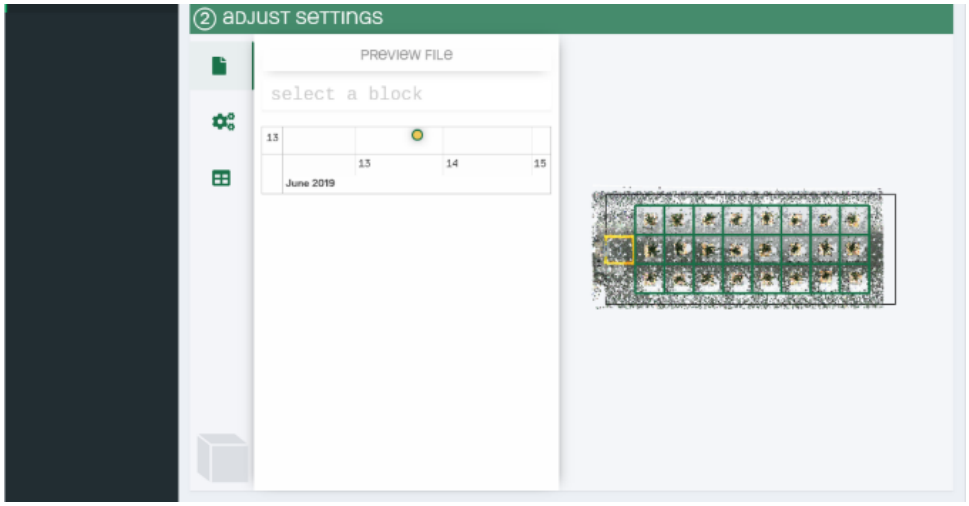
Finish. Reprocessing has been completed, but there were some errors that require corrections.

Done. Reprocessing has been completed without errors and the new dataset was successfully uploaded to the database.

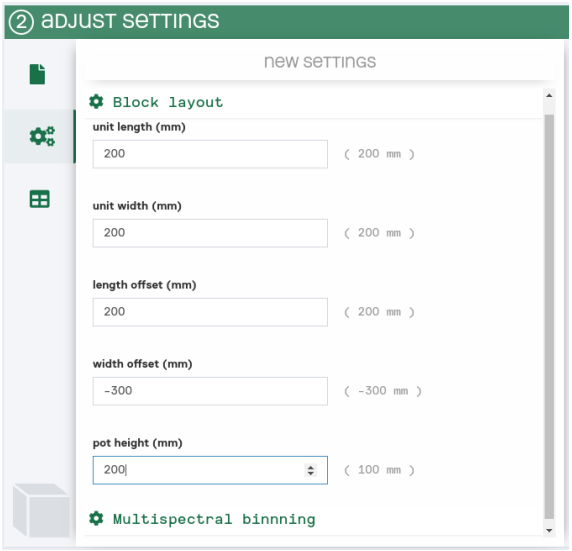
Once an experiment is free you can proceed to Step 2, where you will be able to select a scan, apply new settings and view how the new setting will affect your scan images and data. When you are satisfied with the new settings, you can choose to start reprocessing, which will reprocess **all** scans for the selected experiment.

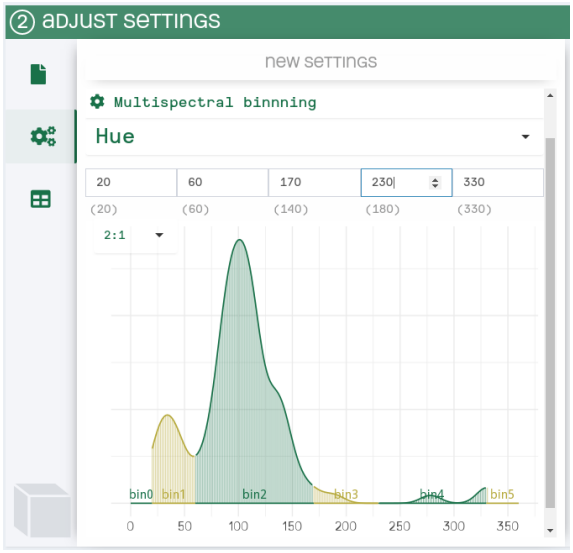
3.3.5.2. Change settings

When a free experiment is selected, you will be able to select a preview scan to optimize your new settings. You can select a preview scan by selecting a block id from the preview file dropdown. This will show you all the available scans for that block. Select a scan, and a 3D view will be loaded.

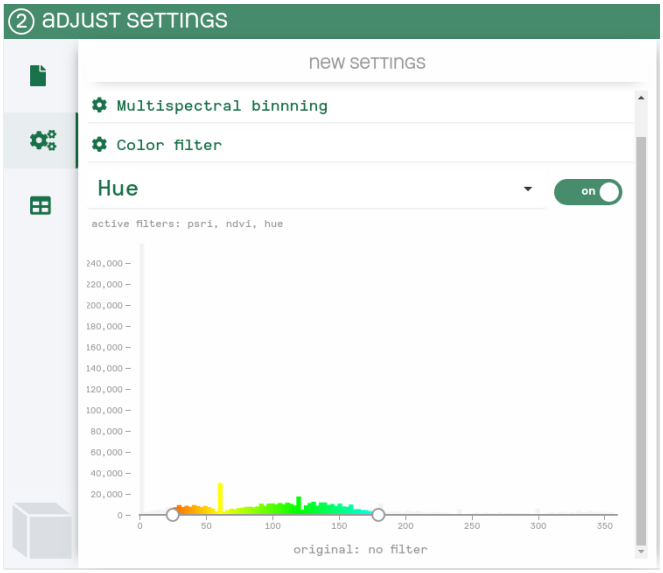


In the left bar new icons will appear, *i.e.* cogs and a table. The cogs will open the settings menu where you can change splitting settings and multispectral bin limits. The grey number in parentheses indicates the old values.

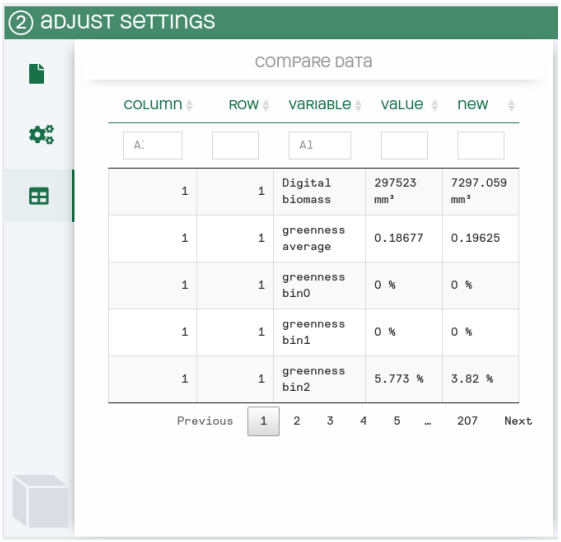




You can also update the color segmentation settings, remove old filters and/or create new ones. The previously set filter values will be specified in gray font under the histogram.

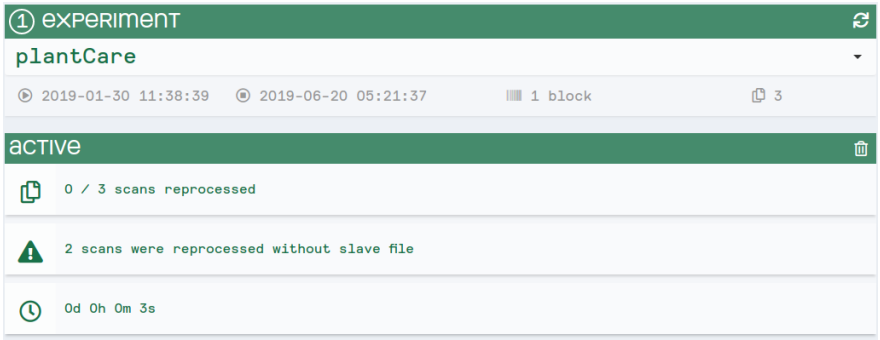


Using the table that is shown after clicking the table icon, you can compare the results between the old dataset and the new dataset.



If you are happy with the new settings and corresponding results, you can start the reprocessing job by selecting the “start” button. A reprocessing job for **all** scans of your selected experiment will be registered. If there are no other jobs running, the experiment will be processed immediately. Otherwise, it will be added to the queue.

While your experiment is being reprocessed you can track its status in the experiment status block. You will also be able to view the number of scans that have been reprocessed, any system warnings, and the elapsed time since reprocessing initiation. You can press the “refresh” button in the top right corner in the experiment selection block to update this information. If you want to remove a reprocessing job, you can click on the trash bin in the top right of the experiment status block.



When reprocessing of an experiment finishes without any warnings, the job will change its state to *done*. Following, the old experiment dataset will be updated with the new dataset, and you will be asked to finalize the reprocessing job. However, if experiment reprocessing finished with one or more warnings, the job state will be changed to *finish*. You will have to confirm that the data can be pushed to the database replacing the old dataset. If you do not wish to replace the old data, you can click the trash bin in the top right corner of the status block, and your reprocessing job will be removed.

3.3.5.3. Safe system shutdown

In order to ensure data safety, we advise to not power off the system when a reprocessing job is running.

3.4. PSX Data Board

Once the experiment is launched, and the data starts to accumulate, it becomes available in the PSX Data board. In addition to the raw data, you can also download analysis for each of the offered modules. Currently, there are five analysis modules: ***Overview***, ***Snapshot***, ***Growth***, ***Germination*** and ***Correlation*** *(PlantEye only)*.

The purpose of this board is to offer you access to the raw data, as well as to visualize and to analyze it. The board is structured so that you have the quickest access to the raw data, which you can then further investigate using the tools that HortControl provides.

3.4.1. PSX Data Modules' Principles

Within each of the PSX Data modules, you can view, filter and download collected data. The first step in each of the modules is the selection of an experiment that you would like to use for the analysis. Use the dropdown list to select an experiment or start typing the name of the experiment that you would like to download and/or analyze. Once you have selected your experiment you will get its general information – set number of blocks, defined number of units these blocks contain, number of created sample groups (unique combinations of genotype and treatment), as well as the sample size (number of units within the same sample group i.e. replicates).

3.4.1.1. Displaying data

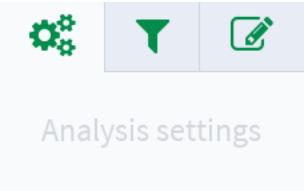
Data visualization is always displayed in the center of the module. Different views can have similar elements displayed.

Navigation bar. A navigation bar is displayed above the step bar. It contains the name of the selected experiment and the selected analysis module.

Variable dropdown. A very important part of the analysis modules is the settings sidebar on the right. It has the same structure in all modules and consists of three parts: analysis settings, filter settings and view settings.

Settings sidebar. A very important part of the analysis modules is the settings sidebar on the right. It has the same structure in all modules and consists of three parts: analysis settings, filter settings and view settings.

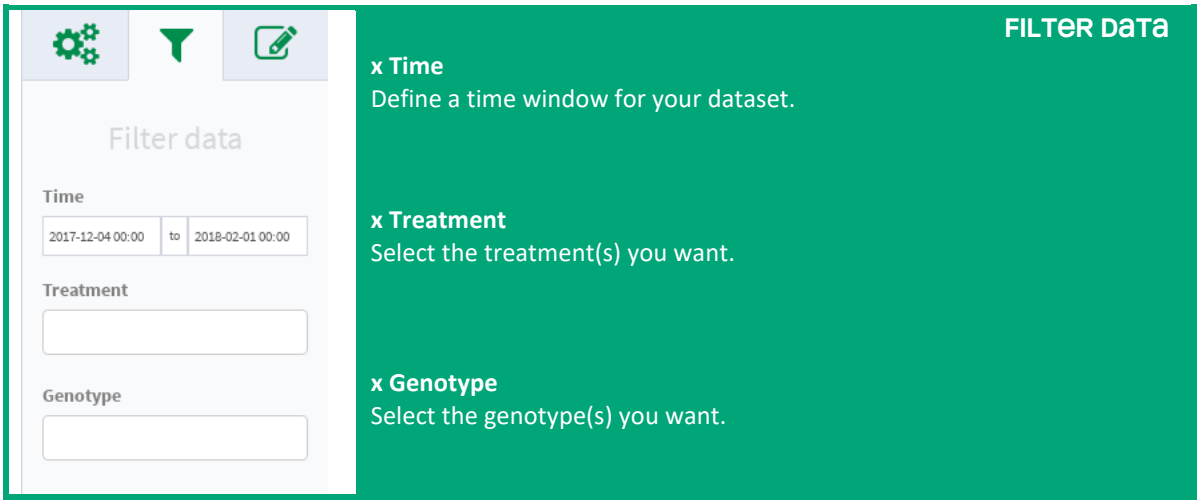
3.4.1.2. Refining data



Collected data can be further refined for each of the modules using three given settings: Analysis settings, Filter Data and Visualization. These settings can be found under the settings sidebar on the top right corner.

Analysis settings will differ across modules. At the bottom of the analysis settings you will always find a “download” button. Generated data will then reflect current analysis settings applied on the (filtered) dataset.

Filter settings have been briefly mentioned before in the description about filtering the selected experiment dataset. Since your data is refined in this step, only part of the original dataset makes it to the analysis module. You can filter your data to select specific units, blocks, genotypes, and/or treatments, and you can define the time window in which your analysis should take place. If there is nothing selected in the filter fields all genotypes and treatments from the experiment will be used for further analysis.

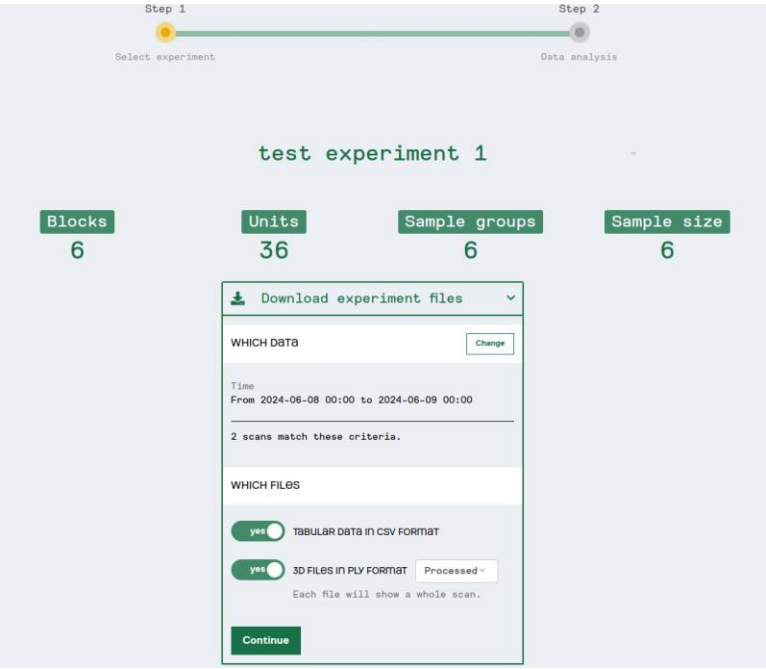


Visualization settings will allow you to adjust view perspective without drastically changing the appearance. For some settings multiple modules may be used at a time, e.g. toggling the legend, while others are module specific.

3.4.1.3. Downloading data

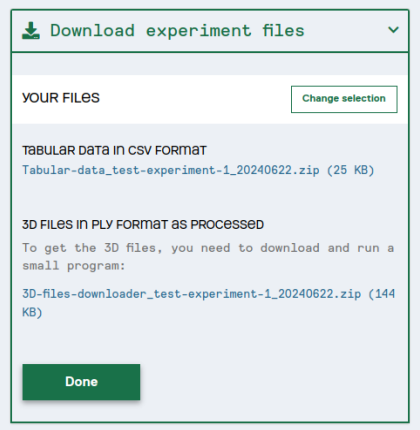
You can download data at any point of your experiment from the Overview module. There are two types of data that you can collect from HortControl. In the Overview module, you can expand the Download tab to filter the data you want to download from the experiment and select which data you want to download, i.e. tabular data and 3D files in case of a PlantEye.

By default, the tabular data will comprise all data collected from the PlantEye, DroughtSpotter and/or the weather station for the selected experiment. If you wish to extract information for any specific treatment, genotype, or species of dates, you can do so by applying necessary filters.



Only if you have the PlantEye sensor in your product, you can select the type of data you want to download (tabular and/or 3D files). Select which data you want to download and press continue. The 3D files can be downloaded either as Processed file (file of entire scans) or Unit file (file of the individual units).

After you pressed “Continue” HortControl will prepare the downloads and serve them as download links.



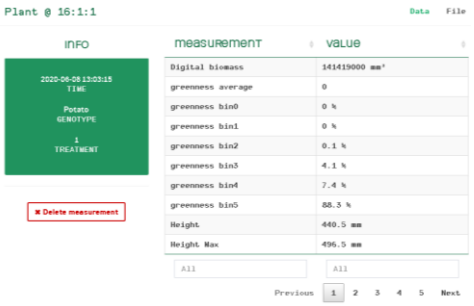
A link will be prepared to download the tabular data in CSV format. Clicking it will start a download of a zip file which contains all PlantEye, DroughtSpotter and/or Weather Station data.

If you have a PlantEye system and selected to download 3D files, a download link is generated for a download script which you can run on your system to download the selected 3D files directly from your computer. The 3D file download script is accompanied in a zip file by a detailed manual on how to use the script to eventually download all the 3D files from the system. With the download script you have full control when and where you download all the 3D files. Place the download script in the folder you would like to have your 3D files downloaded and run it according to the instructions.

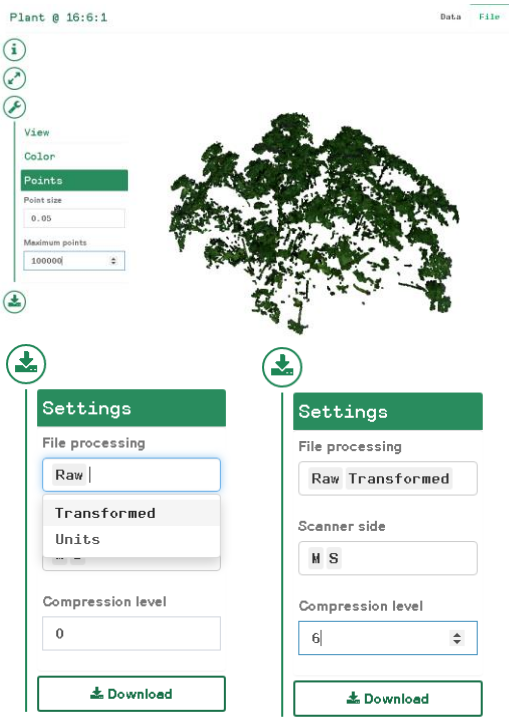
Download 3D model (.ply file)

PLANTEYE

In this step you can also download .ply files. This can only be done for a single time stamp and unit at a time. To do so, select a desired point and you will be prompted to the information window.



Once in the window, select File, and you can preview 3D image of the data point you have selected.



Within .ply files you have an option to download different file types like *Raw* and *Transformed* files (which contain the image of the whole block), as well as *Units* files (which contain separate files for each of the units within the block). See below for more information about the file types and their use cases.

For the dual scan system, please select both M and S in the Scanner side window. Otherwise, only part of your scanned image will be downloaded.

Maximum recommended download compression level is 6, but you do not have to select a value in this window.

Select the Download button to begin your 3D image download.

3D file types explained

We have two processing engines in our products, either Phena 1.0 or Phena 2.0. Both versions are developed to deliver high quality output parameters. With Phena 2.0 we were able to include more features, without adjusting the Phena 1.0 output many of our clients rely on. Because of the extra features, the output of Phena 2.0 includes more different types of 3D files to download. These engines convert the raw 3D file via different processing steps into digital plant parameters and can output 3D files along these processing steps. In order to give you as much access to, and flexibility with the data, HortControl allows you to download the 3D files from these intermediary processing steps. Both engines offer three file types for download: “Raw”,

"Transformed" and "Units". When your product is running with our newest processing algorithm, Phena 2.0, there are two more file types you can download, i.e. "Processed" and "Annotations". Below we describe the different file types you can download, what data you can expect and how you could use it.

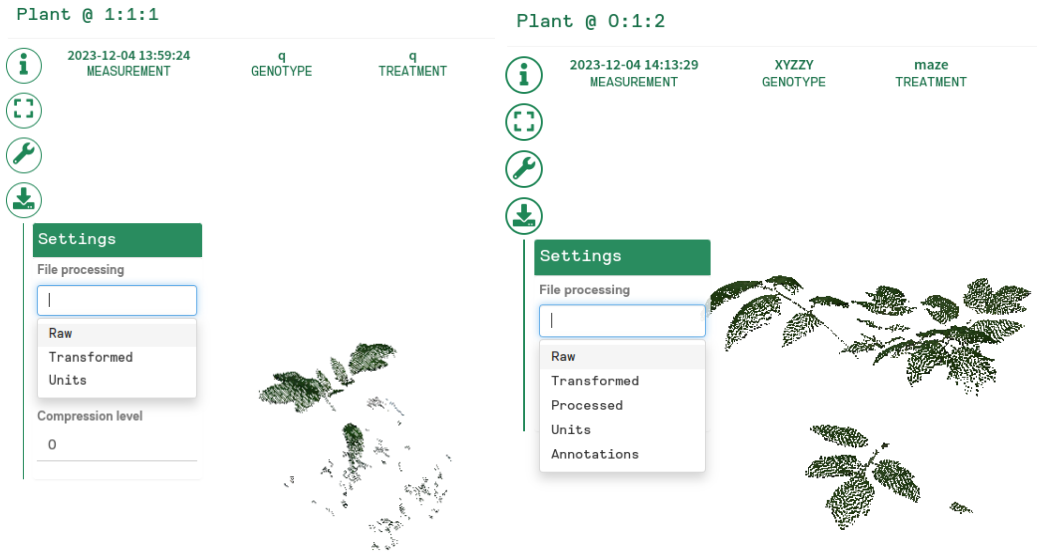


Figure: All the file types you can download for a system running with Phena 1.0 (left) and Phena 2.0 (right).

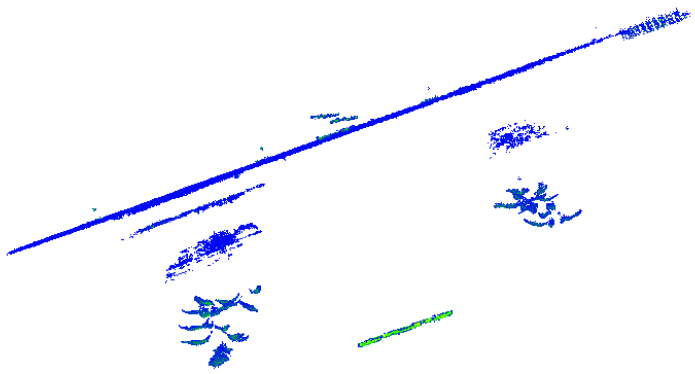
In the table below you can find information about the processing steps the engine performs before it creates the different file types. Afterwards more details about each file type can be found. When you are an advanced user and want to implement your own processing steps, these different types can already give you a head start for your needs.

	Processing steps performed by the processing engine			
File type	***Coordinate Transformation***	***Merging 3D files***	***Background removal***	***Plant splitting***
Raw				
Transformed				
Units		Phena 2.0 only*		separate files per plant
Processed (Phena 2.0)				plants labeled in one file
Annotation (Phena 2.0)	These files do not contain 3D plant data, they only contain data to visualize the convex hull of each plant			

*As described in the chapter 'Unit files': DualScan systems using a Phena 1.0 engine generate 3D files for each scanner separately. On the other hand, DualScan systems with a Phena 2.0 engine produce these files already combined into a single downloadable file.

Raw files

These are unprocessed 3D files as the PlantEyes in your product created them before they are sent through the processing engine. In this file all objects are in scanner coordinates with the origin in the middle of the glass of the scanner. It means that if you open this file in a 3D viewer, it will display your plants upside down or even in an angle when your PlantEye is scanning in an angle. In case of a dual scan setup you can download the raw 3D file generated by each PlantEye, labeled M and S.



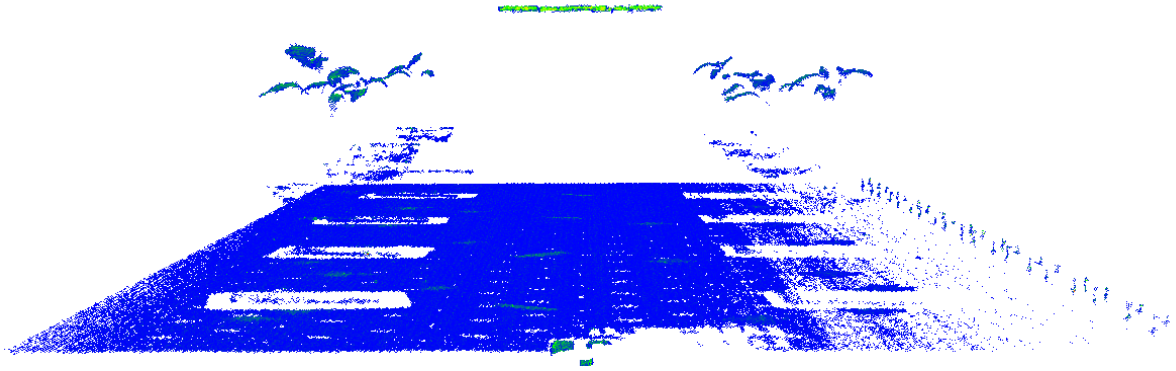
Example of a raw file (front view).

Use cases

- **Backup**. These files can be reused to calculate plant parameters again when sent through our engine. Therefore these are recommended to be stored for backup.
- **Custom processing algorithms** (for advanced users). If you know your way around 3D files, you will experience the most freedom using these raw files. You could even design your own transformation algorithm. Other custom processing you could do is: background removal, plant splitting and plant parameter calculation.

Transformed files

These are 3D files that are converted into your location system (or coordinate system). Think of it as a system that helps us know where things are. The location system has a starting point in the top left corner of the table or ground where you placed the plants and where the scanning starts. If you open these transformed files in a 3D viewer, you will see the plants are now in the right orientation (they will not be upside down anymore). If you have multiple plants in one scan they will still all be together in this file. In case of a dual scan setup you can download the raw 3D file generated by each PlantEye, labeled M and S.



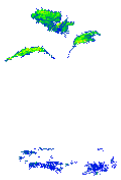
Example of a transformed file (front view).

Use cases

- **Visualization**. You can open these files in a 3D viewer, have an overview of the batch of plants that were scanned and assess them.
- **Custom processing algorithms** (for advanced users). If you know your way around 3D files, but you want to save yourself the time of implementing a transformation and background removal algorithm to get the plants in your coordinate system, these files give you a good start to implement customer processing algorithms. When you have all separated your plants, you can create algorithms to extract digital plant parameters.

Unit files

These 3D files will show each plant separately, in the right coordinate space with the background removed. In case you have a DualScan setup working with Phena 2.0, the 3D data of both PlantEyes were merged into this unit file (in contrast to the previous files). For Phena 1.0 you can only download scans from both sides.



Example of a unit file (front view).

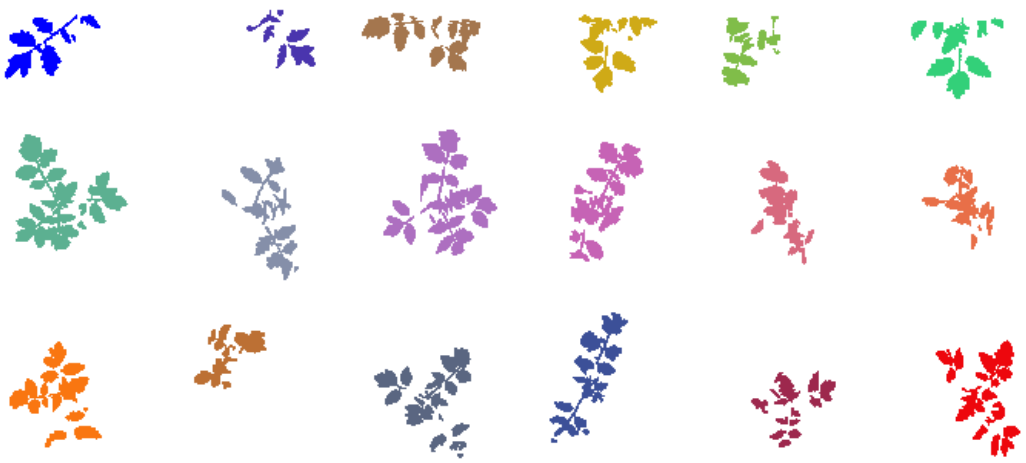
Use cases

- **Visualization.** You can open these files in a 3D viewer, have an overview of the batch of plants that were scanned and assess them.

- **Custom processing algorithms** (for advanced users). You can immediately start implementing a processing algorithm to calculate your plant parameters or extract structural information for that plant, without spending time to process the raw files and separating plants and background first.

Processed files (Phena 2.0 only)

The processed files are 3D files that are converted into your coordinate space. So the origin will be at the bottom and upper left corner of your scanning area. If you open these files in a 3D viewer, you will see the plants are now in the right orientation (they will not be upside down anymore). In case you have a DualScan setup, the 3D data of both PlantEyes were merged into this processed file. Additionally, the background has been removed, the vertices have been triangulated, and the vertices carry a unit ID that represents the plant to which it belongs according to the engine's splitting algorithm. If you have multiple plants in one scan they will still all be together in this file, but you could visualize them separately through coloring them by unit ID.



Example of a processed file (top view). Each color represents a different plant as labeled by the vertex unit ID.

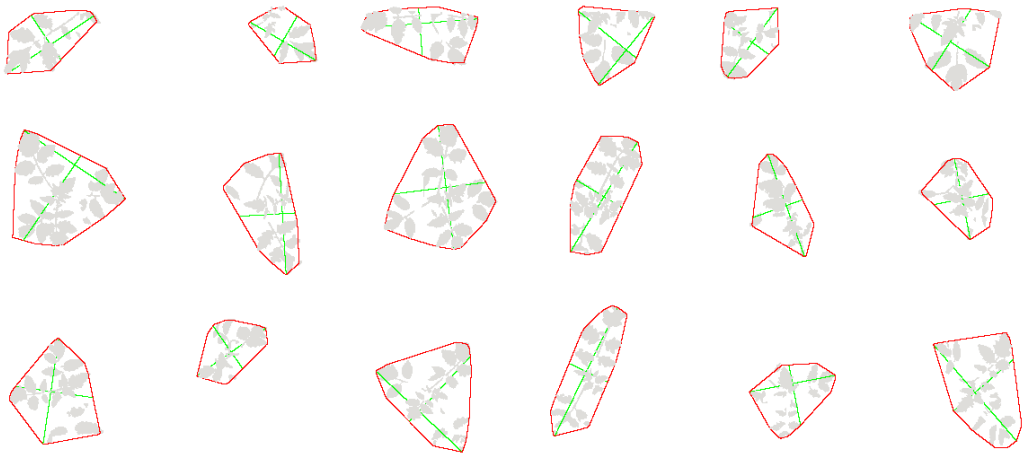
Use cases

- **Visualization**. You can open these files in a 3D viewer, have an overview of the batch of plants that were scanned and assess them.
- **Custom processing algorithms** (for advanced users). If you know your way around 3D files, these files give you a great head start. You can immediately start implementing a processing algorithm to calculate your plant parameters or extract structural information for that plant, without having to spend a lot of time processing the raw files, merging them and separating plants and background first.

Annotation files (Phena 2.0 only)

The annotation files provide the information of the convex hull that the processing engine calculated for each unit. When opening it in a 3D visualization tool you can see the convex hull (in red) around each plant as well

as the longest axis, and the longest perpendicular axis at its midpoint (both green) which are used to calculate convex hull related features.



Example of an annotation file (top view). The file only contains the convex hull (red) and longest the perpendicular axes on its midpoint (green). The gray plants are only for illustration purposes and were derived from the corresponding processed file.

Use cases

- **Visualization**. These files are meant for visualization purposes. This way the user can get a visual representation of the convex hull parameters that the Phena 2.0 engine calculates.

Overview of all use cases

The table below explains which file type to choose for the use case you have in mind. For most use cases the backup and visualization functionality is the most important.

File type	Visualization	Backup
Raw		
Transformed		
Units	separate files per plant	
Processed (Phena 2.0)	all plants labeled in one file	
Annotation (Phena 2.0)	Convex hull visualization	

However, if you are an advanced user and experienced with 3D data and wish to perform your own processing steps, these files might have extra use depending on the time you have and the level of custom processing you want to perform.

	What file type to choose for the custom processing you want to perform yourself. (for advanced use only)				
File type	***Coordinate Transformation***	***Merging 3D files*** *(DualScan only)*	***Background removal***	***Plant splitting***	***Parameter calculation***
Raw					
Transformed					
Units		Phena 1.0 only*			
Processed (Phena 2.0)					
Annotation (Phena 2.0)					

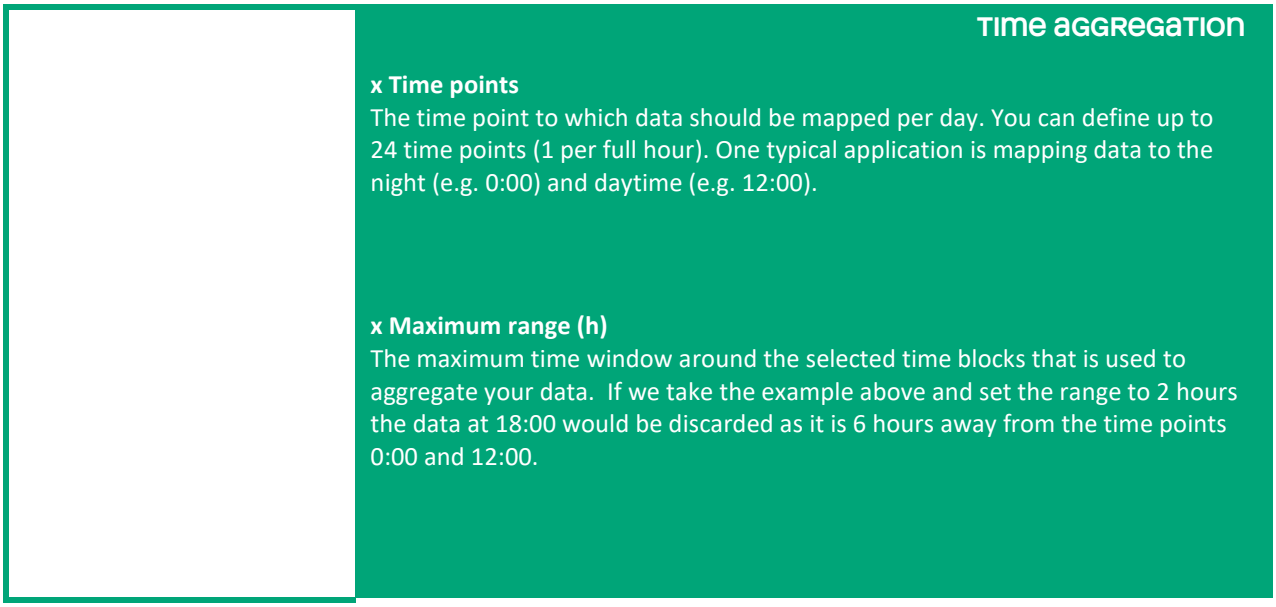
**As described in the chapter 'Unit files': DualScan systems using a Phena 1.0 engine generate 3D files for each scanner separately. On the other hand, DualScan systems with a Phena 2.0 engine produce these files already combined into a single downloadable file.*

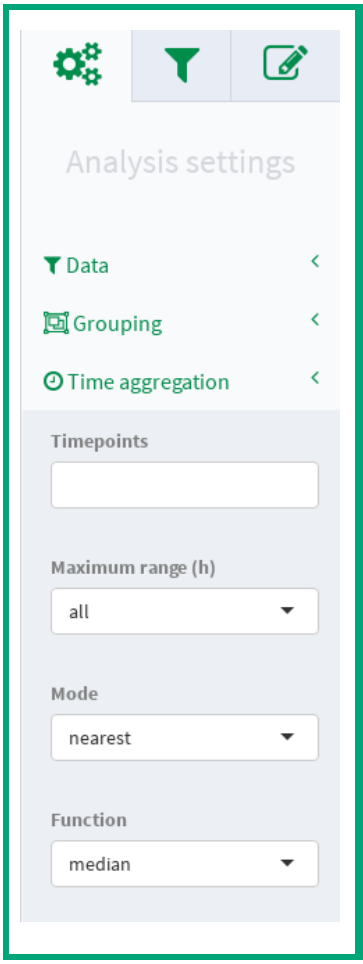
3.4.2. Overview Module

Your system generates a time series with predefined time intervals for every plant. Using the Overview module, you can aggregate your dataset by time, treatment and/or genotype to get more information from it.

3.4.2.1. Analysis settings

Time aggregation. One thing that the overview module offers is data aggregation in time blocks. Aggregation allows combining multiple data points that are within a user-specified time range into one data point. This can be used to simplify your data and make the time series systematic. Periodic data makes it easier to compare between days and plants. For example, in a system that scans 120 plants from 12:00 - 14:00 there will be too many one-minute time points. By setting an aggregation to 13:00 you could normalize all measurements to that time for further analysis.





x Mode
With multiple selected time points, there are three possibilities or modes to decide which data point belongs to which time point.
Before. Only data points earlier than the time point will be mapped to that time point. E.g., 10:00 would be mapped to 12:00 as it is earlier than 12:00 but later than 0:00.
Nearest. The default mode, where each time point is mapped to its nearest time point. E.g., 10:00 would be mapped to 12:00 because it is only 2 hours away, whereas 0:00 is 10 hours away.
After. Only data points later than the time point will be mapped to this time point. E.g., 10:00 would be mapped to 0:00 as it is later than 0:00 but earlier than 12:00.

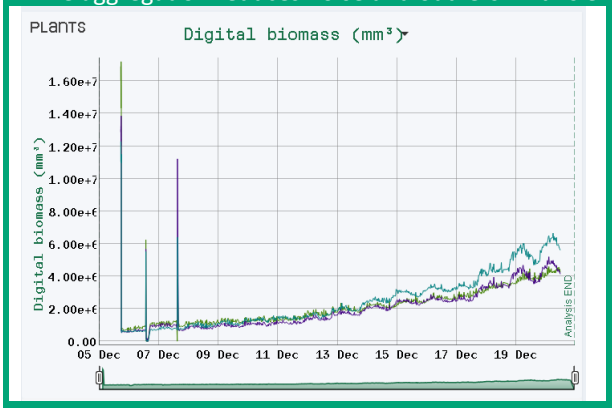
x Function
With the previous settings you define how the raw data should be mapped to discrete time points. Here, you can choose an aggregation function to combine all this mapped data to 1 value per time point. The default method is *median* which will take the median value of all data points mapped to a time point. Alternative methods are the mean (average), maximum or minimum. None is a special case and will only map the data points without aggregation.

Regular time series also allow you to use more advanced analysis algorithms like decomposition. The series decomposition is a mathematical procedure that uses a moving average to estimate the trend-cycle. It is especially appropriate in series with seasonal fluctuations.

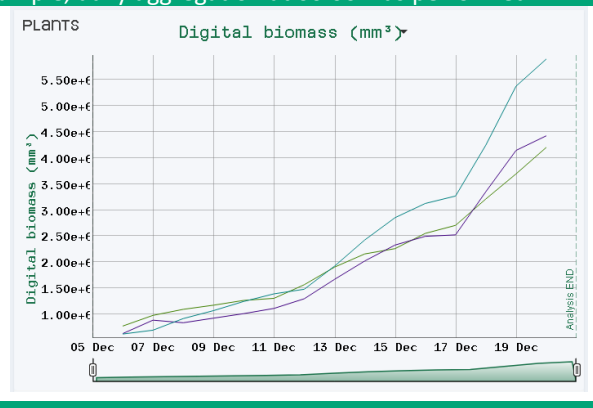
Additionally, there is always technical noise recorded during measurements. Similarly, if you manually measure the area of a plant 2 times, one after the other, the results you will get will be slightly different each time. The overview module uses the repeated measurements that your system performs to reduce this noise. This is achieved by calculating the median of your data per hour. When your data is frequent enough, outliers are likely to be filtered out as well. The image below shows how this filtering cleans your result data.

TIME AGGREGATION EXAMPLE

Time aggregation reduces noise and outliers. In this example, daily aggregation at 00:00 was performed.

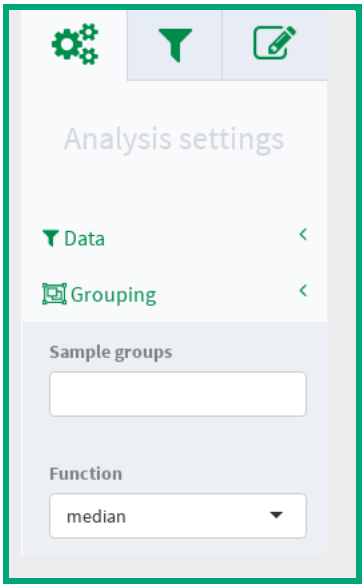


Raw dataset



Time aggregated data set

Grouping. As designated, data is stored per plant. Applying the Grouping filter, you can use the biological information to compare genotypes and treatments. For this, the plant data has to be aggregated per treatment and genotype group. You can use the time point mapping and/or aggregation to combine all plant data and calculate a treatment and genotype value per unique time point.



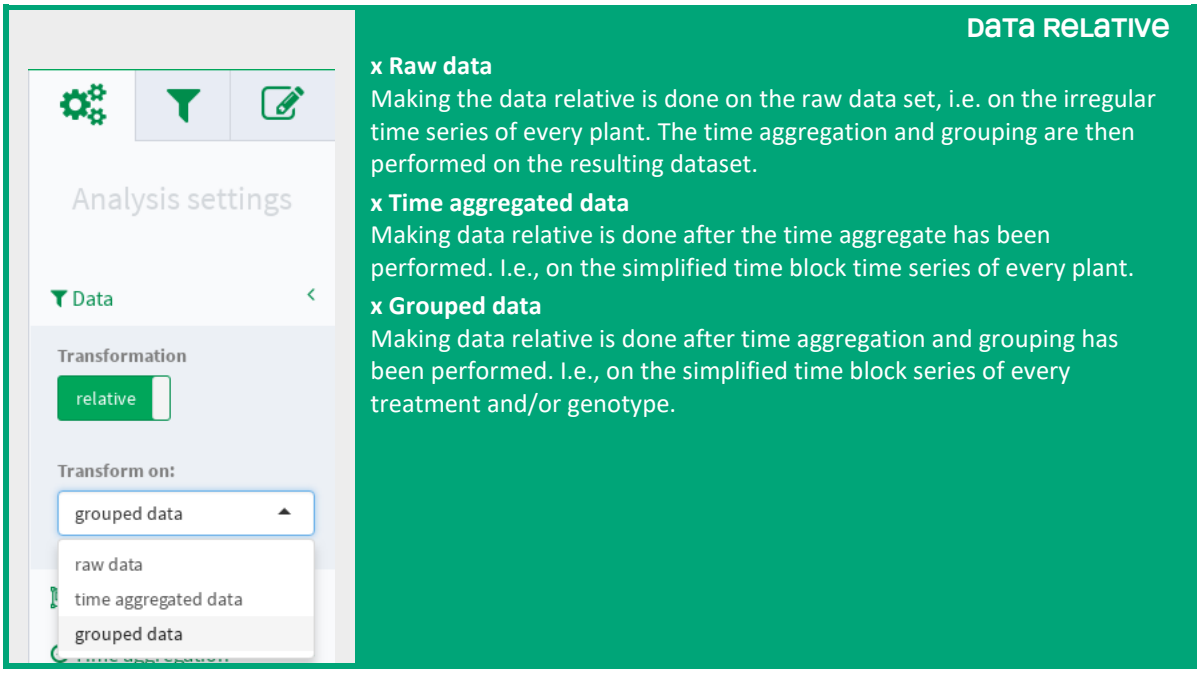
GROUPING

x Sample groups
You can choose to aggregate the plants by treatment, genotypes or both.

x Function
Like in the time aggregation, you can use multiple functions to aggregate the plants into treatment or genotypes. The possible functions are median, mean, minimum, maximum, standard deviation or sum.

Transformation. The plant data stored is absolute. When setting transformation to “relative” you get the value difference between subsequent measurements. That means that if the height of a plant is x_1 at t_1, at t_2 ($t_1 + \Delta t$) it will be equal to x_2 ($x_1 + \Delta x$). The value of Δx is not apparent. By subtracting x_1 from x_2, i.e. making the value relative, a direct measurement for the value change can be determined.

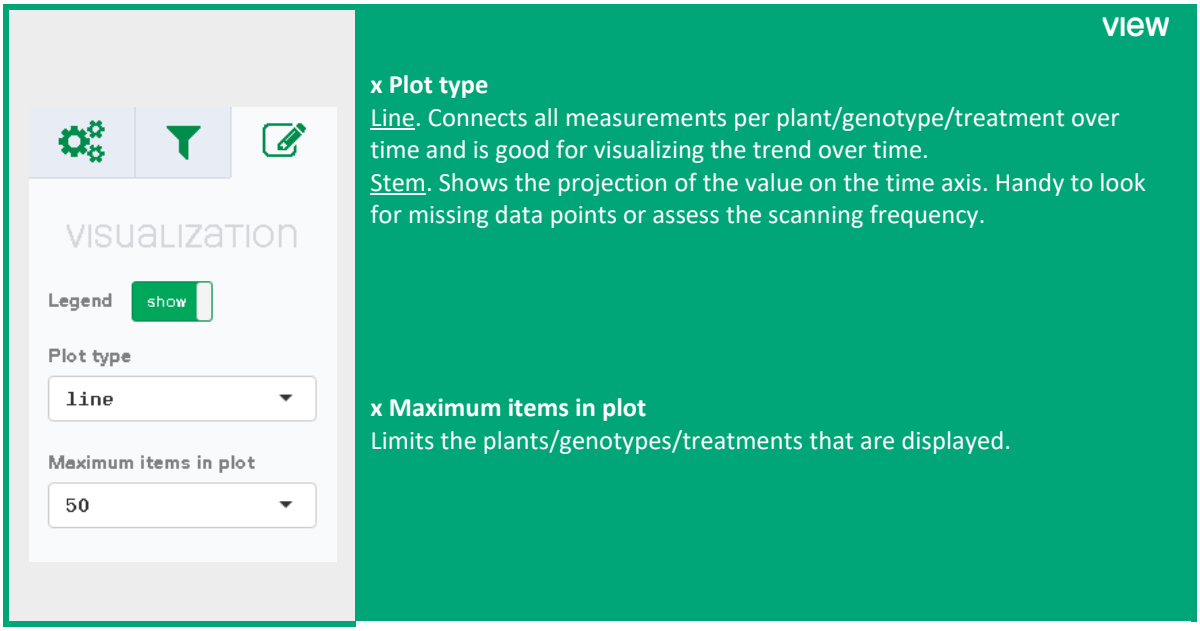
Furthermore, since generally we are dealing with irregular time series (the measurement steps are not done at the same time during the period of the experiment), the value change (Δx) by the time change (Δt) should be normalized. Otherwise, the results may show cyclic, seasonal or irregular movements. Therefore, we divide Δx by Δt, so that they become comparable between the irregular time points. When making the data relative, you can choose at which point during processing you want to perform this action.



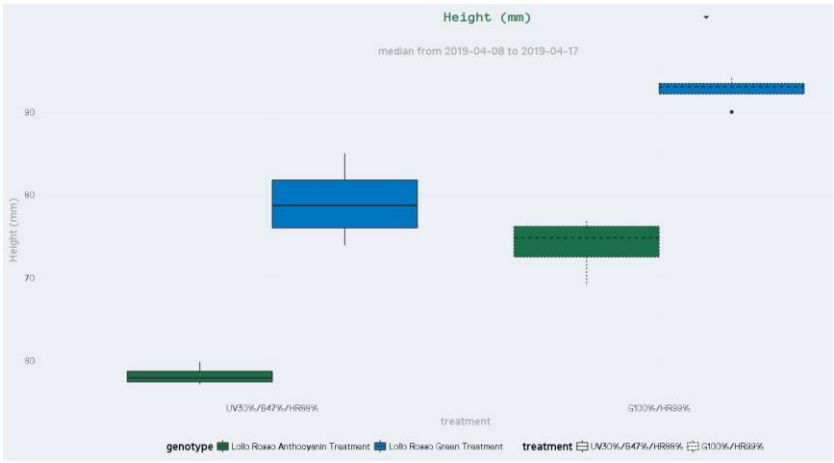
Remember that you can download the aggregated dataset by clicking the “download” button at the bottom of the settings tab.

3.4.2.2. View settings

In the image below, you can find a list of the view settings that work on the overview.



3.4.3. Snapshot Module



With the snapshot module, you can calculate an aggregated plant value of any plant parameter using the time window you define in the time filter settings. There are four aggregation methods available: median, mean, minimum, and maximum. This enables you to calculate a median height for every plant over any *x* hour period. The resulting dataset can be downloaded by clicking on the “download” button in the settings tab, and will be visualized using a boxplot view. In the boxplot view, all aggregated plant values are clustered in their respective treatment/genotype groups and visualized as boxplots (as can be seen in the example below). In the view settings you can choose to color the boxplots based on genotype or treatment. The non-colored category will be displayed on the y axis. In the example below, genotype was selected to be colored.

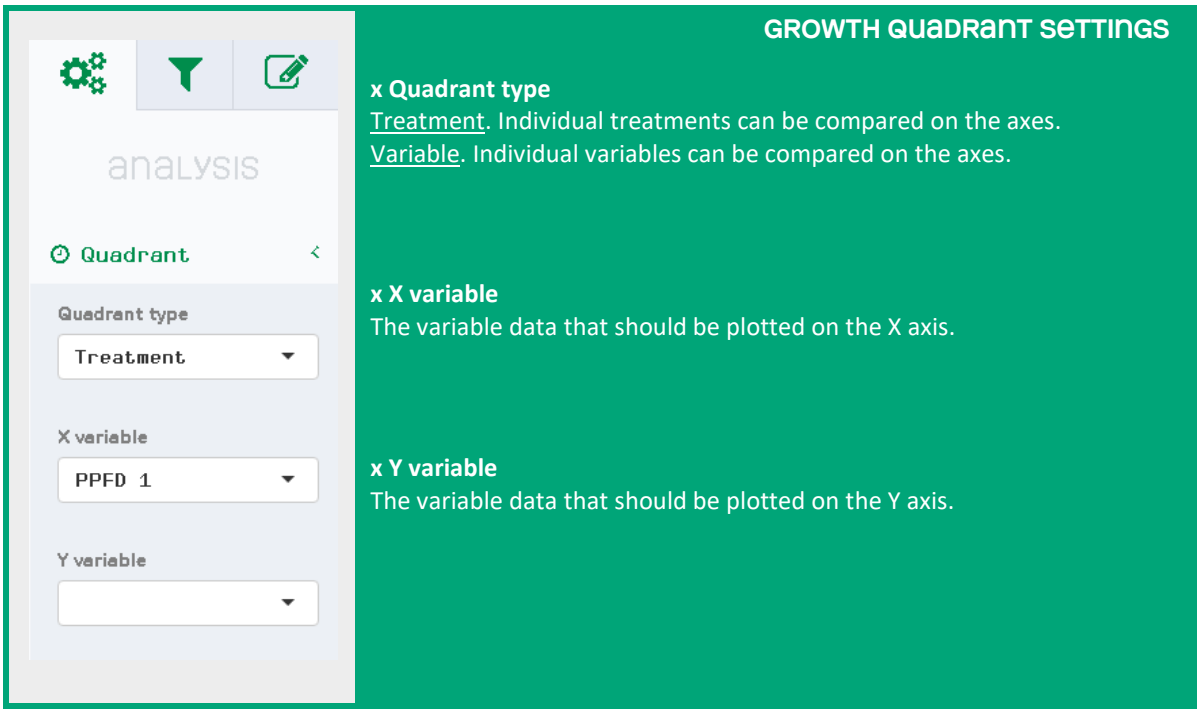
3.4.4. Growth Module

In the growth module the whole time series is combined into a single value for each plant. This gives you the growth rate, or the average growth change of a plant throughout the duration of your experiment. Generated

data can be downloaded at the bottom of the settings bar for the selected variable. These values are grouped per genotype/treatment and presented in two views, the boxplot view and the quadrant view.

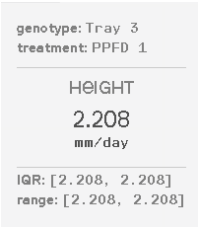
3.4.4.1. Analysis settings

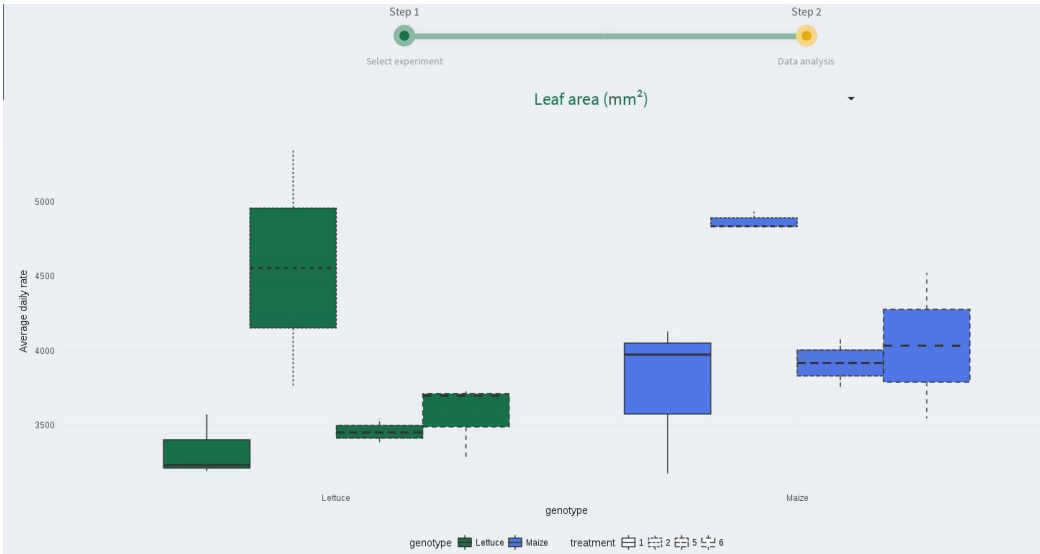
Below is the list of the quadrant view settings that are available for the Growth Quadrant.



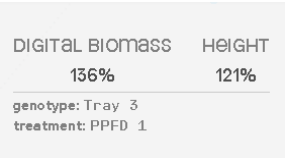
3.4.4.2. Boxplot view

This view is similar to the boxplot view of the germination module. It clusters the growth data of all individual plants by genotype/treatment and visualizes those using boxplots. Also, in this view the box color can be assigned to either genotype or treatment in the view settings. If you place mouse cursor over a boxplot, the tooltip (image on the right) will appear providing you with data about the median growth, the interquartile range and biological information.



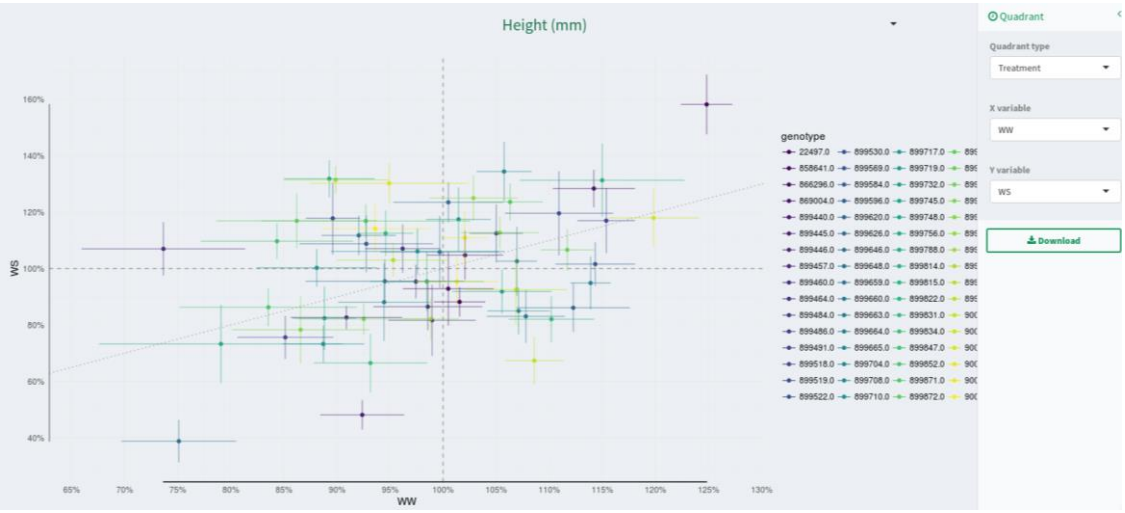


3.4.4.3. Quadrant view



Using the quadrant view, you can compare two different treatments or two different variables. Placing mouse cursor over a quadrant point will provide you with the tooltip (image on the right) that shows axes values and biological information. For the quadrants, the legend can be toggled on and off and coloring can be set to genotype or treatment. The other category will be distinguished by the point shape.

Treatment quadrant. This option allows you to normalize all the plant values to the treatment median. Therefore, every plant is expressed as doing better (> 100%) or worse (<100%) than the median (100%) of its treatment. The normalized data is then clustered per genotype and visualized as a mean and its standard deviation. This is done for the two selected treatments. The result is a scatter plot of genotypes that are divided in 4 quadrants. Each of these quadrants tells you how well each genotype performed for both treatments compared to each other, with the theoretical median (100%) at the origin (0, 0). From the example below it can be seen that the genotype in the upper-right corner outperforms all the others for both treatments (WW and WS), while the one at the far bottom left is performing worst for both treatments.



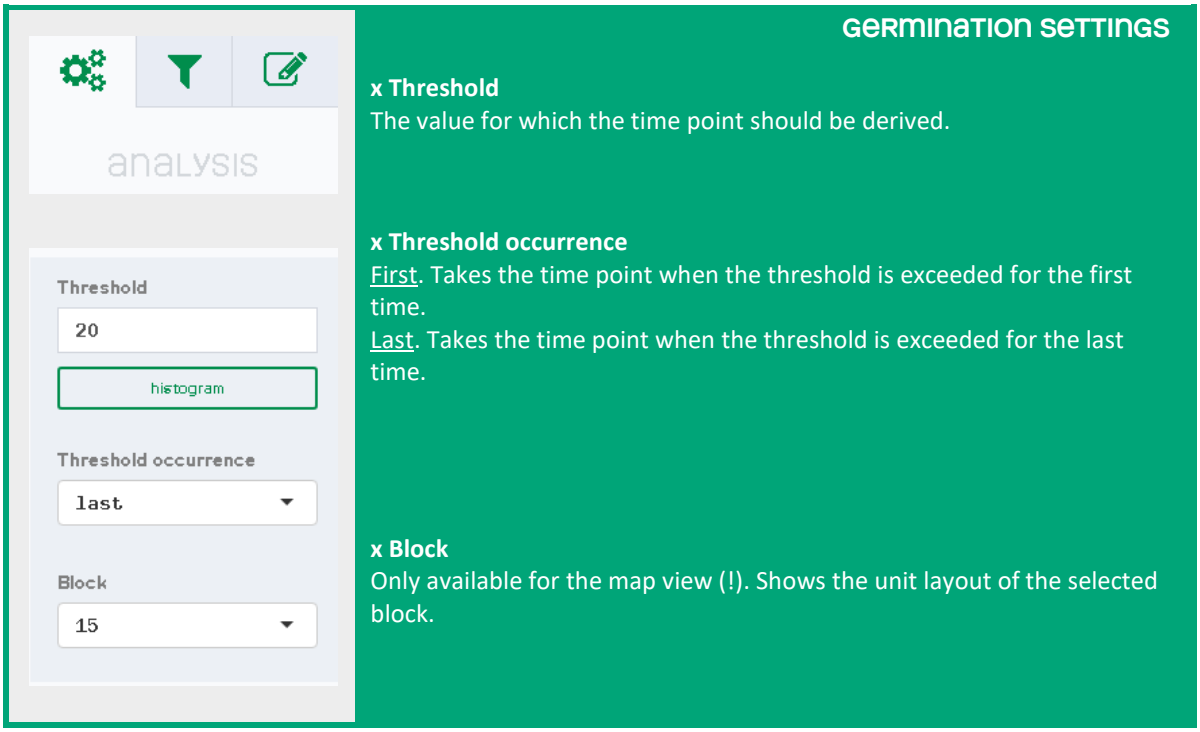
Variable quadrant. Here you can normalize all plant values to the variable median. Similarly to the "Treatment quadrant," every plant is expressed as doing better (> 100%) or worse (<100%) than the median (100%) of the selected variable. The normalized data is then clustered per genotype and treatment, and visualized as a mean and its standard deviation. This is done for the two selected variables. The result is a scatter plot of *genotypes x treatments* that can be divided into 4 quadrants. Each of these quadrants tells you how well each *genotype x treatment* combination performed for both variables in comparison to each other and the theoretical median combination which is represented as the origin of the quadrant plot.

3.4.5. Germination Module

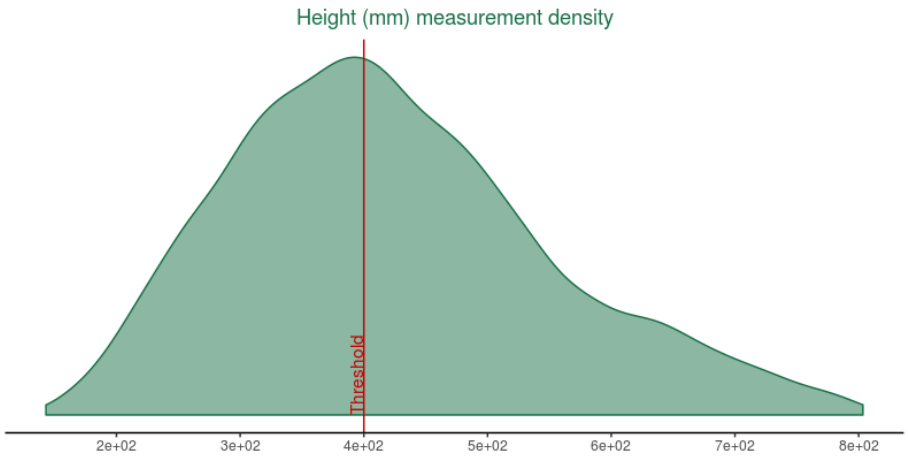
In the germination module, you can calculate the time point at which every plant reaches a certain data value. For example, you can evaluate when your seedlings reach a height of 20 mm.

3.4.5.1. Analysis settings

In the image below, you can find a list and description for each of the Germination analysis settings.



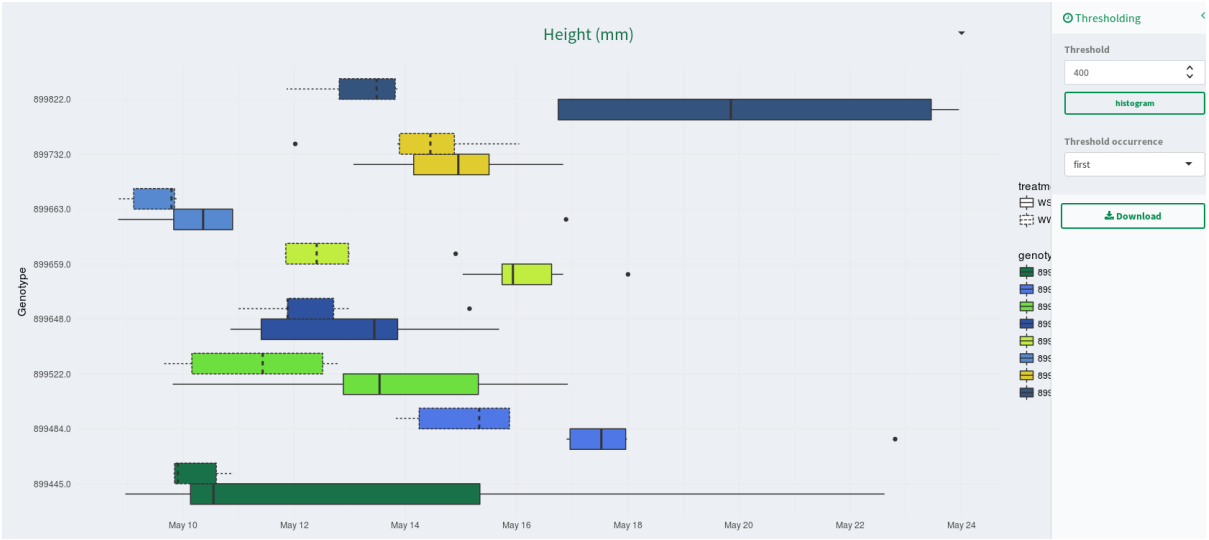
The "histogram" button in the settings bar will open a histogram of all the height measurements in your dataset. This histogram might help you to select a proper threshold.



There are two views available - the boxplot view and map view.

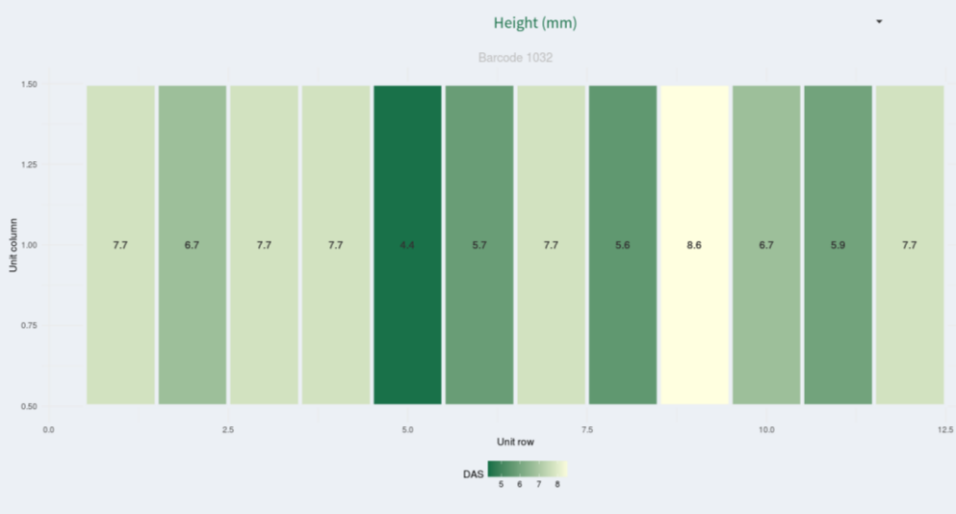
3.4.5.2. Boxplot view

In the boxplot view (shown below), all your plant time points are clustered in their respective treatment/genotype groups and visualized as boxplots. In the view settings, you can select to color the boxplots based on genotype or treatment. The non-colored (non-treated) and colored (treated) categories are displayed along the y axis.

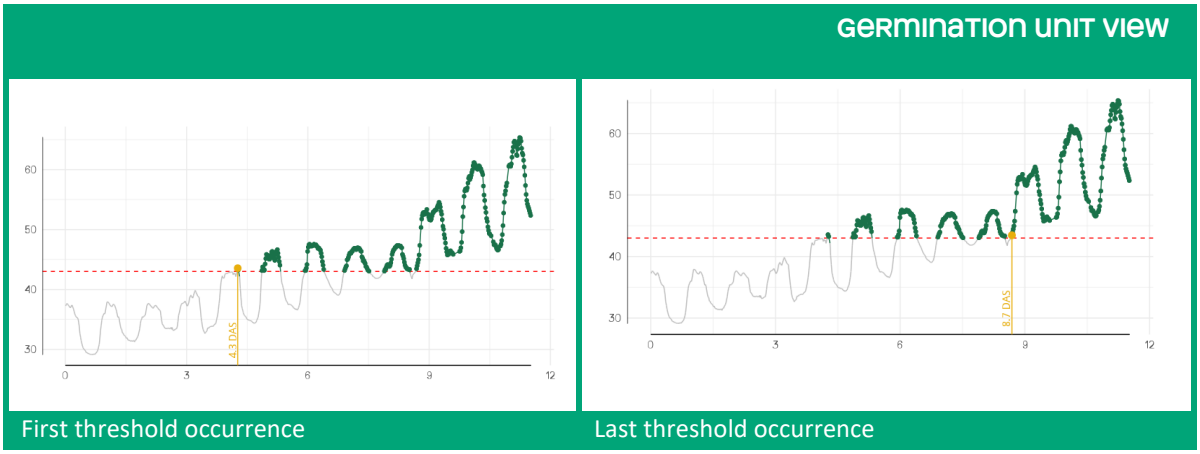


3.4.5.3. Map view

The map view gives a color-coded overview of the units per block. The color coding is based on the time (DAS-days after start) it took the corresponding unit/plant to reach the germination threshold from the start of the experiment. The start of the experiment can be adjusted in the filter settings.



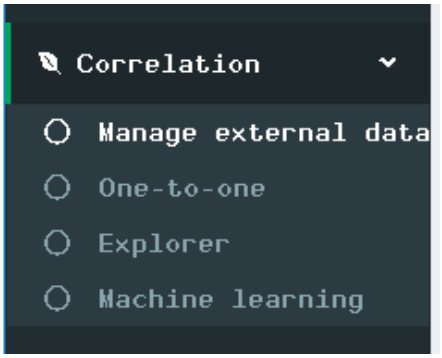
When you click on a unit you can see all its measurements and the time point when the germination was reached. In the image below, you can see that within the Germination Unit View you can either select for the first threshold occurrence or last threshold occurrence to be specified.



3.4.6. Correlation Module

With the correlation module you can import an external dataset to the experiment and search for correlation between the PSX data (generated by your system) and your external dataset.

There are three modes to search for a correlation between both datasets:



1) *One-to-one* mode, for correlating a specific external variable to a specific PSX variable (see 3.4.6.3). This mode can be used to validate manual measurements.

2) *Explorer mode*, to search for the best corresponding PSX variable over time to a specific external variable (see 3.4.6.4). Using this mode will make it easy to find a good proxy for a manual measurement you want to automate.

3) *Machine learning* mode (3.4.6.5), to create new models using PSX data that can incorporate multiple stages of growth in order to predict target features.

In addition, there is a *Manage external data* (3.4.6.2) module, where you can upload desired data.

3.4.6.1. Analysis settings

Below is the quadrant view settings list with all the available variables for the Correlation application. Each one of these steps is explained in more detail below.

GROWTH QUADRANT SETTINGS

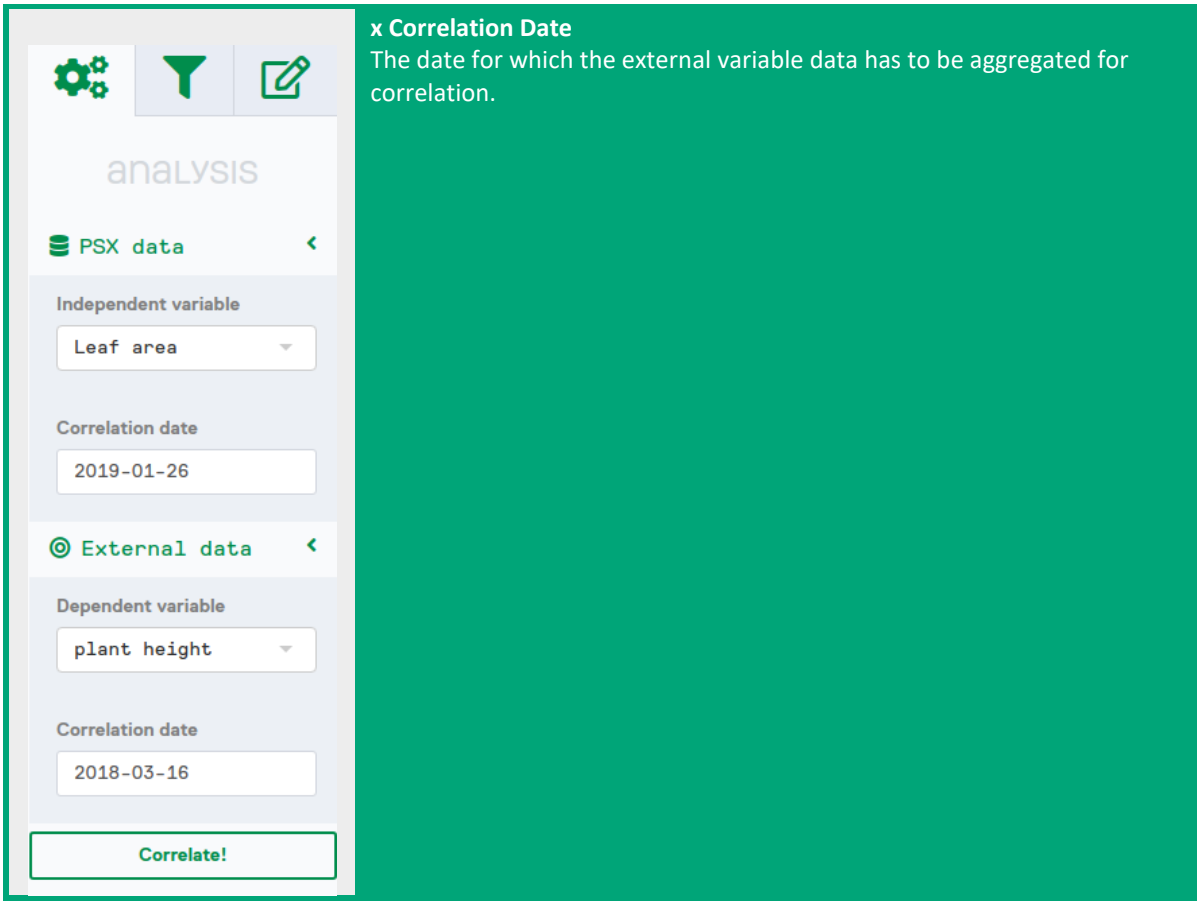
PSX data

x Independent variable
The PSX variable that will be used as the source variable to correlate with external data

x Correlation Date
The date for which the PSX variable data has to be aggregated for correlation.

External data

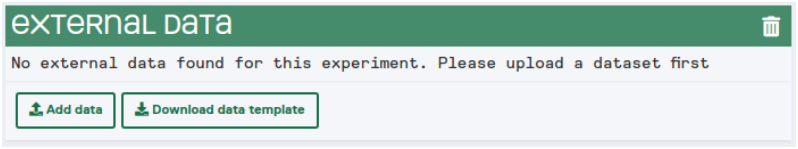
x Dependent variable
The External variable that will be used as the target variable to correlate with PSX data



x Correlation Date
The date for which the external variable data has to be aggregated for correlation.

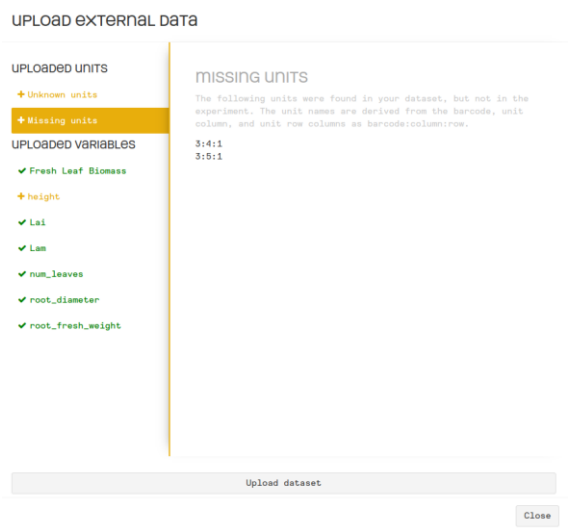
3.4.6.2. External data upload

To upload an external data set you have to open *Correlation Module > Manage external data*.

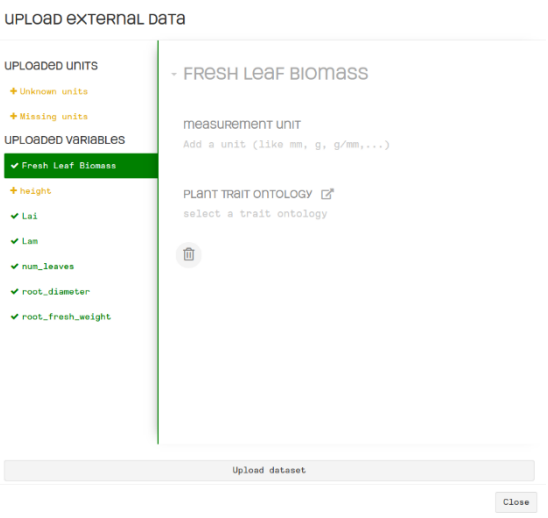


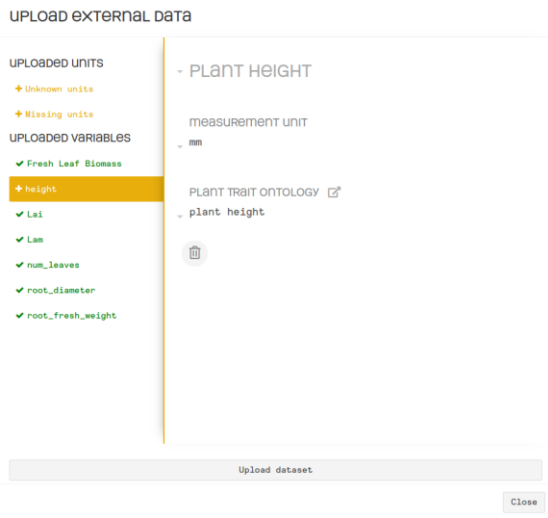
Data template can be downloaded and used as a format for later upload. This file contains a column with all the units of the experiment and a column with correlating timestamps. You can have as many or as few units and timestamps as needed. In order to add other parameters, add a column with the variable name as its header and measured values for each timestamp below. To upload the file, press *Add data* and select a filled file with a unit column, timestamp column, and a column for each external data variable. If the data format is not correct, an error will be shown and you will be asked to update the file again.

Once the data is uploaded, the units and variables in the file will be compared to those of the experiment. You will be informed if any unit in the file does not appear in the experiment (unknown units) or if the file is missing an experiment unit (missing unit).



The variables will be matched with any registered variable in the database. When there is a match, the variable will be colored green. You can still choose to map the variable to another database entry or create a new entry by typing a new variable name, and optionally defining a variable unit and/or trait ontology identifier. The variable color will be yellow for a new entry.





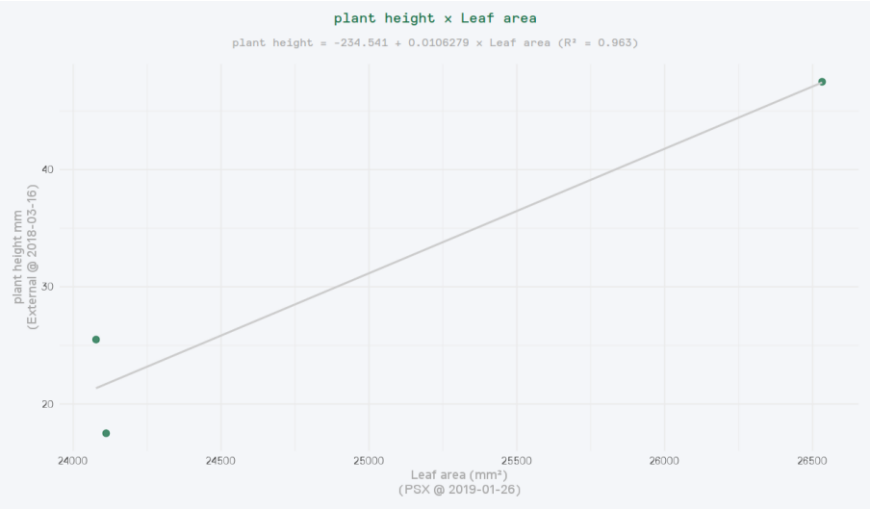
Once you have all desired matching variables on the list, you can choose to upload the external data to the database and attach it to your experiment. You can add as many or as few external data sets as you wish.

To remove the linked external data for any experiment - click the trash bin.

3.4.6.3. One-to-one mode

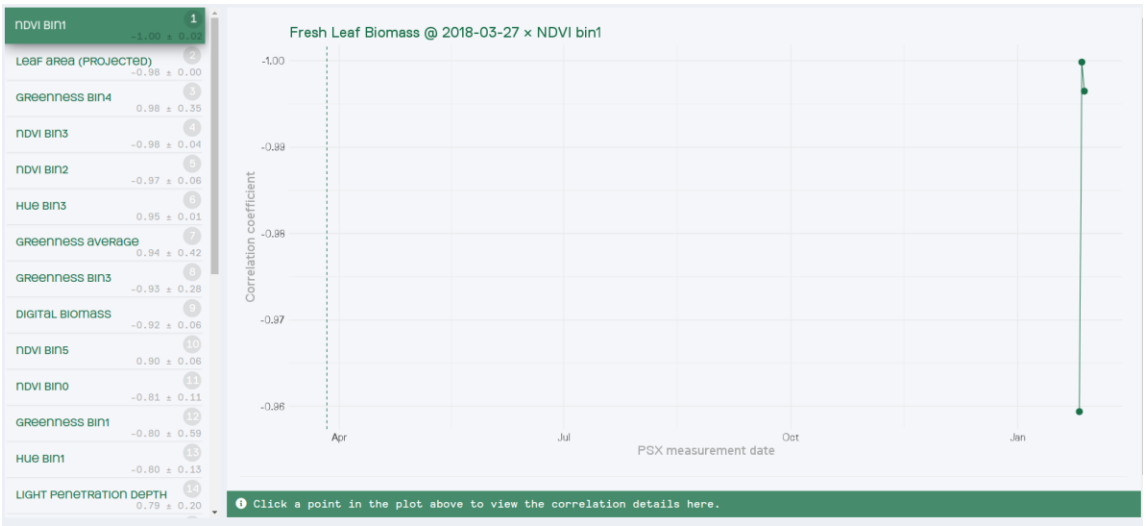
In this mode you can correlate a specific external variable to a specific PSX variable. This mode can come in handy when validating measurements. To use this mode, select necessary variables and their associated dates

in the settings bar on the right. Following that, for every unit all data will be averaged for the selected day and correlated between both datasets.

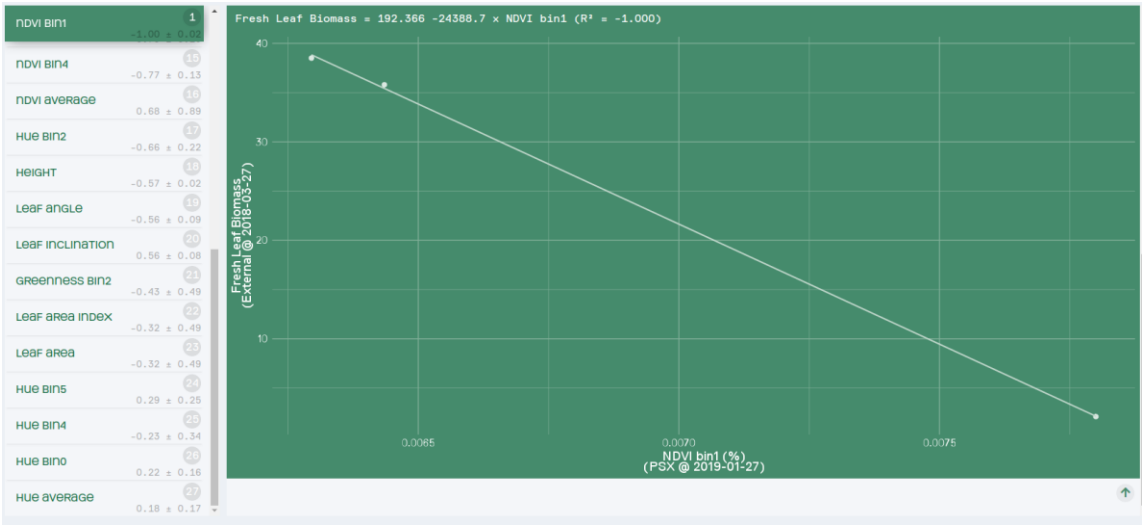


3.4.6.4. Explorer mode

In Explorer mode you can search for the best correlated PSX variable over time to a specific external variable. This mode can be used to find a good proxy for a manual measurement you want to automate. To use the Explorer, select the external variable and the date in the settings bar on the right. All data per unit will be aggregated per day, and the selected external dataset will be correlated to all variables and all measurement dates of the PSX dataset. On the left you will see a rank of the best correlated PSX variables to the selected external dataset. The PSX variables are ranked based on the average correlation coefficient. When you click a PSX variable you can see the correlation coefficient over time.



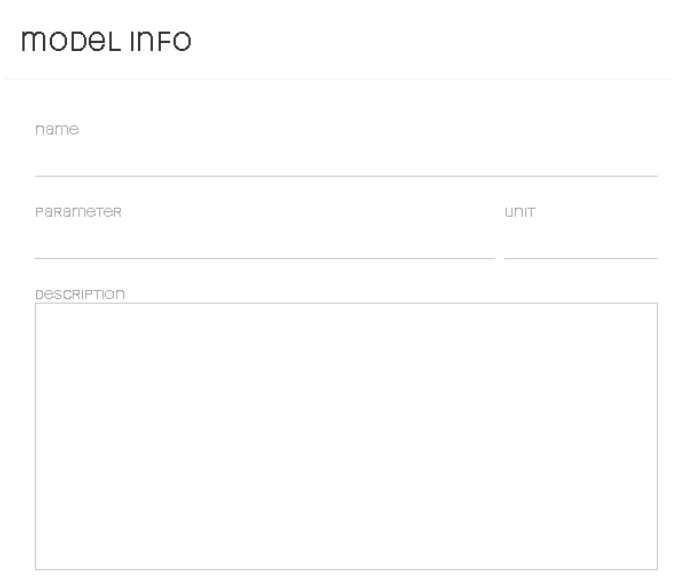
When a point on the correlation timeline is selected, a detailed view of the correlation will open.



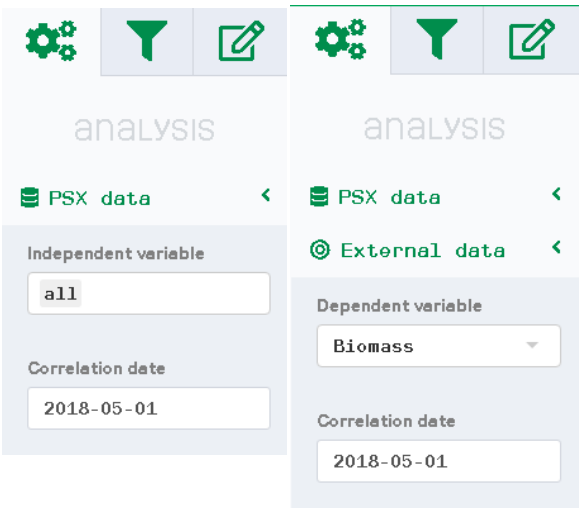
3.4.6.5. Machine learning

In the above described modes, it is possible to correlate only one source variable against one target variable. The new machine learning mode allows you to select as many source variables as needed to predict a target variable. In addition, you can store newly created models for later use in the other data modules. For example, you could build, store and re-use a model that would estimate a disease score or biomass.

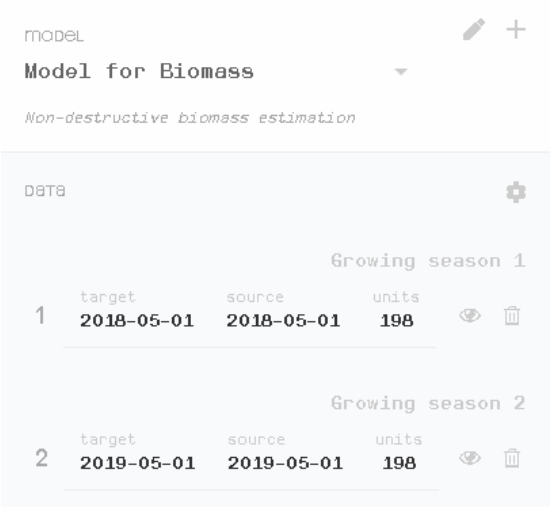
As with previous modules, first we select the name of the experiment for which we would like to do machine learning analysis. Once in Step 2, we have to create a model. On the left-hand side window, click on **+** and fill in relevant information. You can always go back and edit this form by selecting the pencil icon next to the name of your model.



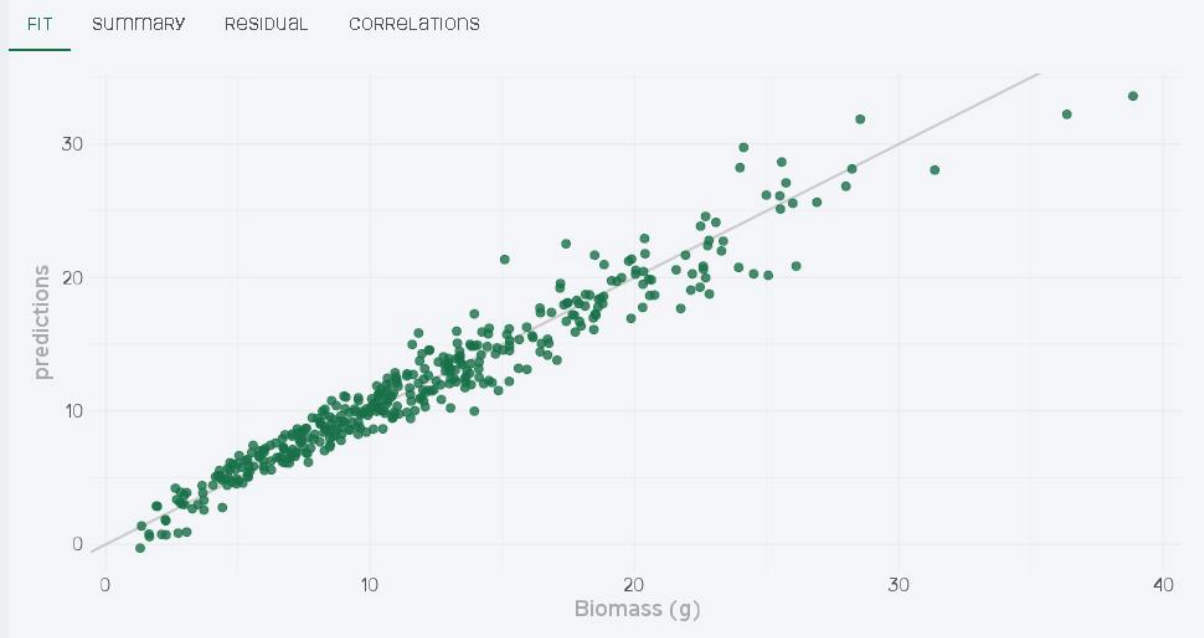
Once the model is created, you can select PSX and external data, which you are interested in correlating. For PSX data, you can add as many or as few variables as you wish. For the external data, you can select a single variable per model.



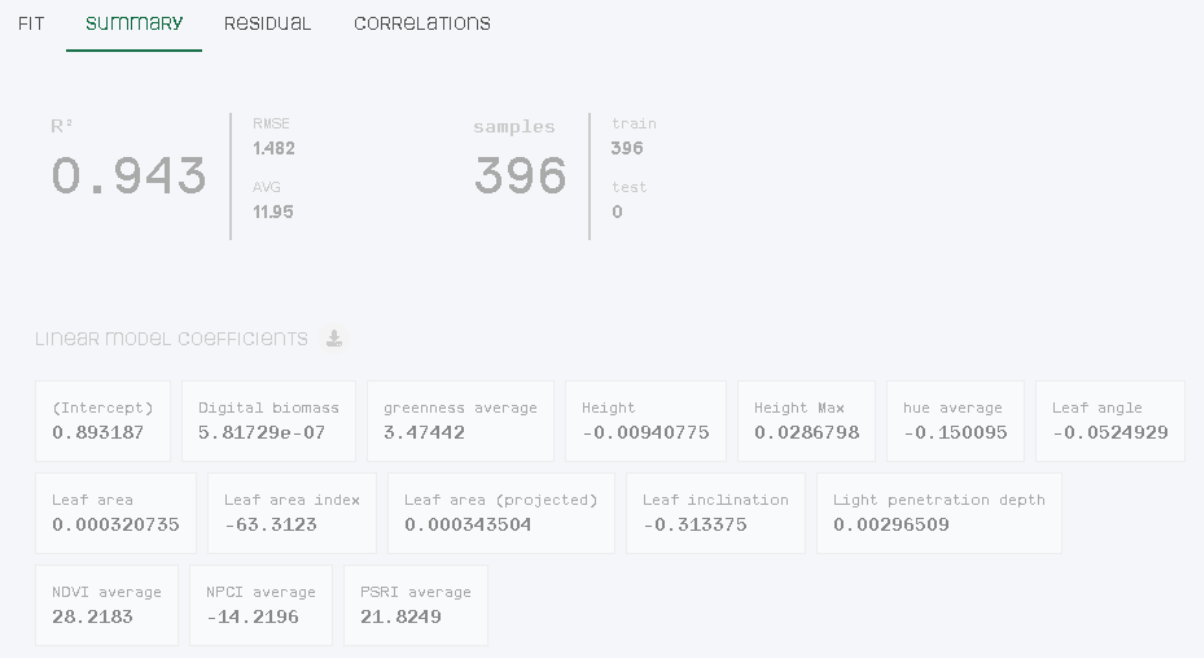
Multiple datasets can be attached to a model. This allows you to build models during a growth cycle, or even combine data across different experiments to acquire a better supported model for you target plants.



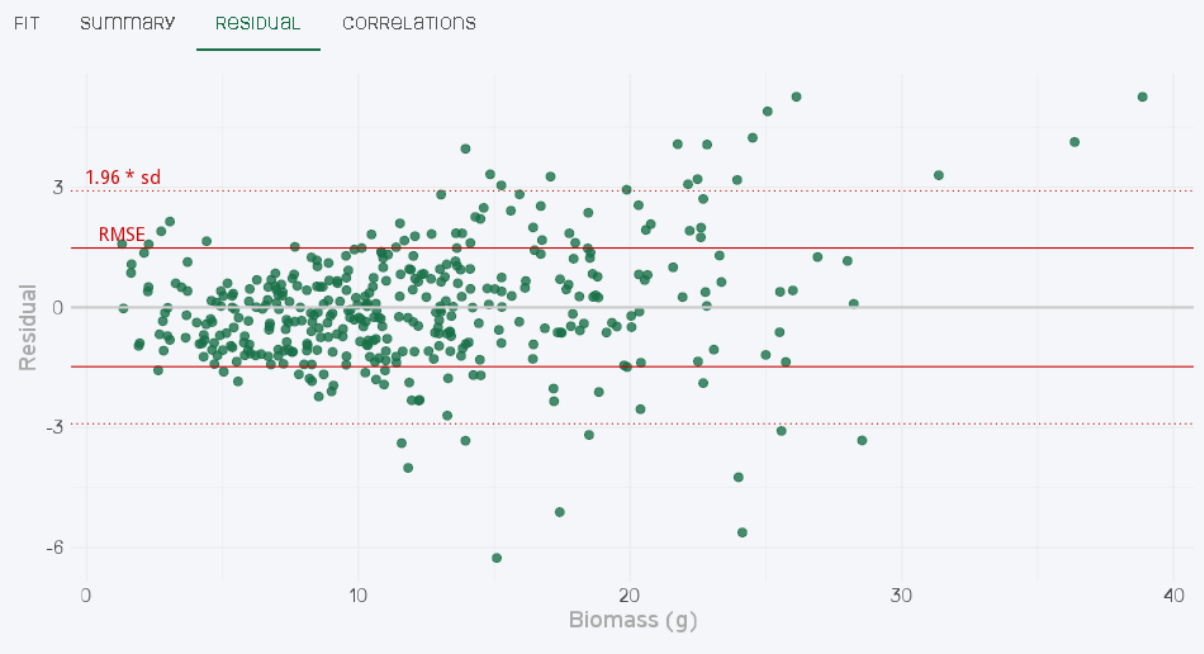
Furthermore, you can filter your data sets by time frame, treatment and genotype. For the best model fit it is advised for both PSX and external data sets to have matching days. Once you add desired data sets and select filters, you are ready to visualize data. In the FIT tab, you can view a simple prediction plot.



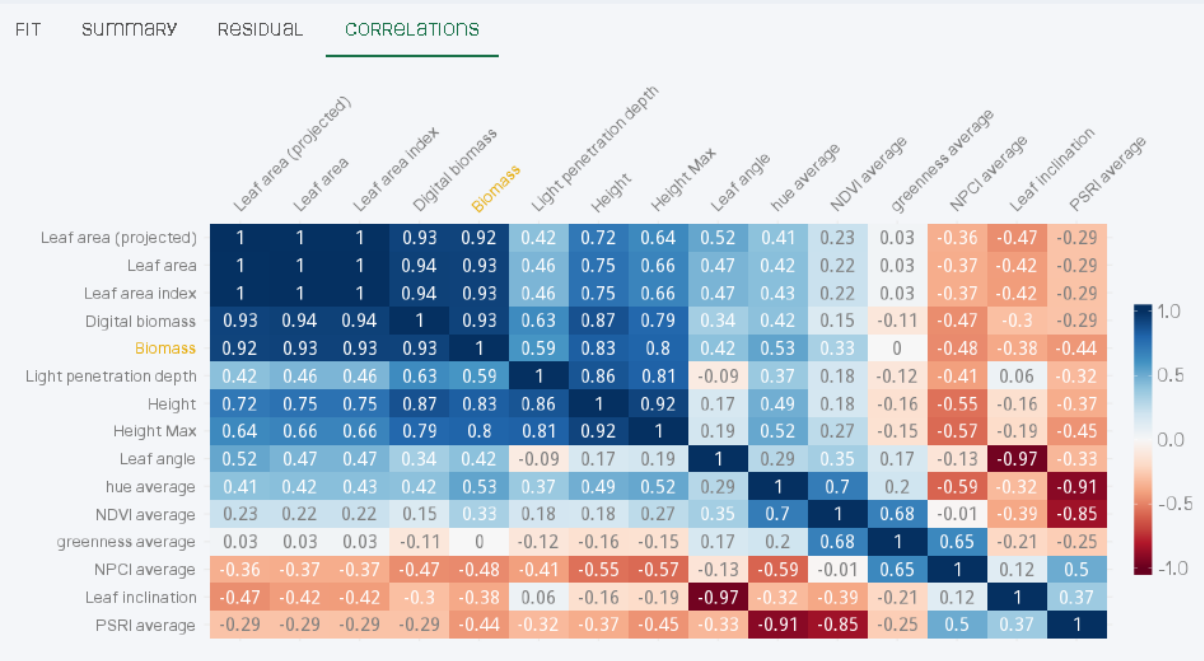
To view data, and information associated with this model, please go to SUMMARY tab. Here you can view correlation coefficients of your linear model for all selected variables. Other details of the model include R^2, root mean squared error (RMSE), as well as sample size.



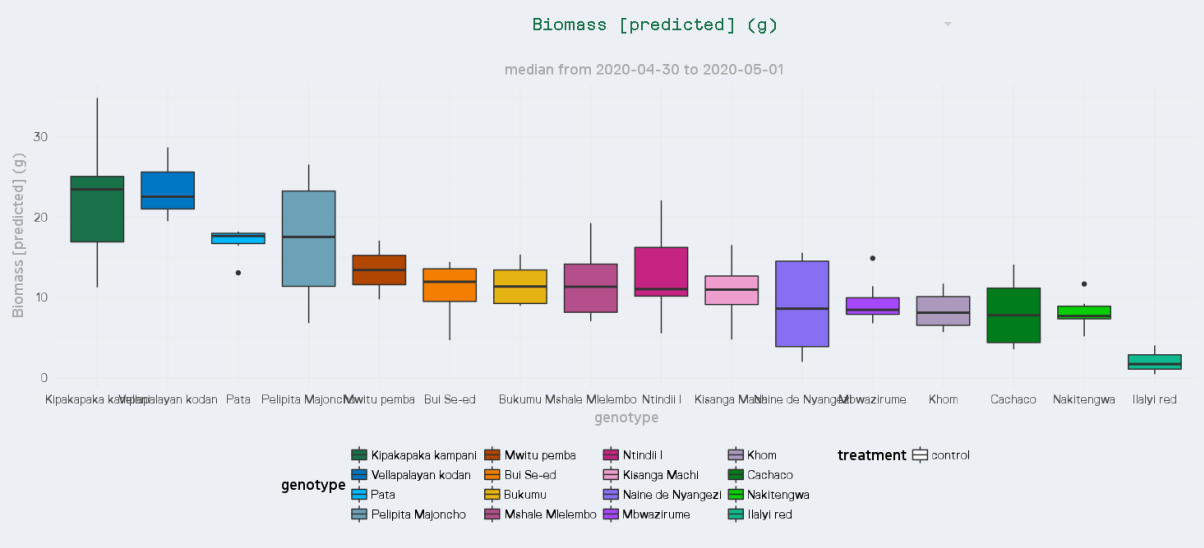
Error distribution is visualized over a range of target values in the RESIDUAL plot. It is determined based on the difference between fitted and target values.



CORRELATIONS plot represents relationships between all specified variables. This summary gives you a good overview of the data structure.

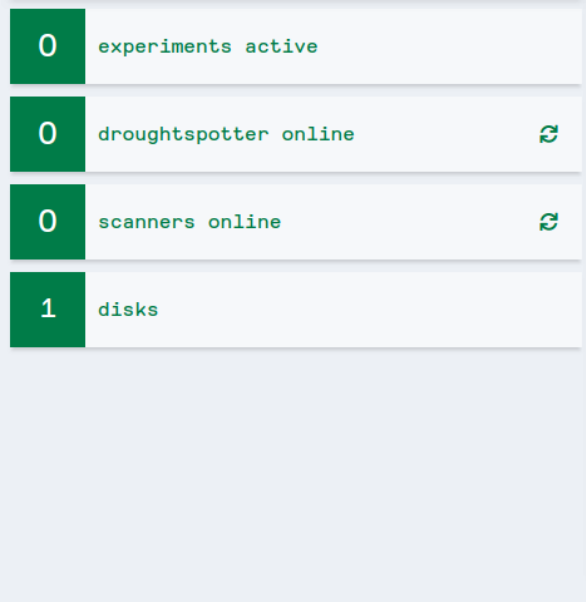


The models can later be used in other PSX Data modules. In the example below, built model is incorporated with the snapshot module. Here, the data originally collected over two growing seasons is used to estimate new features in growing season 3.


Biomass [predicted] (g)
median from 2020-04-30 to 2020-05-01
Biomass [predicted] (g)
30
20
10
0
Kipakapaka kampani
Vellapalayan kodan
Pata
Pelipita Majoncho
Mwitu pemba
Bui Se-ed
Bukumu
Mshale Mlelembo
Ntindil I
Kisanga Machi
Naine de Nyangezi
Mbwazirume
Khom
Cachaco
Nakitengwa
Ilalyi red
genotype
genotype
Kipakapaka kampani
Vellapalayan kodan
Pata
Pelipita Majoncho
Mwitu pemba
Bui Se-ed
Bukumu
Mshale Mlelembo
Ntindil I
Kisanga Machi
Naine de Nyangezi
Mbwazirume
Khom
Cachaco
Nakitengwa
Ilalyi red
treatment
control

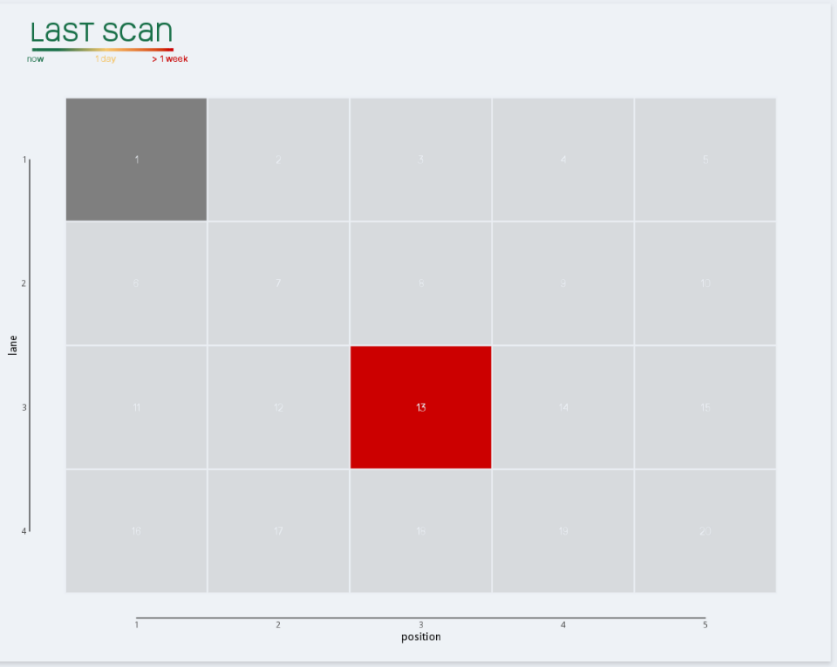
3.5. Dashboard

In the dashboard you can monitor the state of your system. On the left will be a list of numbers which can be expanded. These numbers indicate the active experiments, products that are online, and the disk usage of the device.



The overview module also provides a system overview on the right with the active blocks color-coded based on the selected feature above. The selectable features are dependent on the Phenospex sensors that are attached to the system. The two features are:

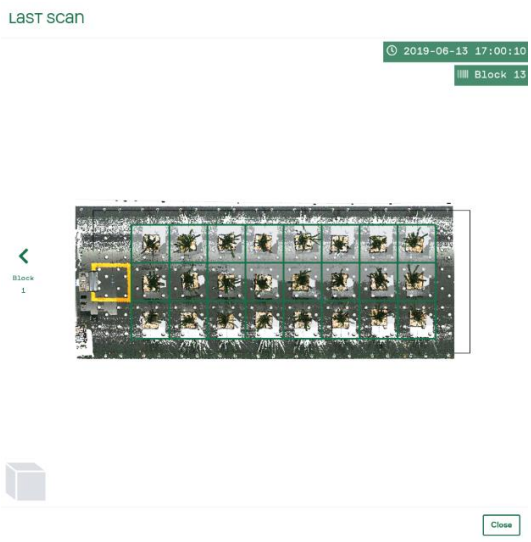
- **Last Scan** (planteye), time that elapsed since the last scan was made for the corresponding block and goes from green (now) over yellow (1 day ago) to red (1 week ago). Dark gray blocks have not been scanned yet whereas light gray blocks do not belong to any active experiment.
- **Last weight measurement** (DroughtSpotter)**,** time that elapsed since the last weight measurement was made for the corresponding block and goes from green (now) over yellow (1 day ago) to red (1 week ago). Dark gray blocks have not been scanned yet whereas light gray blocks do not belong to any active experiment.



PLANTEYE

In the top left there is a window that shows the latest scan. Whenever a new scan is made, a “refresh” option will become available, allowing you to update your view to the latest scan.

You can click any of the active blocks in the overview to visualize the last scan that was made for that block. Clicking left or right from the visualization will easily allow you to go to the latest scan of the previous or next active block.

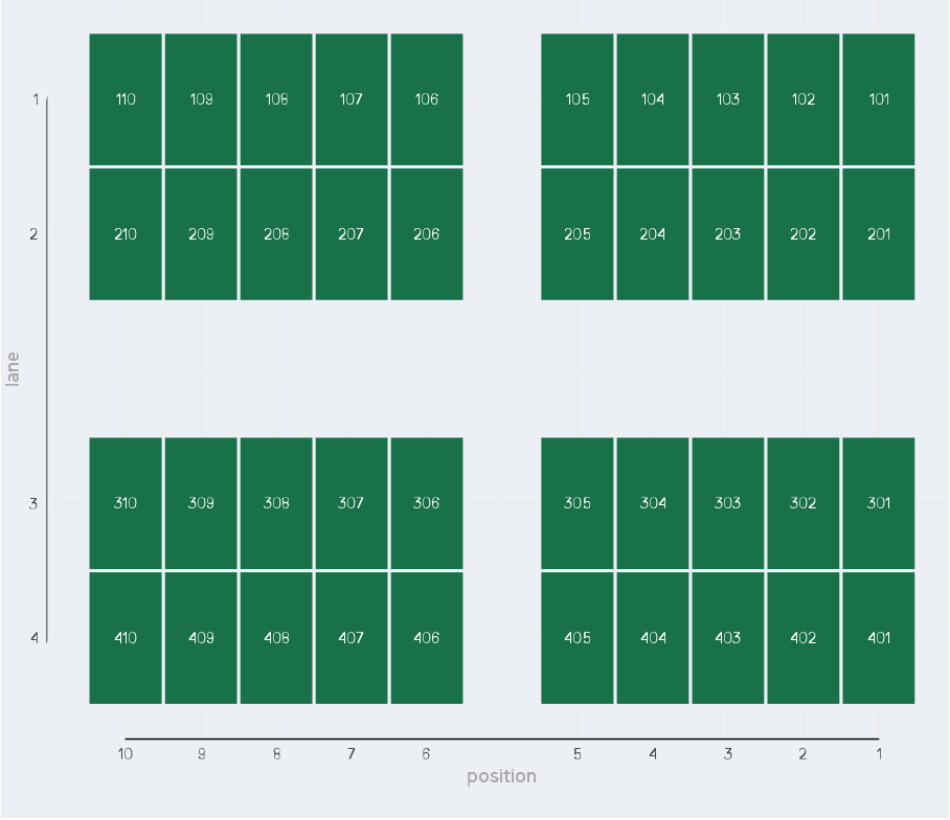


3.6. System Board

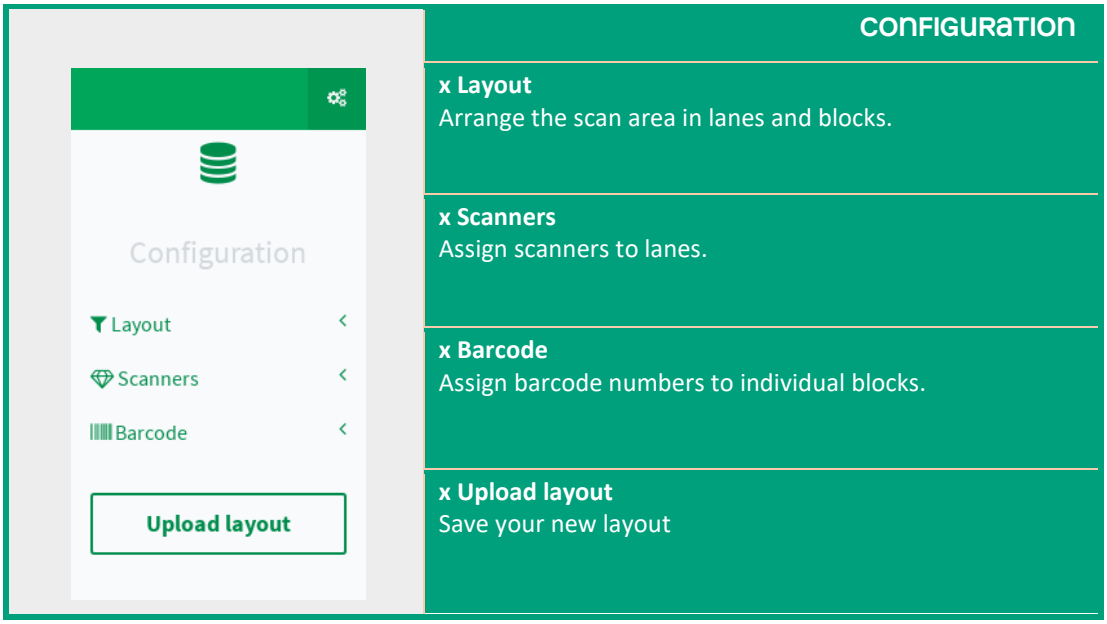
The system board is only accessible by users with an admin role. It allows you to manage and configure the systems to your specific needs. The board consists of 4 modules: Layout, PHENA, database and users.

3.6.1. Layout Module

In HortControl we often make use of the system ***Layout***. It is a visual representation of your experiment setup that is separated in lanes (vertical) that are further divided in numbered blocks with unique IDs from 0 to 9999. These blocks are the core reference points to a part of your system. In the example below, you have a total of 40 blocks within the 4 lanes.

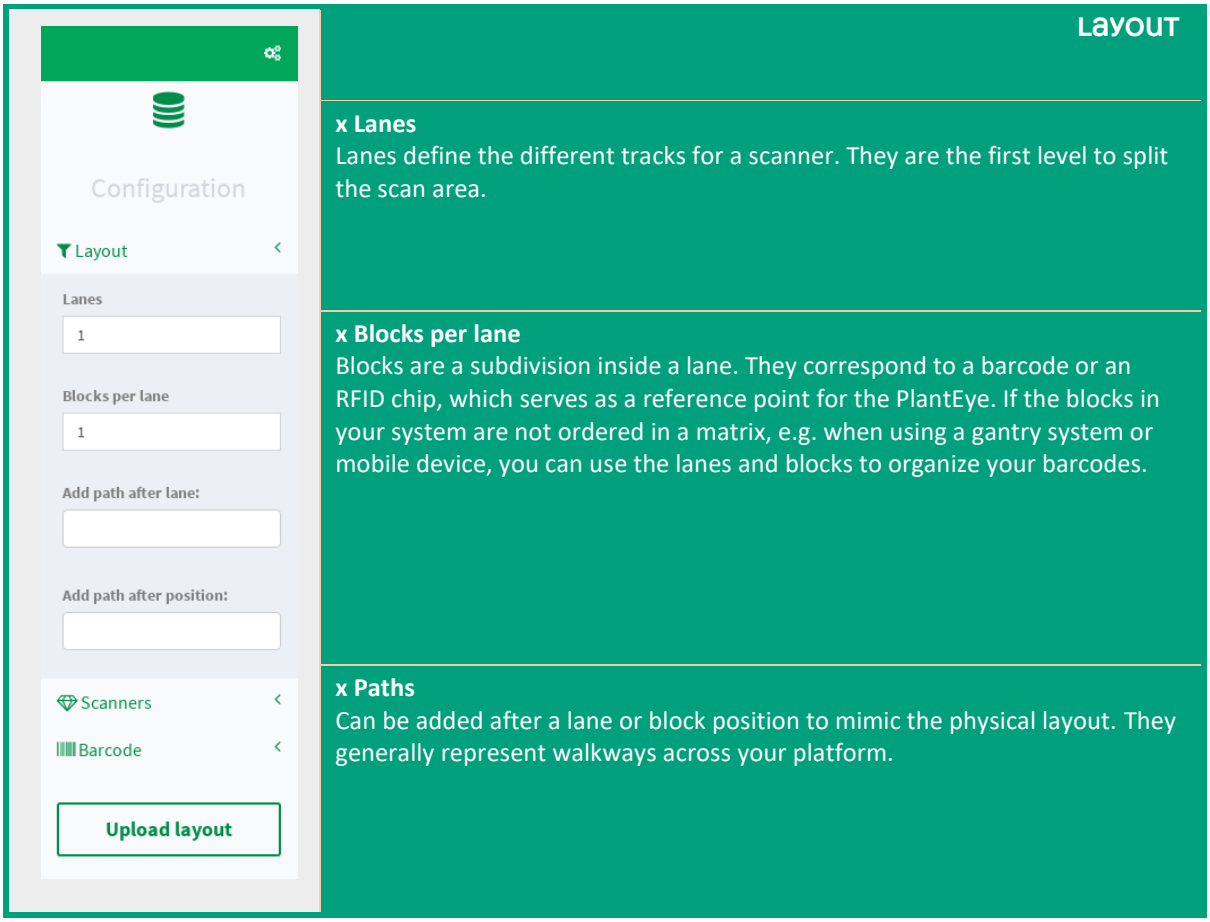


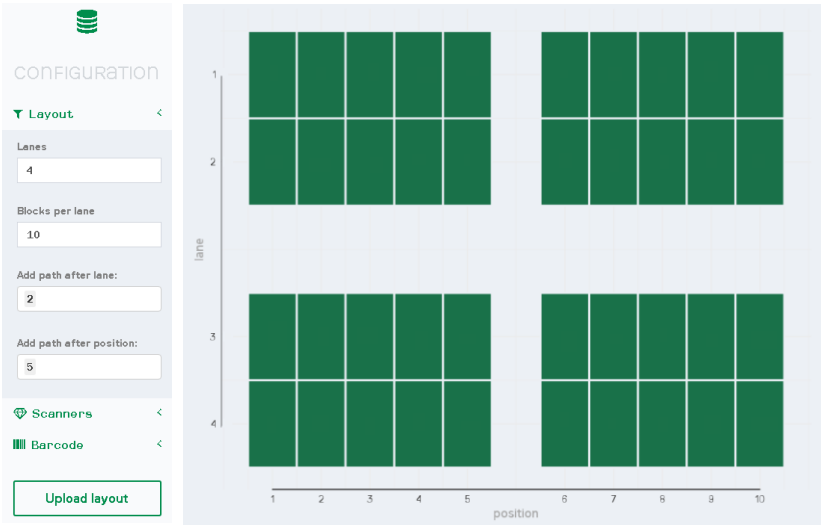
Our system is flexible and the layout can be changed in order to reflect the physical layout of the field, the greenhouse or the walk-in growth chamber. By default, Phenospex provides an initial layout appropriate for the system you just bought. However, this layout can be adjusted if the configuration of the physical layout changed and/or you want to add extra barcodes. Setting up a layout follows three steps. These steps are organized in settings groups in the settings sidebar. To open the sidebar, click on the settings icon in the top right corner.



3.6.1.1. Layout configuration

The first step involves subdividing your scan area into lanes and blocks. For this you select the **Layout** setting tab for more options. Below you can find each of the options and their descriptions.

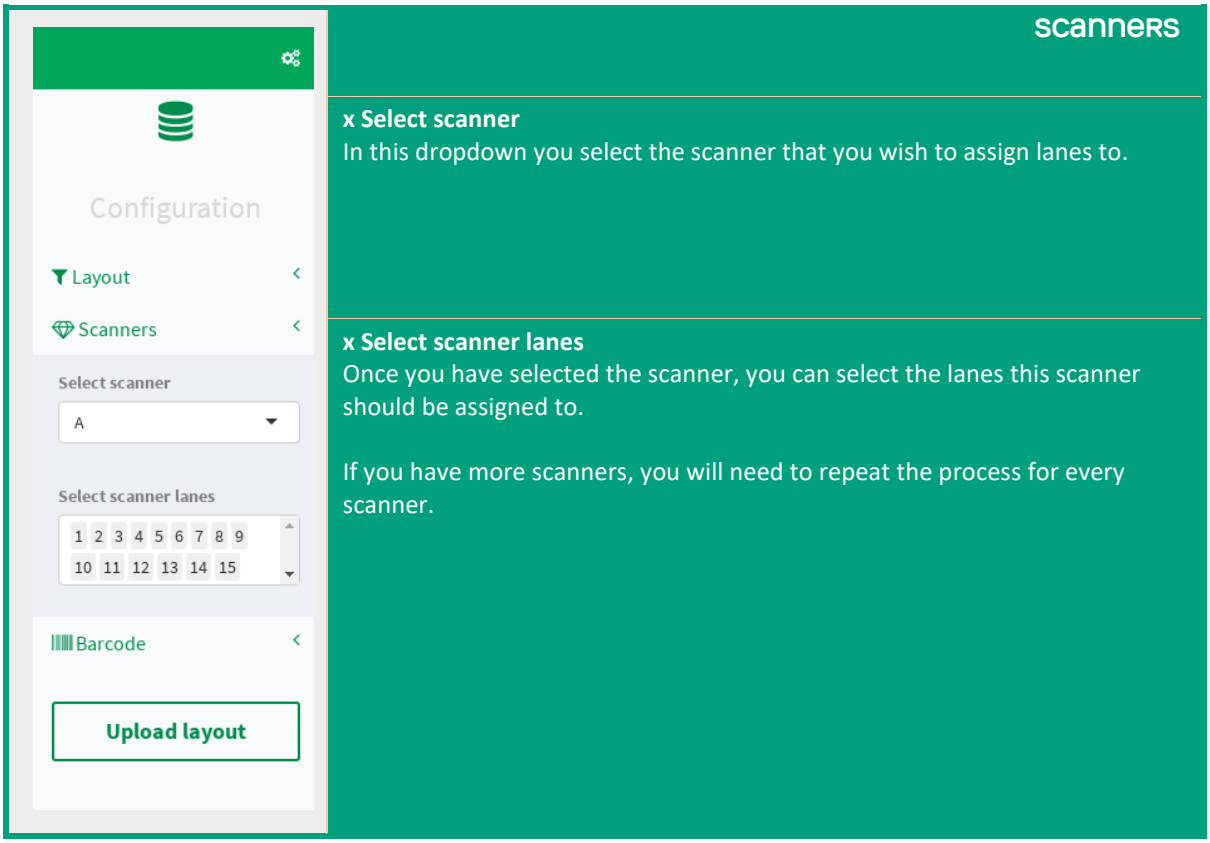




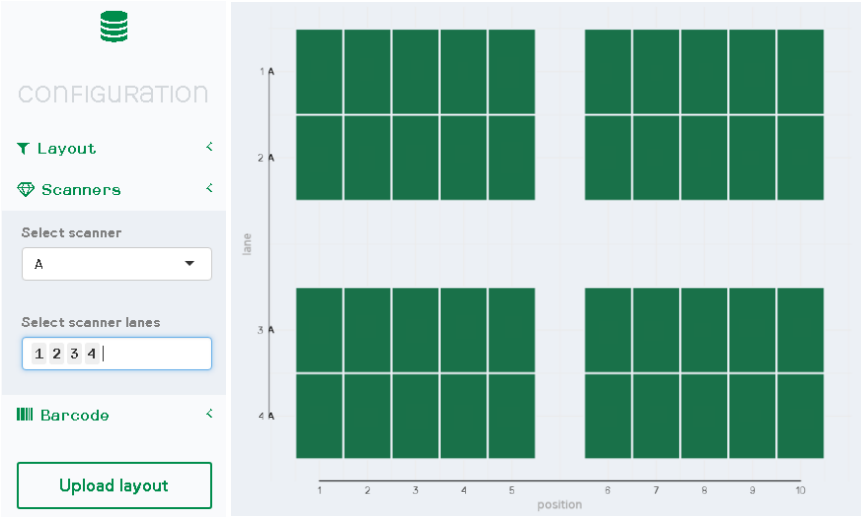
In the example on the left, we have set up a layout with 4 lanes and 10 blocks per lane. We added a horizontal path (parallel to the scanner's direction) after lane 2, and a vertical path (perpendicular to the scanner's direction) after position 5.

3.6.1.2. Scanner assignment

Now that we have divided our scan area, we need to assign a scanner to each lane. Therefore, we expand the **Scanner** setting tab.



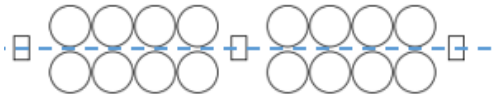
In the example on the right, we assign all 4 created lanes to a single scanner A.



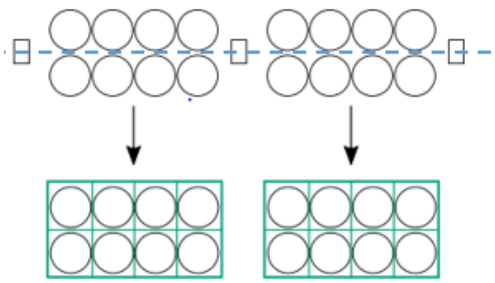
3.6.1.3. Barcode assignment

Each block within HortControl's layout has to be linked to a position within the scan area. The most common identifiers in Phenospex products are barcodes (image of barcode on the holder on the right).

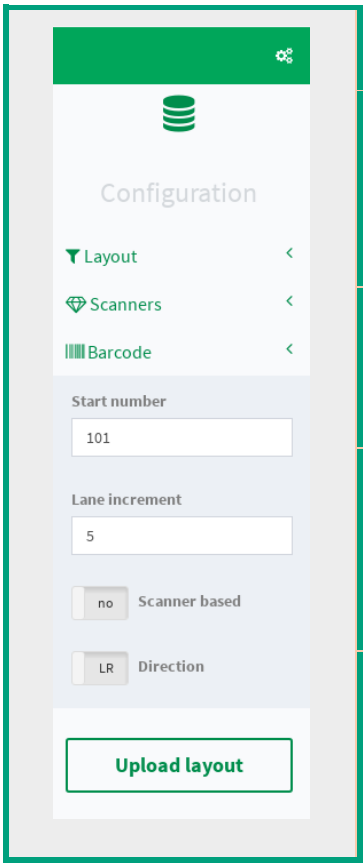
In this step, barcodes are configured to match your setup. In most cases, those will be provided to and set up for you by Phenospex. However, if there is ever a need to change the setup in the field, please make sure you change the configuration within HortControl as well. Barcodes should be placed in the linearly ascending or linearly descending order. If there are multiple lanes, fill in the first row first, then move over to the next. In some cases, when there is a large number of plants per lane, it may also make sense to place multiple barcodes within a single lane, sub-diving it as shown on the image below (blocks represent barcodes, circles – plants, and blue dashed line – PlantEye path).



The above example should be translated into HortControl in the Experiments Board as follows (with each of the plants occupying its own block):



Within the Configuration step, a “Start number” or the number of your first barcode should be specified. Furthermore, under the “Lane increments” you should identify how many blocks are between the barcodes, or per each lane. If you have multiple scanners, and for each of the scanners there is the same set of barcodes (two scanners, with barcodes numbered 101 through 501 per each), the “Scanner based” option should be set to *NO*. In the case of a single set of barcodes, each with a unique number, that preference should be set to *YES*. The “Direction” should incorporate the position of the initial barcode with respect to the direction of the PlantEye.



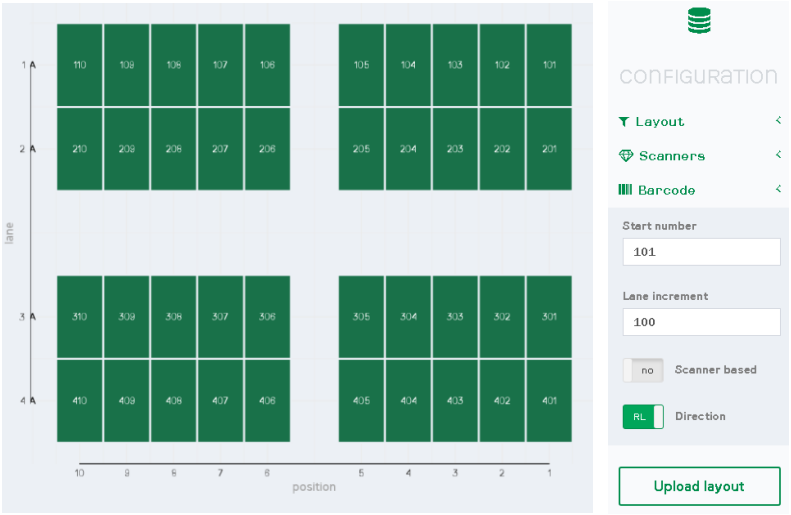
BARCODE

x Start number
The barcode number for the first block of the first lane. The subsequent blocks of the lane are numbered incrementally.

x Lane increment
Indicates the step size of the blocks between lanes.

x Scanner based
NO if you want to restart barcode numbering per scanner.
YES if you want unique barcode numbers in your system.

x Direction
ON starts first block of a lane is positioned left.
OFF starts the first barcode of a lane at the right side.



In the example on the right, we start the barcode numbering from 101. For each new lane, the block number will be incremented by 100. We use unique barcodes throughout the system and start barcode numbering from right increasing to the left, following the direction of the scanner.

Now that the layout is set up you can press the “Update layout” icon, which will update your layout. You can now use the new layout for your next experiments.

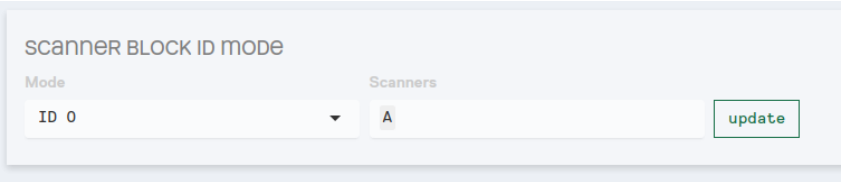
IMPORTANT

Barcode setup is one of the most crucial steps for your experiment. Barcodes should also be fully visible to a scanner. Incorrect positioning, or setup can result in incorrect or complete loss of data.

3.6.1.4. Block ID mode

PLANTEYE

Block ID mode offers a way of manually setting the block id mode of your system. The block id mode specifies how your system stores scans. There are three modes available, which you can select, assign to a scanner and update.



Metal barcode mode

When a scanner recognizes a physical metal barcode (provided by Phenospex), it will translate it to the corresponding block id. The scanner will then assign any subsequent scanning area to a file identified by that block id.

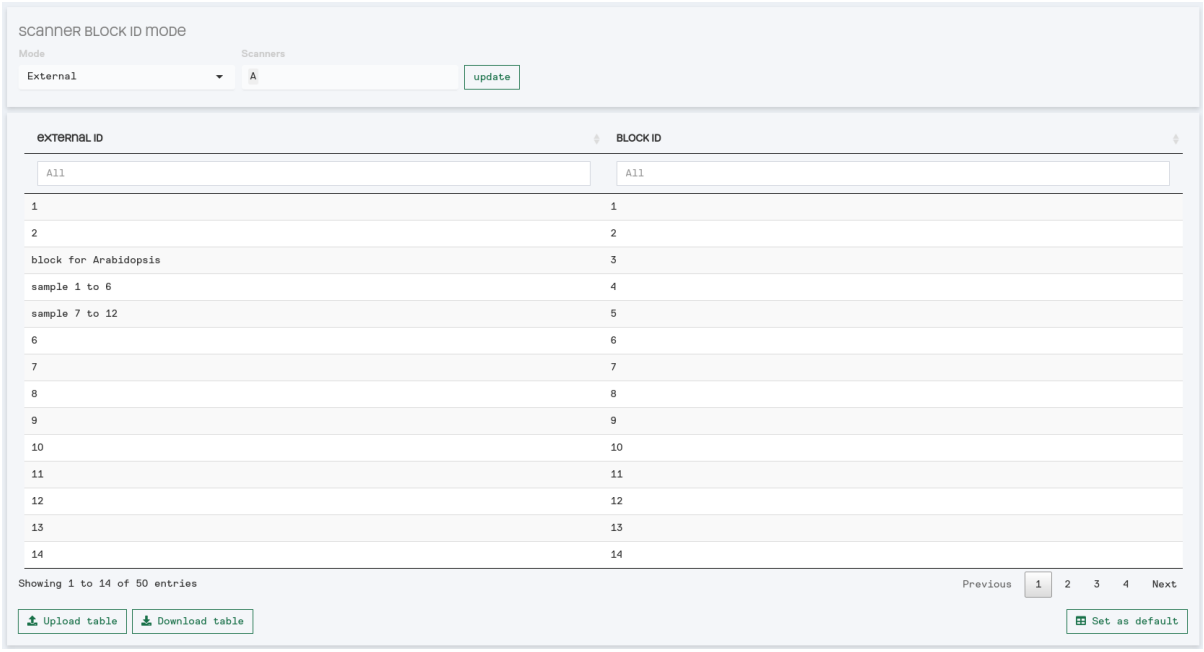
ID 0 mode

In ID 0 mode no block ids are used. All scanning area will be assigned to block 0.

External mode (live mode)

In External mode the user has the possibility to translate a custom number or string to a system block number. E.g. a user can assign “block for samples 1-6” to system block number 1. This mapped block identifier can be selected in the *Live* module of the Experiment (3.3.3) Board and set as the next block id for the scanner to assign data to. For customers with a TraitFinder, Phenospex distributes a physical barcode scanner that can be coupled with their HortControl. This scanning system allows customers to use any 1D barcode as a corresponding block id. When this mode is selected you will need to create the “translation” table from your external block identifier to the internal block number of your Phenospex system. You can choose to manually update any entry in the table, or download and re-upload a CSV table that you can adjust using text editor or excel.

After a PlantEye scan in external mode, you can select if the external barcode has to be discarded or kept for a next PlantEye scan using the “After scan?” toggle button. Discarding the external barcode after a scan is a fail-safe option to avoid that a new scan would be assigned to the previous (wrong) external barcode.



The translation table can also be generated using the physical barcode scanner, where an external barcode digit is translated into its corresponding block id digit, i.e. external barcode 1 would translate to block id 1, external barcode 2 would translate to block id 2, etc. For this purpose a barcode formatted as **GENERATE %number%** will generate such a translation table for the specified number of blocks. E.g. **GENERATE 250** will auto-generate a translation table for blocks 1 through 250.

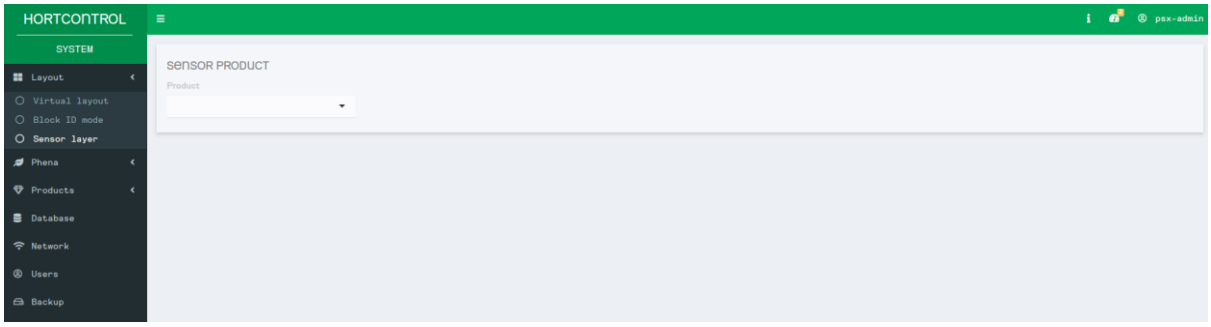
The physical scanner input also supports the barcode **DELETE ALL** to delete the translation table and start over.

If the scanned barcode is not in the translation table yet, a new entry will automatically be created with the next unassigned block id.

3.6.1.5. Sensor layer mapping

DROUGHTSPOTTER

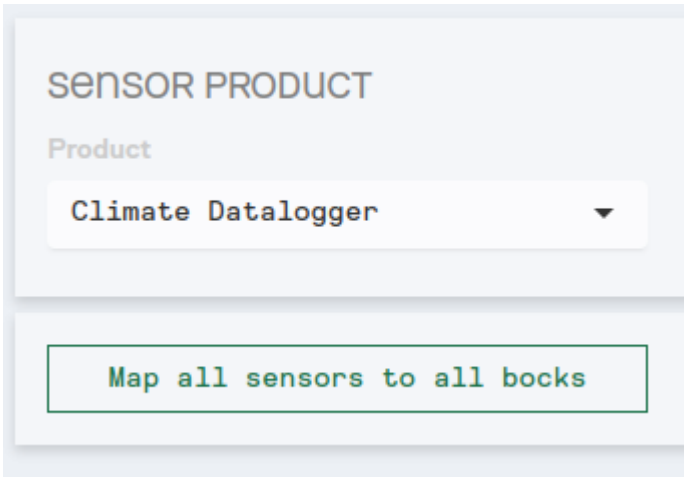
Every time a new virtual layout is created, you need to map the connected sensors, such as DroughtSpotter and datalogger, to it. This can be achieved using the sensor mapping module.



In this module select the sensor and map it to the new virtual blocks accordingly.

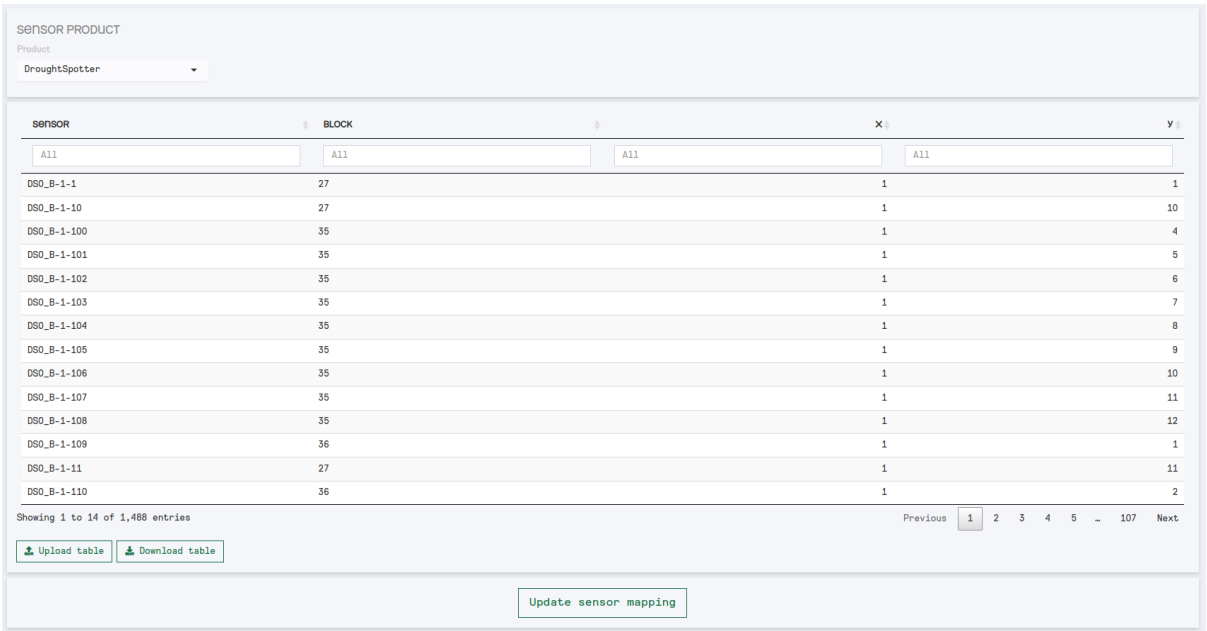
Climate Datalogger

The climate datalogger can be mapped to all blocks after selecting it in the Product dropdown and clicking the map button.



DroughtSpotter

Every DroughtSpotter scale has to be mapped to a x/y coordinate within the virtual blocks. This can be achieved by selecting the DroughSpotter in the Product dropdown menu and filling out the table by means of the UI or file upload. Click “update sensor mapping” to confirm the mapping.



3.6.2. Phena Module

Another system board module is PHENA, the toolchain that converts raw sensor data into plant parameter data. This conversion happens in a few steps, separated in different settings within HortControl:

Fundamentals of each of these steps are described below. Understanding these steps in more detail is not required, as Phenospex optimizes all the settings individually for your setup. If more information is required, please inquire about additional material.

Transform: The purpose of this step is to transform the coordinates from the scanner's coordinate system to the user's coordinate system. PlantEye can be integrated in very diverse systems and setups, thus, looking at the plant from different perspectives. By transforming coordinates, we correct the view to our perspective.

Segment: Once the transformation of detected points is completed, the segmentation process begins. During this step, groups of points are segmented within the 3D point cloud. The segmentation algorithm is based on region growing techniques.

Triangulate: During the triangulation step, at least three points are merged together to form a surface object in 3D space. These triangles give us area information.

Splitting: A scan of a block is then divided into multiple units. These units are the most detailed positional identifiers in your system. The scan is split along the x and y axis to create equal sized rectangles.

Merge: This step is utilized only in dual scan systems, and is skipped for a single scan. Here, the overlapping objects are merged in order to avoid repetitive information and noise.

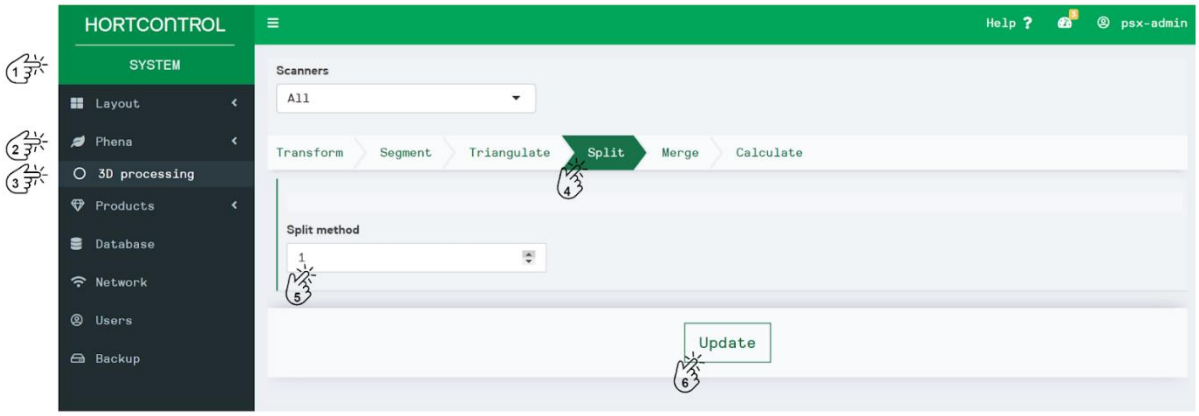
Calculate: Once a scan has been preprocessed, the calculation process will extract plant information for each unit. For a complete list of the resulting parameters and detailed description please refer to section 4 Calculated Plant Parameters.

3.6.2.1. Split Methods

After scanning a block, the 3D processing pipeline divides the scan into smaller parts called units. These units help extract the individual plants within the block and calculate the digital plant parameters accordingly.

To access the split methods setting on HortControl, navigate to ***SYSTEM > Phena > 3D processing> Split***.

If you cannot view or modify these settings, ask your IT admin to grant you psx-admin rights.



The “split method” is an integer value that can be set to 1, 2, or 3.

1: Hard Border Cut

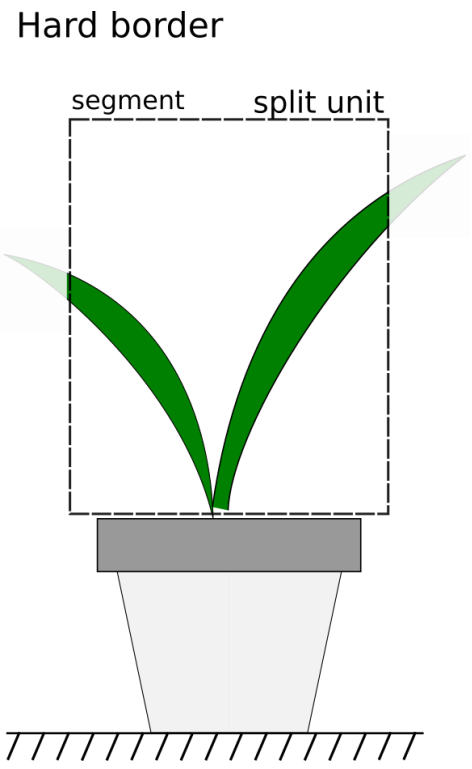
2: Center Of Mass

3: Lowest Point (Phena 1.0 only)

Note: Updating the split method will immediately affect all future scans. To maintain data comparability, ensure that no experiments are actively running before updating the split method.

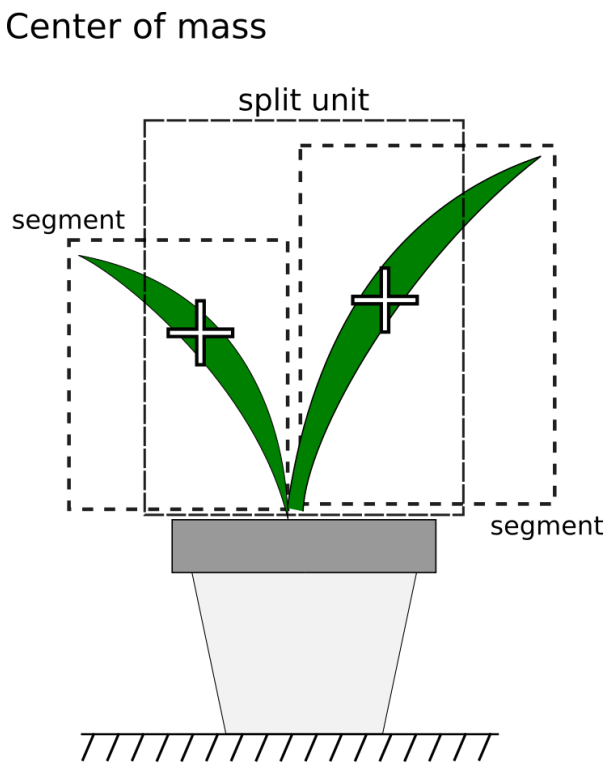
1. Hard Border Cut

Only the points that are located inside the split unit are used for the parameter calculation for the plant. All points outside this splitting unit are excluded even if they are part of the plant. This method is useful if the split unit's size is bigger than the plant and covers all segments including this split cube.



2. Center Of Mass

For each detected segment, the center of mass is calculated. All segments whose center of mass is inside the split unit are used for parameter processing. Therefore, segments extending beyond the split unit are also included in the calculation if most points are located inside it.

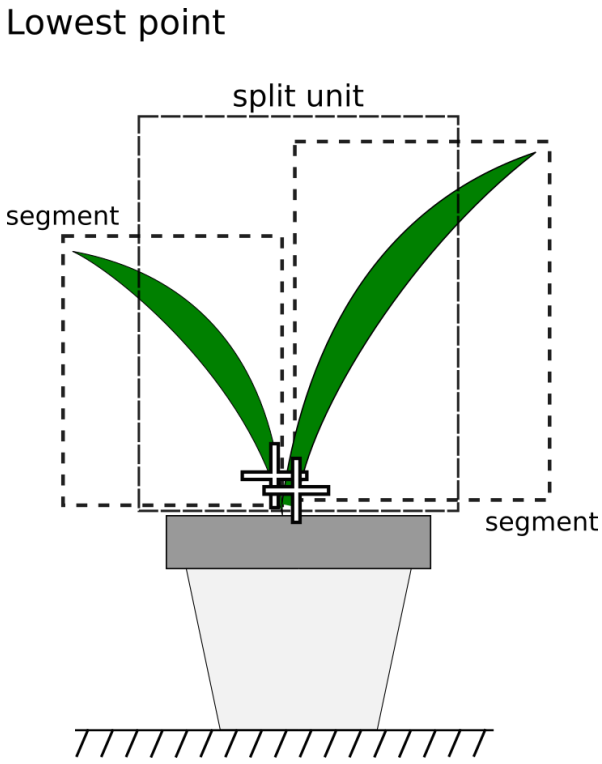


Limitations:

If most points related to a plant part are located outside the split unit, this segment will not be detected as an element of the split unit. To avoid this problem, an increase in the size of the split unit is necessary, which requires more distance between the specimens.

3. Lowest Point (Phena 1.0 only)

For each detected segment, the lowest points are determined. If this point is inside the split unit cube, it is considered part of the plant. This method follows the segment downwards to its root. It requires a continuous connection to the split unit.



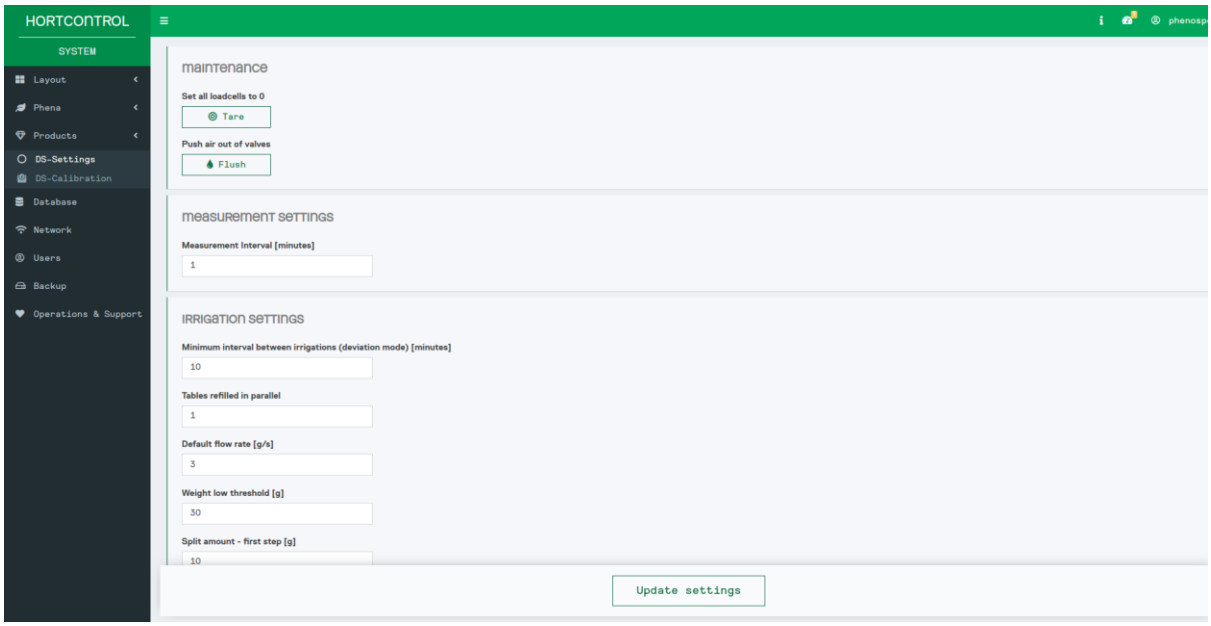
Limitations:

For plants with a very horizontal orientation of their leaves, the lowest point is often determined by the leaves themselves. The leaves can also cover the stem during the scan. Consequently, no connection from the leaves to the stem can be established, and therefore the stem is not detected as part of the plant.

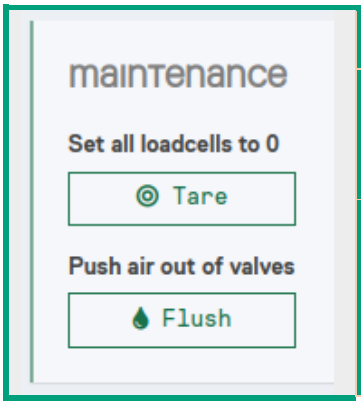
3.6.3. Products module

The products module allows you to configure product specific settings. It has currently two submodules, “DS-Settings” and “DS-Calibration” where DS stands for DroughtSpotter. It indicates that the submodules are there to configure DroughtSpotter.

3.6.3.1. DS-Settings



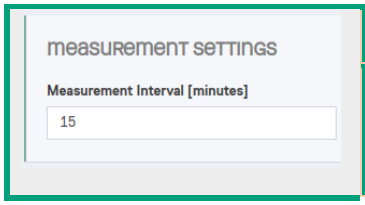
The settings are briefly explained below.



maintenance

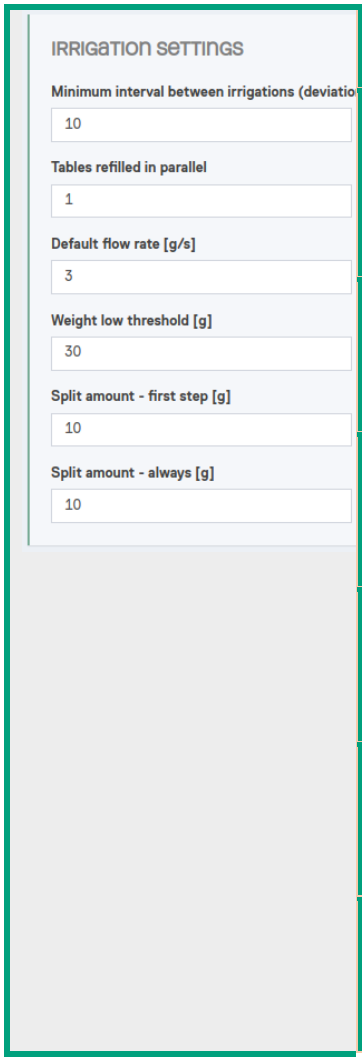
x Tare
Set the value of each scale to 0.

x Flush
Opens the valves of each scale one by one for a short time in order to get the air out.



measurement

x Measurement interval
The time interval between data capturing of the scale weights.



IRRIGATION

x Minimal interval between irrigations
Time between two irrigation attempts.

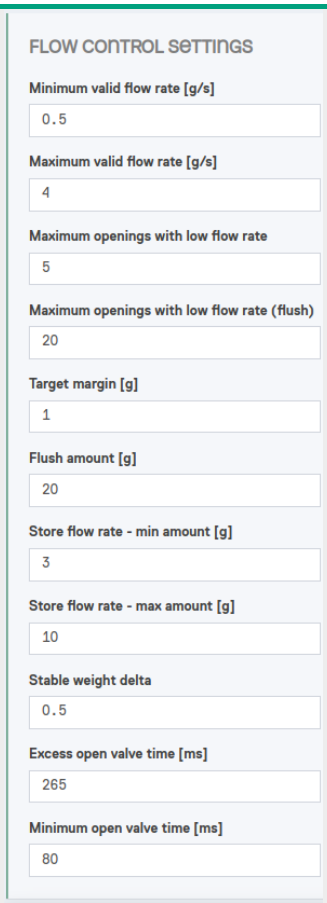
x Tables refilled in parallel
The number of blocks that should be watered in parallel. Be aware that too many tables will cause a pressure drop and might prolong the time to reach target weight.

x Default flow rate [g/s]
The flow rate at which the system has to start.

x Weight low threshold
Interrupt refilling when weight is under this threshold

x Split amount - first step
The minimum amount of irrigation at the first step, up to 50% of the difference with the target weight will be irrigated.

x Split amount - always [g]
The minimum amount of irrigation at the next steps, up to 50% of the difference with the target weight will be irrigated.



FLOW CONTROL

x Minimal valid flow rate
Minimum at which the flow rate will be considered valid

x Maximum valid flow rate
Maximum allowed flow rate

x Maximum openings with low flow rate
Maximum number of times the valves wlll be opened when a low flow rate is detected.

x Maximum openings with low flow rate (flush)
Maximum number of times the valves wlll be opened when a low flow rate is detected during a flus procedure.

x Target margin
Only refill when the difference between the current weight and the target exceeds this number.

x Flush amount
The amount of water that should be flushed during a flush procedure.

x Store flow rate - min amount
Store the measured flow rate after refilling at least this amount.

x Store flow rate - max amount
Store the measured flow rate after refilling maximum this amount.

x Stable weight delta
Allowed deviation between different weight measurements and this measurement to consider the measurement stable.

x Excess open valve time
The maximum time a valve can be opened longer.

x Minimum open valve time
Minimum amount of time that a valve should be opened.

3.6.3.2. DS-Calibration

DROUGHTSPOTTER

With this module, you can calibrate all the scales of your system that are not in an active experiment. Calibration adjusts the conversion of the scale's electrical current signal to match the actual weight. This relation can drift over time, reducing the accuracy of the measurement. We recommend calibrating your scales before the start of every experiment to achieve the best results. Calibration follows a stepwise procedure, and the **5 steps** to perform are as follows:

1. Select a DroughtSpotter system
2. Set your calibration weight
3. Select the scale you want to calibrate
4. Start the calibration of the selected scale
5. Finalize the calibration of the selected scale

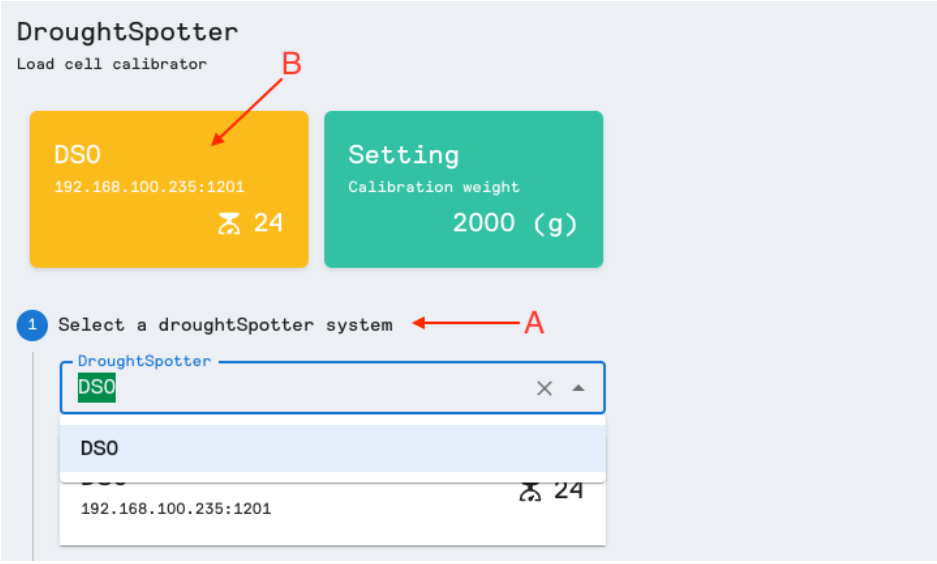
To get you started quickly the calibration tool will come with a set of defaults. The first DroughtSpotter system will be selected by default already (usually you only have one system). Also the latest calibration weight is filled in as a default. If all this information is correct, you can immediately proceed with selecting your target unit for calibration (step 3).

Important

It is important that your DroughtSpotter system is online and connected to HortControl in order to calibrate!

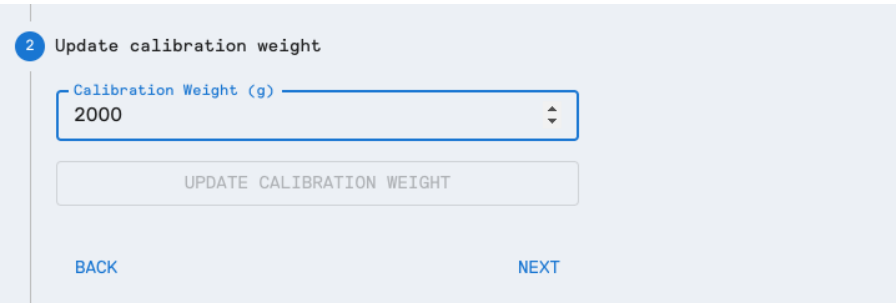
Step 1: Select a DroughtSpotter system

If necessary, update the DroughtSpotter system you wish to calibrate. Select the relevant step (A in the image below) and select the correct system. At the top the selected system will be indicated (B in the image below).



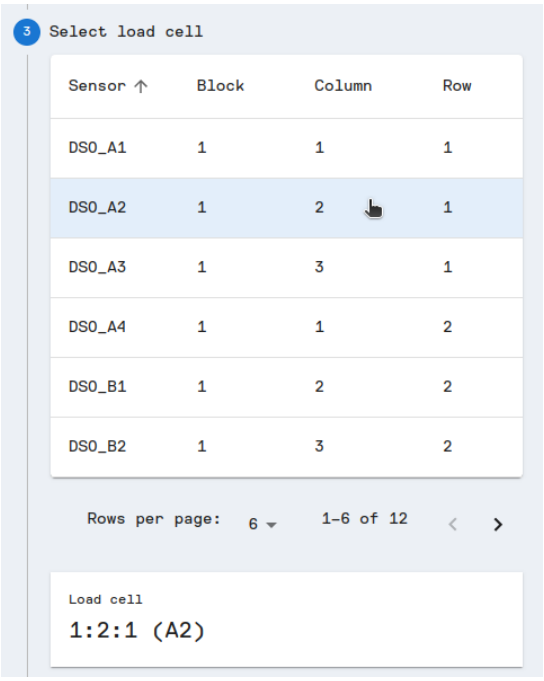
Step 2: Set your calibration weight

In this step you can define the weight of the calibration object you will use. Select the step and update the weight in grams if necessary. The weight should be between 1 and 500000g. Then click the “UPDATE CALIBRATION WEIGHT” button and make sure it was updated successfully.



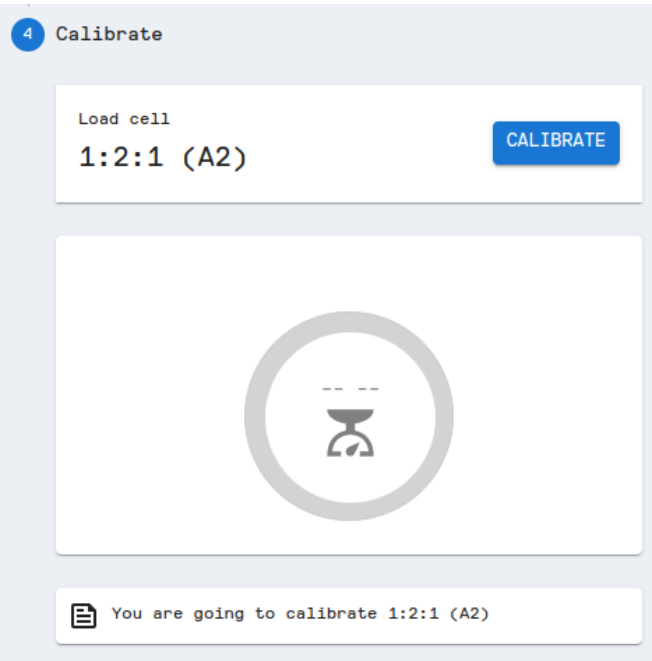
Step 3: Select the scale you want to calibrate

In this step you have a tabular overview of your scales. Click on the step and select the scale you want to calibrate by selecting the row in the table. The selected scale will be indicated below the table as a unit name for confirmation.



Step 4: Start the calibration of the selected scale

In this step, the calibration process is presented through a three-card layout, each providing vital information and functionalities.



The first box indicates the scale you selected and presents a button “CALIBRATE” you can click to start the calibration process. The button can take on three states depending on where you are in the calibration process.

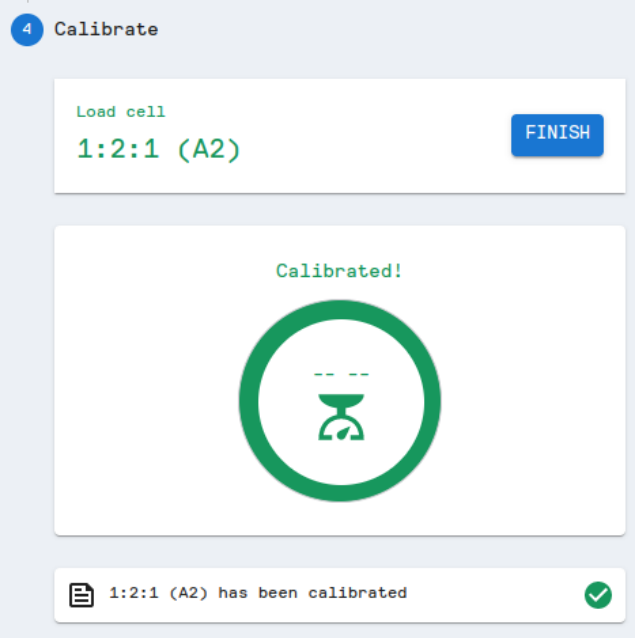
CALIBRATE	There is no calibration going on. Clicking on the button will start a new calibration process for the selected scale
CANCEL	You are running a calibration process for the selected scale. Clicking the button will stop that process and revert the scale to its previously calibrated state.
FINISH	The calibration process has ended. Click the button to finalize the process

The white box with the scale icon will take you through the process. For the calibration to succeed the calibration weight has to be put on the scale after starting the calibration process and needs to be left on there for at least 10 seconds to stabilize. This box will keep you up to date with the calibration process and eventually inform you when the calibration ends.

The third box with the file icon will instruct you which steps have to be undertaken by yourself during the process.

Step 5: Finalize the calibration of the selected scale

When the scale has finished calibration, it will display a green icon with the text 'Calibrated!'.
Click 'Finish' to return to the starting screen, as shown in step 1. From here, you can proceed to calibrate the next scale by going directly to step 3 and selecting the scale you want to calibrate.



3.6.4. Database Module

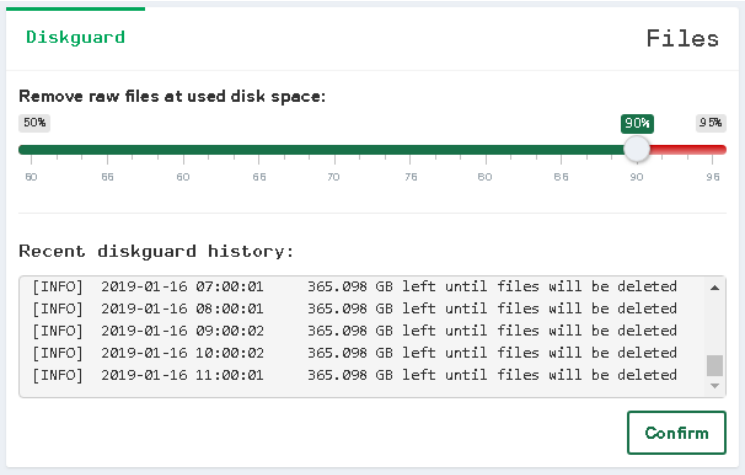
In this board you will find a few data related clean up settings.

3.6.4.1. Remove experiments / block layout

You can either remove experiments or block layouts by clicking the corresponding tab and pressing the ✖ Remove button. This is commonly done to remove unwanted experiments and/or to free up disk space. Removing your experiment will delete all biological information and measurements of the experiments from the database, as well as associated 3D scans.

3.6.4.2. DiskGuard

DiskGuard is a safety feature in HortControl that will remove the oldest 3D files when the filesystem is close to being completely filled. When the filesystem is full, HortControl cannot accept 3D files from the scanners or data from other devices anymore, meaning no new data will be processed and stored in the database. As the processed data of the oldest files were already safely stored in the database, Diskguard will remove these files first. It will do so until a defined threshold for the filesystem size is reached, allowing new files to come in, and further to be processed and stored. The threshold can be set in the DiskGuard module. The module also shows a log of the last removed files.



In this example, the oldest 3D files will be removed when the filesystem is more than 90% full.

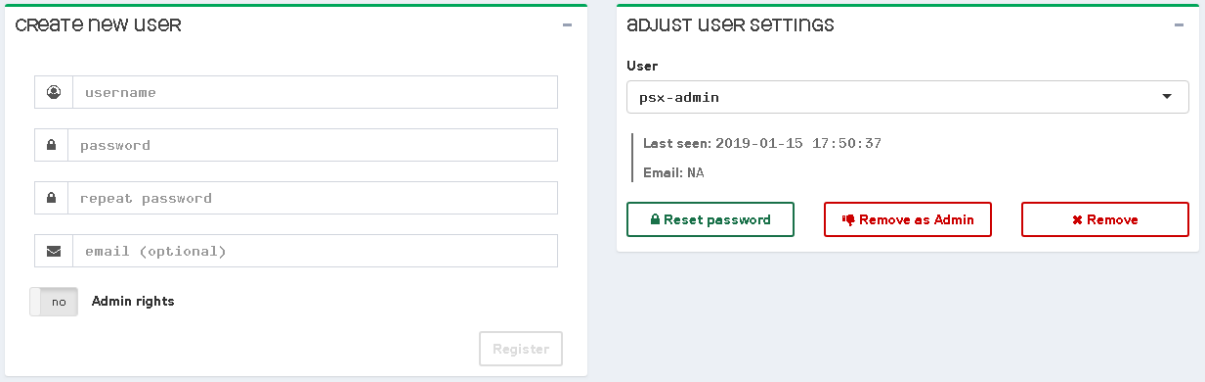
When the mount share point is provided, diskguard can be configured if required. By default – this feature is not activated.

IMPORTANT

Do not rely on the NFS share for your data backup.

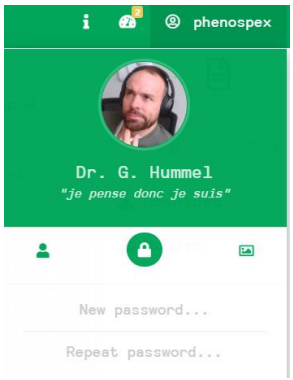
3.6.5. Users Module

This module allows the admin to manage users in the system. Users can be created, updated or removed. The minimal requirements for creating a new user are a unique username and a password. Toggle admin rights on if you want to give the new user admin rights. User rights for the different account types are mentioned in the login chapter.



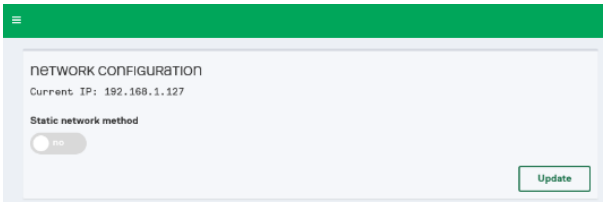
3.6.5.1. User Password reset

You can set new passwords for all users expect yourself here. Everybody can set a new password by opening their personal menu in the top right corner and then clicking on the lock icon



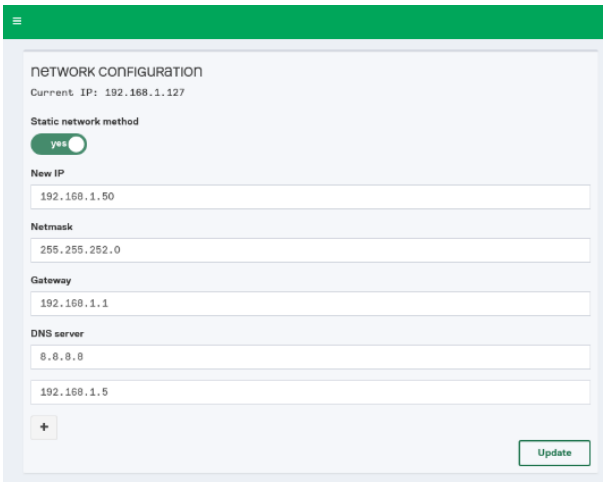
3.6.6. Network Module

In the network module, the settings can be changed in order to integrate HortControl into your own network. By default the network is set to dynamic.



If you would want to assign a static address, you need to toggle off dynamic mode. After that, you will be able to fill in the IPv4 address, netmask, gateway and DNS servers.

If you want to change back to dynamic mode, you will need to finalize the changes by browsing to: <new dynamic ip>:1612/device/network/confirm.



Restoring IP

When anything fails during this process or if the new IP cannot be confirmed within 20 minutes, the network settings will be restored to the previous settings.

3.6.7. System Backup Module

With this module you can manage complete HortControl system backups. You can create a new backup and download the latest backup. We offer both a frontend (UI) and backend (REST API) backup management system. It is advised to create, download and remotely store a HortControl system backup regularly.

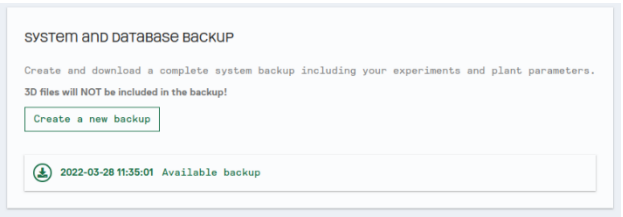
For data security the backup is encrypted. In the unlikely event of a system failure the Phenospex team can help you to restore your system to the state of the latest backup you can provide.

IMPORTANT

1. **It is the user's responsibility to create, download and store backups regularly on a private system. Phenospex will not store customer data and backups remotely, and can therefore not be held responsible for permanent data loss due to unforeseen system failure.**
2. **3D files are not included in the system backup. Processed plant data will be included in the backup.**

3.6.7.1. System backup using the User Interface

Click the "*Create a new backup*" button to start the creation of a new backup. It will take some time, while you will be informed about the progress. To download the last backup click the download icon next to text "*Available backup*". In the overview you will see the time when the last successful backup was performed.



3.6.7.2. System backup using REST API

We offer REST API calls to help you set up an automated backup routine on your private machine. You can find the backup documentation by browsing to the URL below on your HortControl machine:

<HORTCONTROL IP>:1612/documentation/index.html#tag/Backup

3.7. BrAPI

Automate the data transfer from HortControl into your workflow or system.

The Breeding API (BrAPI) project is an effort of the plant research community to enable interoperability among plant databases. BrAPI is a standardized RESTful web service API specification for communicating plant data. We implemented the plant phenotyping calls that are compatible with the data that are generated by our Phenospex products.

You can find the supported calls by browsing to the following link on your HortControl machine:

<hortcontrol ip>:6988/documentation/brapi

The BrAPI call is always preceded by */brapi/v2*. Therefore the structure of a BrAPI call looks like this:

<hortcontrol ip>:6988 /brapi/v2/<brapi call>

As an example the call to list all available BrAPI calls is shown below:

<hortcontrol ip>:6988 /brapi/v2/serverinfo

4. CALCULATED PLANT PARAMETERS

This document explains how plant parameters are calculated by our 3D processing chain, Phena, their biological significance, and their application in phenotyping experiments.

Plant parameters are categorized as follows:

1. **Digital Plant Parameters**
    a. Morphological Parameters (plant shape and structure)
    b. Spectral Parameters (plant physiology and health)
2. **Technical Parameters**
    a. Morphological Parameters (plant morphology and growth patterns)
    b. Spectral Parameters (plant color and appearance)

Digital plant parameters can be directly applied in phenotyping applications and often correlate closely with plant traits. **Technical parameters** are known parameters in digital phenotyping and/ or used in machine learning models. In many cases these technical parameters correlate closely with one or more plant traits, but the degree of correlation may vary across species or types of plants.

4.1. Phena

Phena is our processing chain. It calculates plant parameters using the raw data collected by PlantEye sensors. These plant parameters can be viewed, filtered, and exported on the HortControl platform. Systems installed before 27 April 2022 use Phena 1.0, unless they have been upgraded to Phena 2.0. Systems installed after 27 April 2022 use Phena 2.0.

	Phena 1.0	Phena 2.0
Plant Height Max	☑	☑
Plant Height Average	☑	☑
Canopy Light Penetration Depth	☑	☑
3D Leaf Area	☑	☑
Projected Leaf Area	☑	☑
Digital Biomass	☑	☑
Leaf Area Index	☑	✗
Leaf Inclination	☑	✗
NDVI Average	☑	☑
GLI Average	☑	☑
PSRI Average	☑	☑
NPCI Average	☑	☑
Convex Hull Area	✗	☑
Convex Hull Area Coverage	✗	☑
Convex Hull Circumference	✗	☑
Convex Hull Maximum Width	✗	☑
Convex Hull Aspect Ratio	✗	☑
Voxel Volume Total	✗	☑
Surface Angle Average	✗	☑
Hue Average	☑	☑
Lightness Average	✗	☑
Saturation Average	✗	☑

4.2. Morphologic Digital Plant Parameters

Morphological digital plant parameters, calculated using the plant's shape and structure, include the plant's height, canopy light penetration depth, leaf area, and biomass. These parameters provide insights into the plant's physical characteristics and architecture.

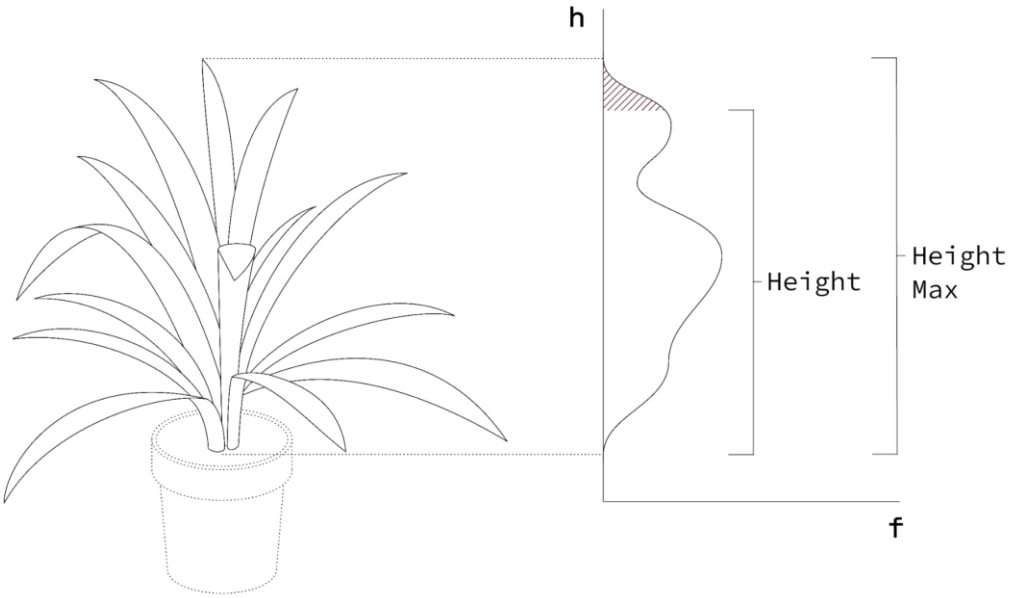
Plant Height Max (mm)

Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 - ∞
Unit:	mm

"Plant Height Max" accurately determines the absolute highest point of the plant, correlating closely with the plant's overall height.

To calculate the parameter, the PlantEye sensor finds the highest domain – a cluster of points in the 3D file – that also contains enough points and is close enough to the other domains. The highest point of this domain is the "Plant Height Max."

This method ensures the precise measurement of the plant's highest point, while also excluding single-noise points and foreign objects effectively.



Plant Height Average (mm)

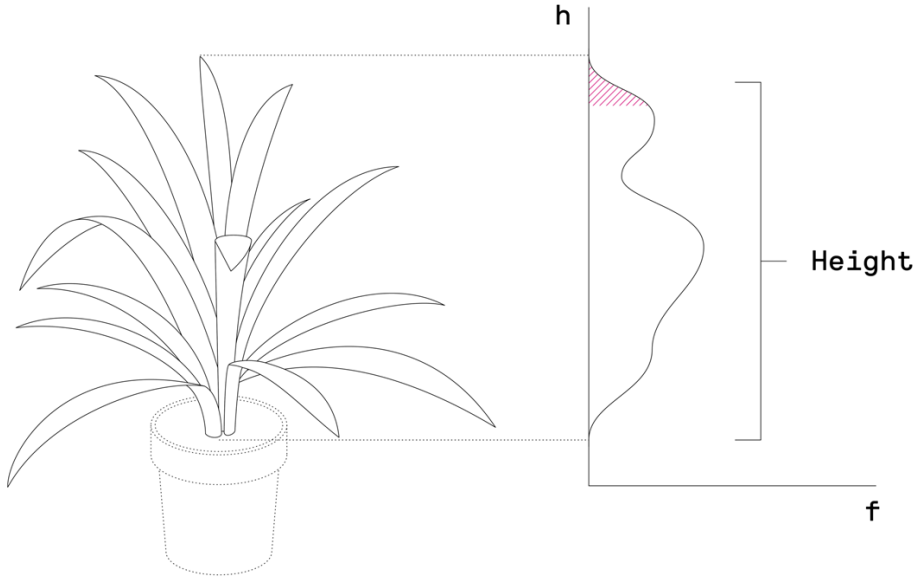
Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 - ∞
Unit:	mm

"Plant Height Average" prioritizes stability over accuracy by minimizing the effect of small movements caused by wind, external factors, or diurnal plant rhythms. The parameter correlates closely with the plant's overall height.

The parameter is calculated by analyzing the distribution of points along the z-axis. First, a histogram is generated to represent the density of points at various heights above ground.

This histogram is then adjusted by cropping the extremes, removing a safety margin from the top and bottom to improve resilience against anomalies.

The "Plant Height Average" is the average of the heights within the top **10%** segment of the plant, measured from the pot height.



Canopy Light Penetration Depth (LPD) (mm)

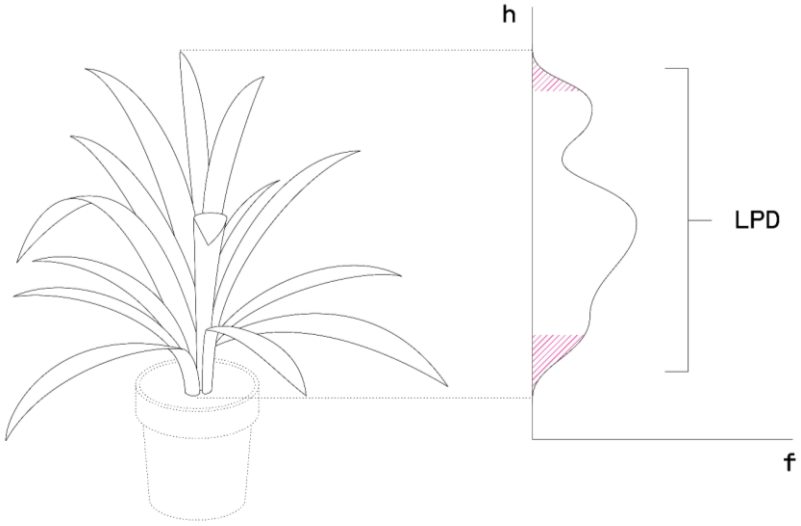
Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 - ∞
Unit:	mm

“Canopy Light Penetration Depth” (LPD) utilizes 3D data to calculate the depth at which laser light can penetrate the plant’s canopy. Very dense plants will therefore exhibit a low value.

The parameter is calculated by analyzing the distribution of points along the z-axis. First, a histogram is generated to represent the density of points at various heights above ground.

This histogram is then adjusted by cropping the extremes, removing a safety margin from the top and bottom to improve resilience against anomalies.

Next, the **bottom 20%** and the **top 10%** are averaged. The “Canopy Light Penetration Depth” is the distance between the top and bottom average values.



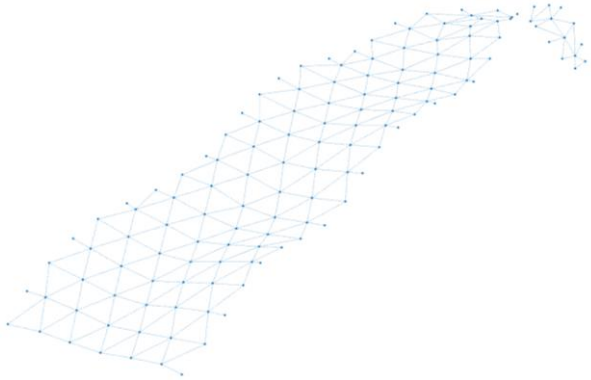
3D Leaf Area (mm²)

Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 - ∞
Unit:	mm²

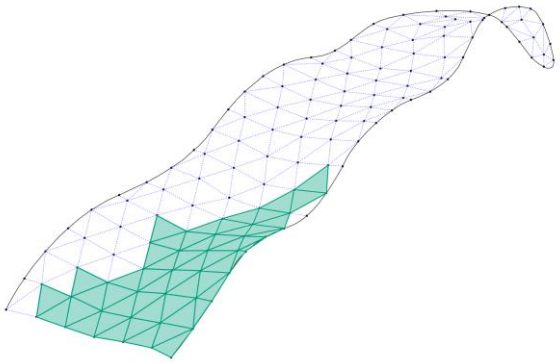
"3D Leaf Area" is the sum of all of the calculated triangle surfaces within the plant's structure, correlating closely with the plant's actual leaf area.

The parameter calculation process begins with a 3D point cloud from which points that are spatially proximate and without intervening points are triangulated.

Given the uneven distribution of points within the 3D point cloud, triangles may vary in size. The PlantEye sensor compensates for this variation by calculating the area of each triangle. This enables precise measurement of the real leaf area, including for leaves at an angle, unlike 2D methods that only consider a flat projection.



Within the plant, domains – clusters of triangles that form continuous, non-overlapping surfaces – are identified. Although the number of domains typically correlates to the number of leaves, this correlation is not necessarily accurate.



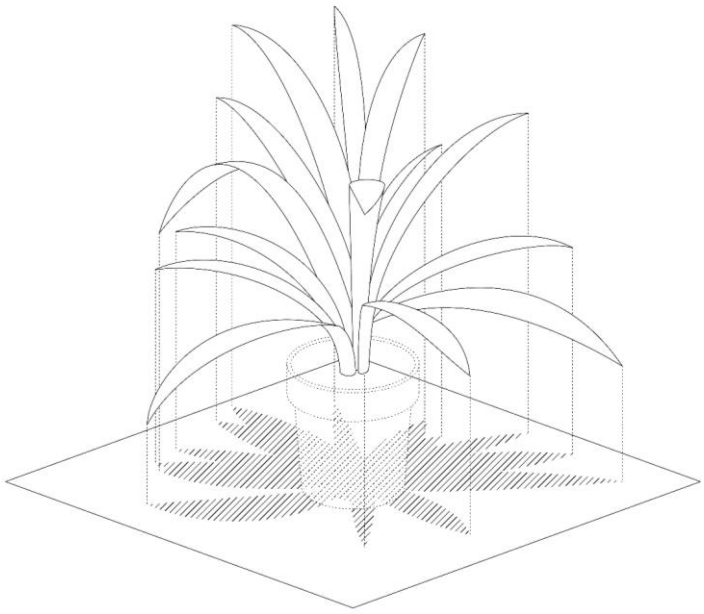
The 3D area of each domain is determined by summing the areas of its constituent triangles. The plant's total "3D Leaf Area" is then calculated by summing the areas of all the domains in the unit.

Projected Leaf Area (mm²)

Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 – sector size
Unit:	mm²

"Projected Leaf Area" is calculated by mapping all the triangles onto the X-Y plane.

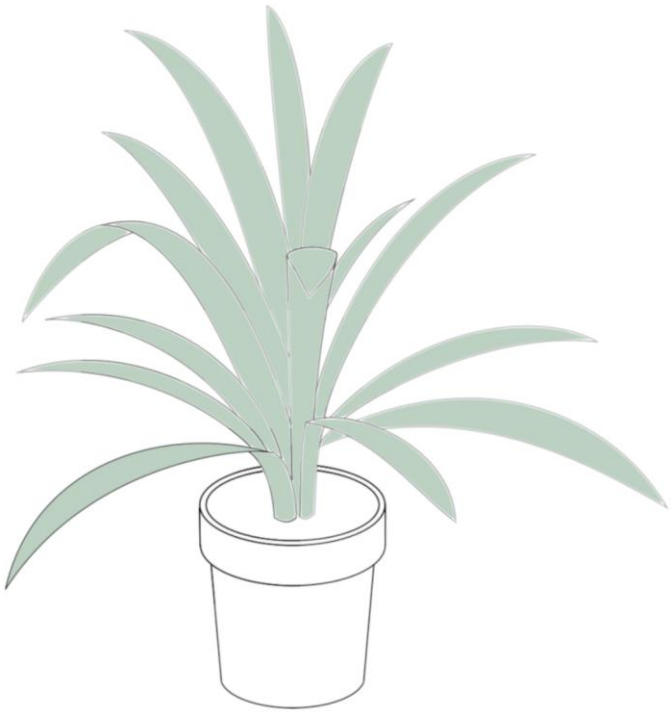
By transforming the plant's 3D structure into a simplified 2D representation, the "perspective effect" associated with 2D imaging is avoided. This effect causes objects further away from the camera to appear smaller – with fewer pixels and thus a smaller measured area – and objects closer to the camera to appear larger, with more pixels and a correspondingly larger area.



Digital Biomass (mm³)

Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 – ∞
Unit:	mm³

“Digital Biomass” is calculated by multiplying “Plant Height Average” by “3D Leaf Area.” Numerous studies have proven a strong correlation between our “Digital Biomass” parameter and actual biomass. However, the value will only be accurate if the plant has a uniform structure, allowing its volume to be determined through its height and area dimensions.

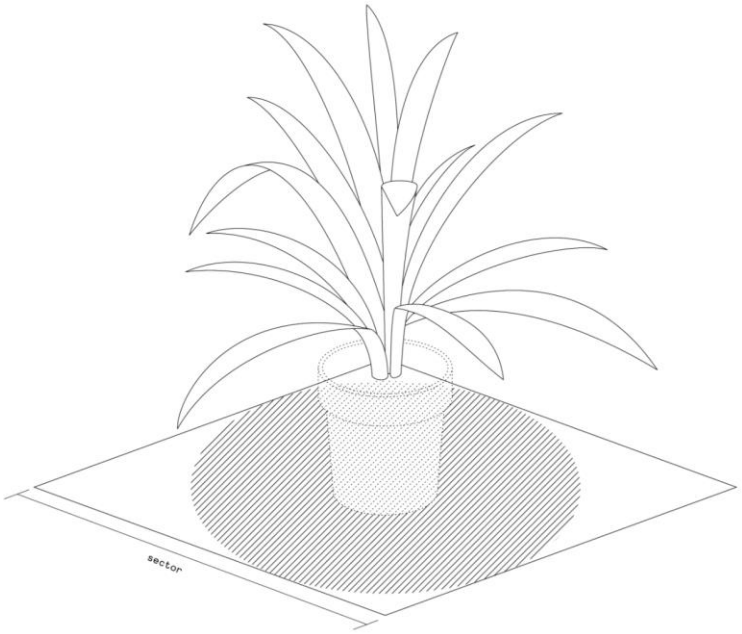


Leaf Area Index (mm²/mm²)

Phena 1.0 ☑	Phena 2.0 ✗
Value Range:	0 – ∞
Unit:	-

“Leaf Area Index” quantifies the leaf layer density of a specified area. It is calculated by dividing the “3D Leaf Area” by the unit area, which is the space allocated to each plant during experiment set-up.

“Leaf Area Index” is only relevant in a dual-scanner set-up, where two scanners assess the canopy from opposing angles. These scanners enable a detailed capture of leaf coverage, including where leaves overlap.



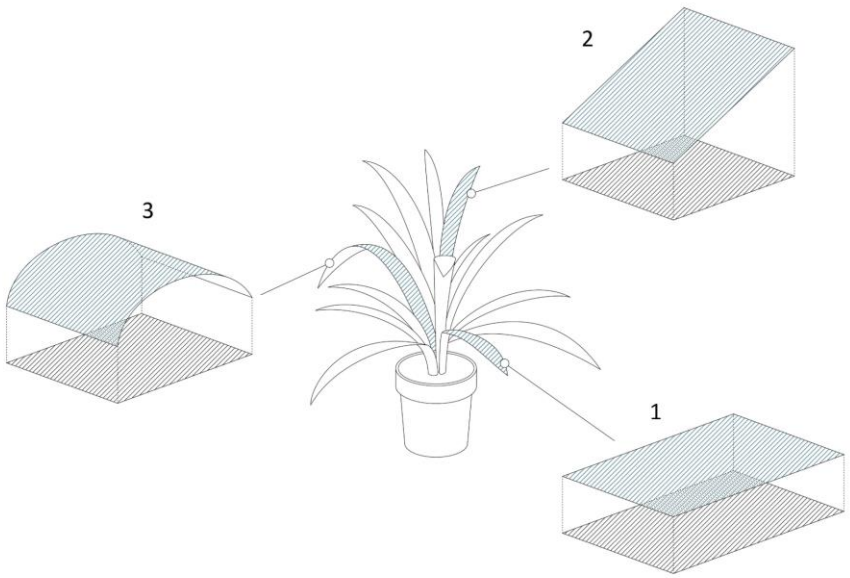
Leaf Inclination (mm²/mm²)

Phena 1.0 ☑	Phena 2.0 ✗
Value Range:	0 – ∞
Unit:	-

"Leaf Inclination" measures the average orientation of a plant's leaves, indicating how upright or angled they are. It is calculated by dividing the plant's total leaf area by the "Projected Leaf Area."

Leaves laying flat have a value of 1 because their total leaf area and "Projected Leaf Area" are equal. As leaves become more upright, angled, or bent, their total leaf area increases but the "Projected Leaf Area" stays the same, resulting in a higher "Leaf Inclination" value.

Example



1: Flat Leaf	2: Upright Leaf	3: Bent Leaf
Total leaf area: 10cm²	Total leaf area: 15cm²	Total leaf area: 15cm²
"Projected Leaf Area": 10cm²	"Projected Leaf Area": 10cm²	"Projected Leaf Area": 10cm²
Individual leaf inclination: 1	Individual leaf inclination: 1.5	Individual leaf inclination: 1.5

The plant's overall "Leaf Inclination" is calculated by averaging all the individual leaf inclinations for each single domain.

4.3. Spectral Digital Plant Parameters

Spectral digital plant parameters, calculated using spectral data like RGB and NIR wavelengths, include NDVI, GLI, PSRI, and NPCI. These parameters provide insights into various aspects of the plant's physiology and health, like greenness, senescence, and chlorophyll content.

The PlantEye color channels shown below and the wavelengths corresponding to these channels are used in the calculation of spectral digital parameters.

Color Channel	Peak Wavelength (nm)
Red (R)	624 - 634
Lime green (G)	530 – 540
Blue (B)	465 – 485
Near-Infrared (NIR)	720 – 750

NDVI average

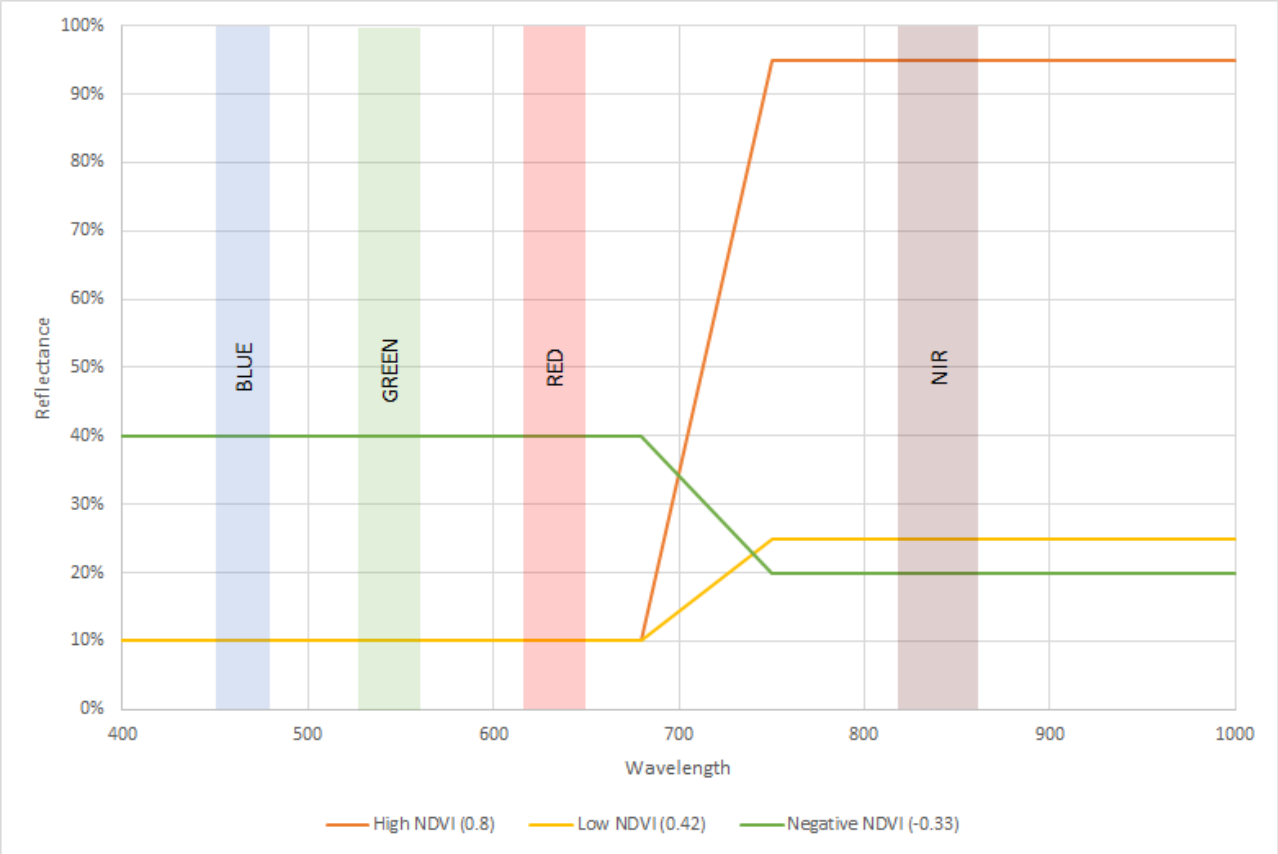
Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	-1 - 1
Unit:	-

Normalized Difference Vegetation Index (NDVI) is a widely-used parameter in plant science and has been shown to correlate with photosynthetic efficiency. It is calculated for each 3D point as follows:

```
(NIR – RED) / (NIR + RED)
```

NDVI values are analyzed in two main ways:

1. "NDVI Average": The average NDVI across all the 3D points in the unit
2. NDVI bin (%): The percentage of 3D points in a specific NDVI range compared to the total number of 3D points in the unit



— High "NDVI Average"
(NIR – RED) / (NIR + RED)
(95 - 10) / (95 + 10)
"NDVI Average": 0.8
Plant health: Good

— Low "NDVI Average"
(NIR – RED) / (NIR + RED)
(25 - 10) / (25 + 10)
"NDVI Average": 0.43
Plant health: Moderate

— Negative "NDVI Average"
(NIR – RED) / (NIR + RED)
(20 - 40) / (20 + 40)
"NDVI Average": -0.33
Plant health: Dead

GLI Average in Phena 2.0 / Greenness in Phena 1.0

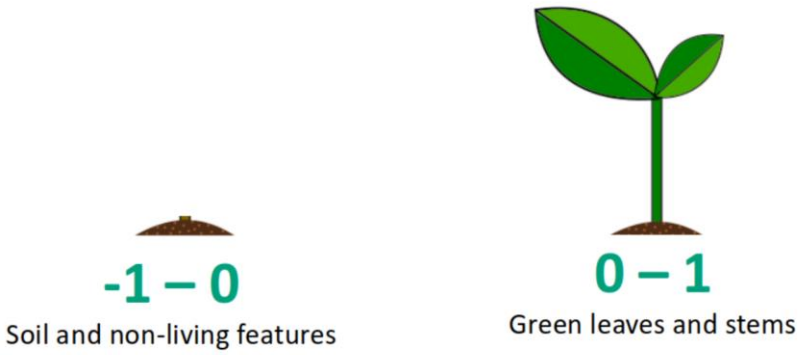
Phena 1.0 ☑	Phena 2.0 ☑	
Value Range:	-1 - 1	
Unit:	-	

Green Leaf Index (GLI) is a parameter used in plant science to quantify the green parts of the plant. It is calculated for each 3D point as follows:

```
(2*G-R-B)  / (2*G+R+B)
```

GLI values are analyzed in two main ways:

- "GLI Average": The average GLI across all the 3D points in the unit.
- GLI bin (%): The percentage of 3D points in a specific GLI range compared to the total number of 3D points in the unit



PSRI average

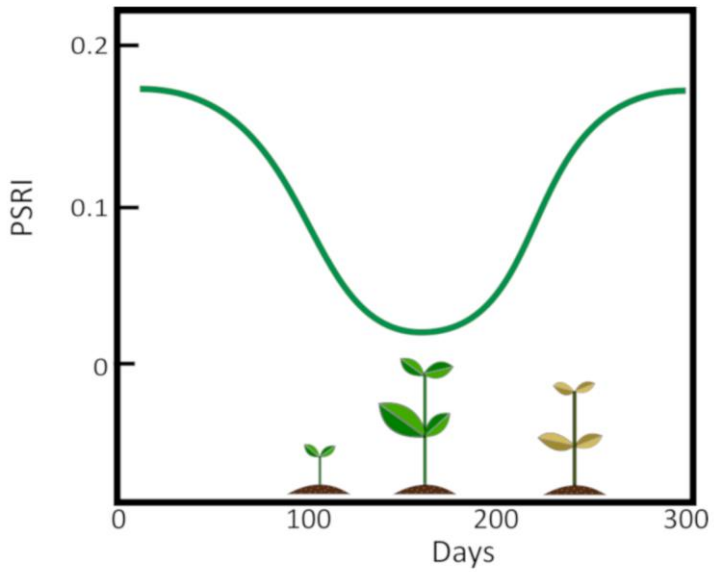
Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	-1 - 1
Unit:	-

Plant Senescence Reflectance Index (PSRI) is a parameter used in plant science to evaluate leaf senescence. It is calculated for each 3D point as follows:

`(RED − BLUE) / (NIR)`

PSRI values are analyzed in two main ways:

- “PSRI Average”: The average PSRI across all the 3D points in the unit
- PSRI bin (%): The percentage of 3D points in a specific PSRI range compared to the total number of 3D points in the unit



NPCI average

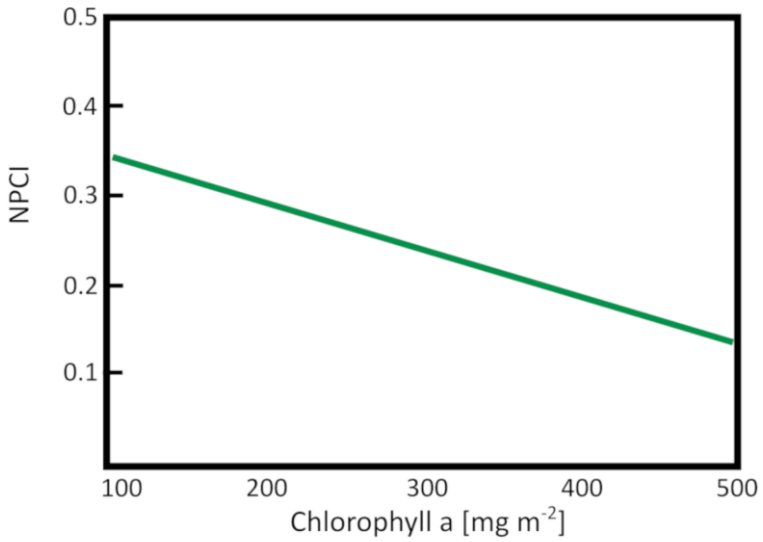
Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	-1 - 1
Unit:	-

Normalized Pigment Chlorophyll Index (NPCI) is a parameter used in plant science to estimate chlorophyll content. It is calculated for each 3D point as follows:

`(RED − BLUE) / (RED + BLUE)`

NPCI values are analyzed in two main ways:

- “NPCI Average”: The average NPCI across all the 3D points in the unit
- NPCI bin (%): The percentage of 3D points in a specific NPCI range compared to the total number of 3D points in the unit



4.4. Morphologic Technical Parameters

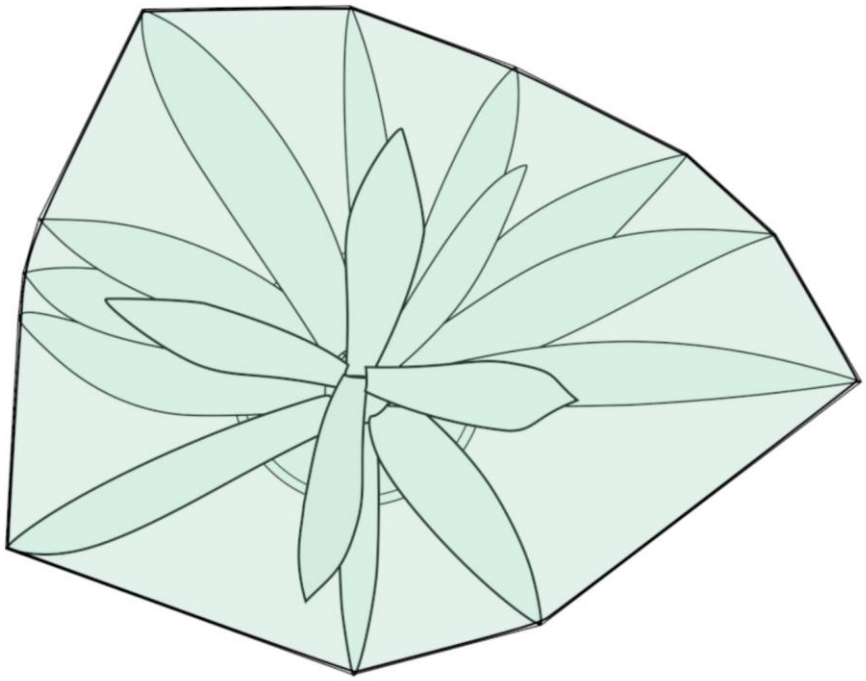
Morphological technical plant parameters, calculated using the plant's geometric properties and structure, include the convex hull's area, circumference, and maximum width. These parameters provide insights into plant shape and spatial characteristics, facilitating the characterization of plant morphology and growth patterns.

Convex Hull Area (mm²)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	-
Unit:	mm²

"Convex Hull Area" is the area of the geometric shape that encloses the bird's-eye 2D projection of the plant. It is a measure of the maximum space a plant could occupy at its current size, even if its leaves move.

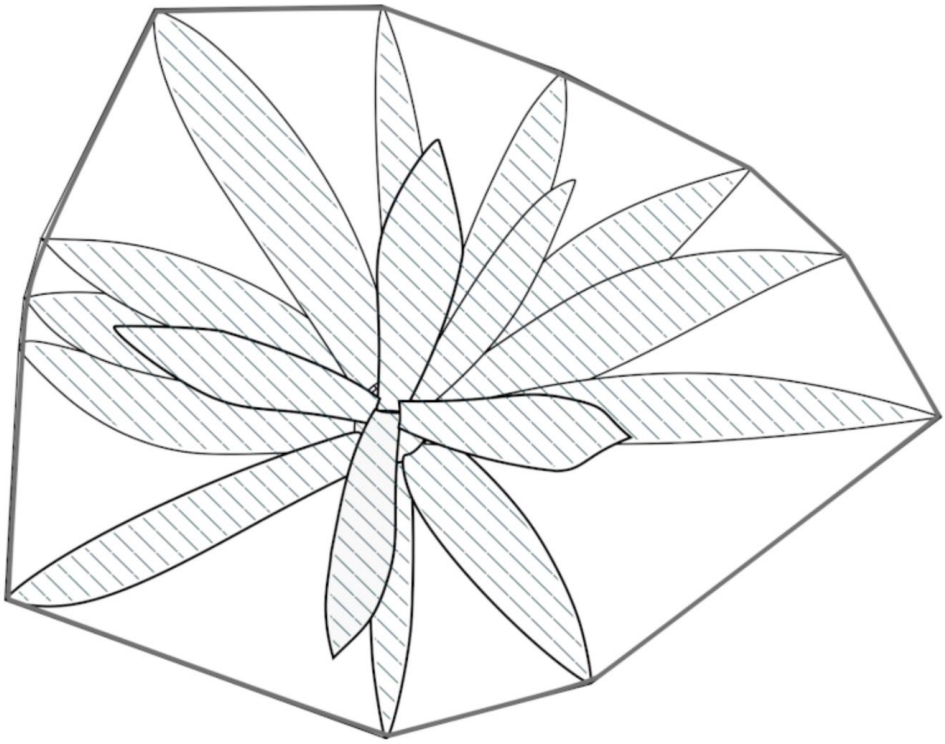
To obtain high-quality computed values, ensure plants do not overlap with each other's units.



Convex Hull Area Coverage (%)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	-
Unit:	%

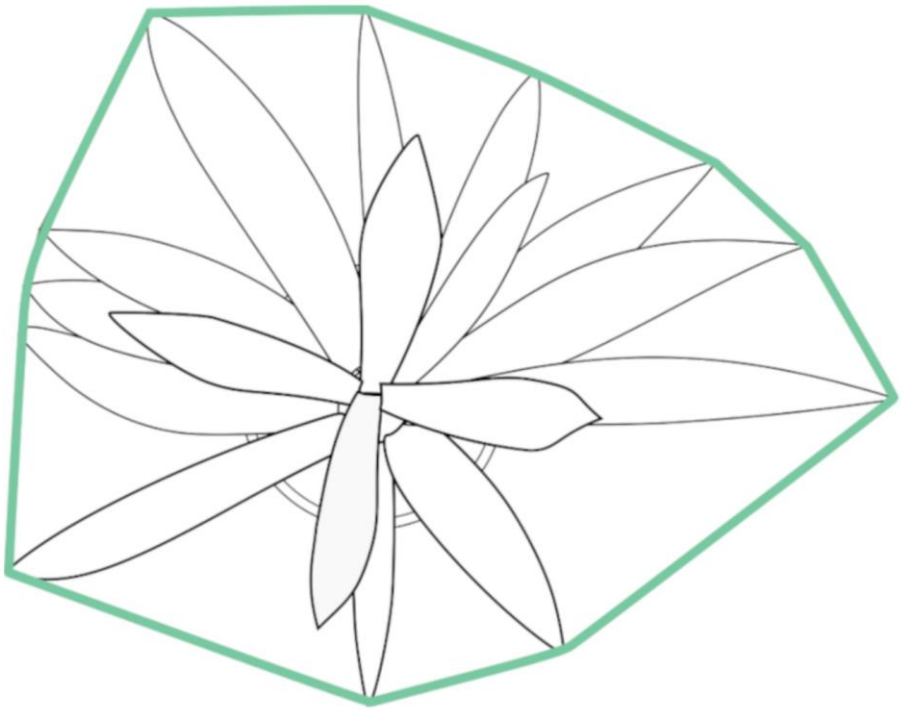
“Convex Hull Area Coverage” is the percentage of the hull area occupied by the plant’s 2D projection. It correlates with the morphological structure of the plant.



Convex Hull Circumference (mm)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	-
Unit:	mm

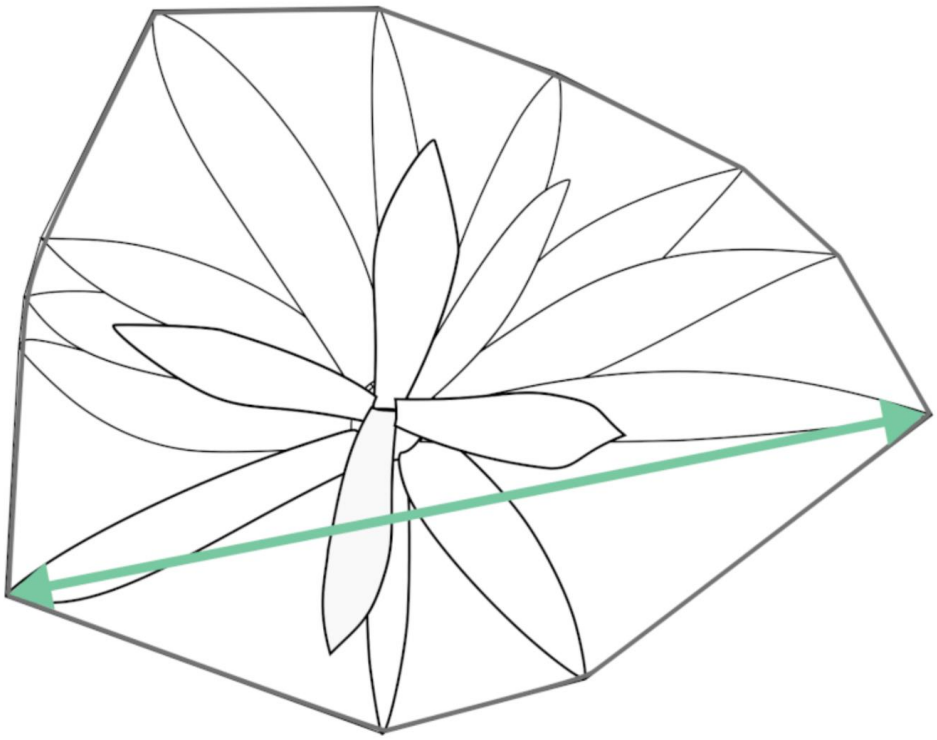
“Convex Hull Circumference” is the distance around the convex hull. It can be used in combination with the “Convex Hull Area” as a morphological shape descriptor.



Convex Hull Maximum Width (mm)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	-
Unit:	mm

“Convex Hull Maximum Width” is the distance of the longest straight line that can be drawn from one point on the convex hull circumference to another.

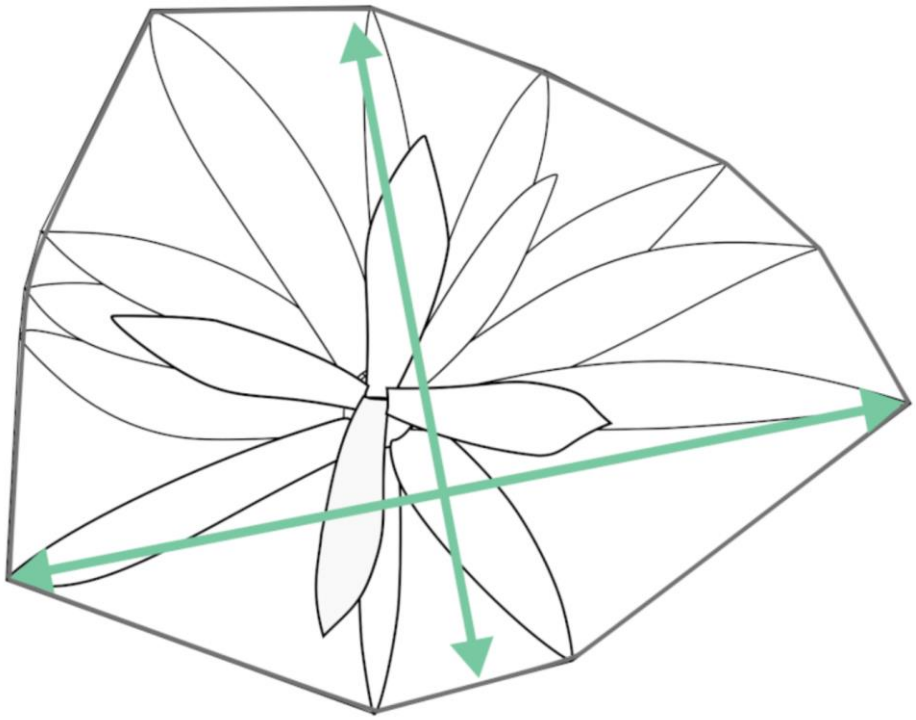


Convex Hull Aspect Ratio

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	-
Unit:	%

“Convex Hull Aspect Ratio” is the ratio between the “Convex Hull Maximum Width” and the distance of the perpendicular line that intersects with the maximum width line at its midpoint, from one point on the convex hull circumference to another. It is expressed as a percentage (%).

A widely used parameter, the “Convex Hull Aspect Ratio” correlates with the growth stage of a plant and can distinguish between different morphologies.



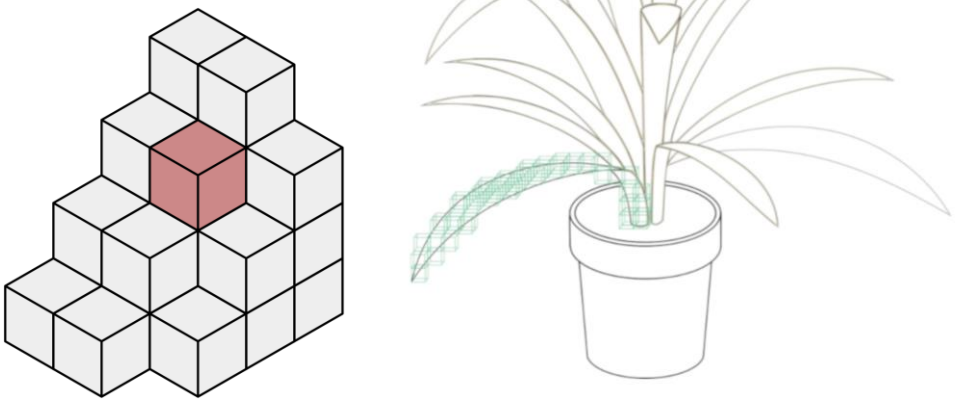
Voxel Volume Total (mm³)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	-
Unit:	mm³

A voxel grid is a 3D grid used to represent a 3D image. It's similar to how a 2D image is made of pixels (small rectangles), but in 3D, it's made of voxels (small cubes). Each voxel has its own position in the grid and contains spectral information, just like a pixel does in a 2D image.

“Voxel Volume Total” is the total number of visible voxels multiplied by the voxel volume.

This parameter correlates with biomass in specific plant structures and applications.

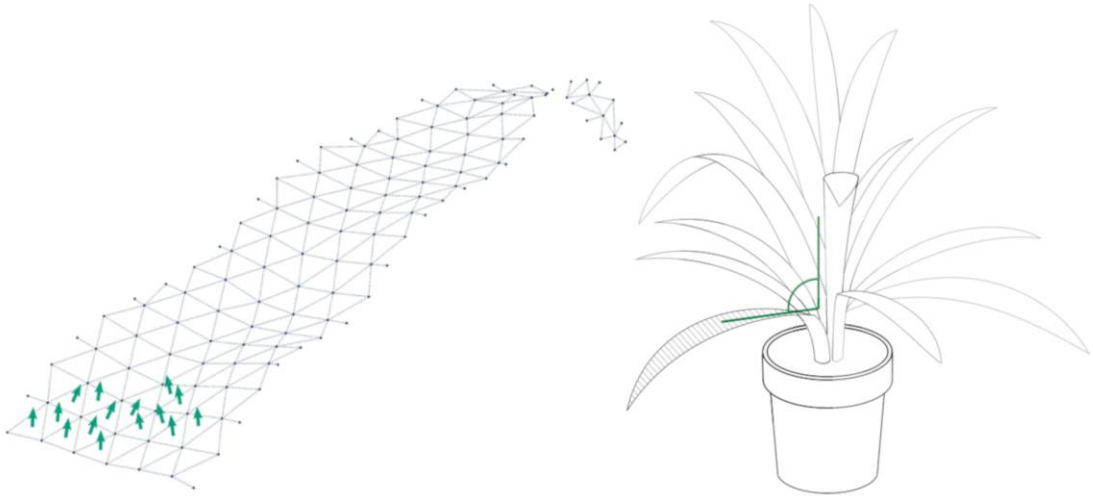


Surface Angle Average in Phena 2.0 / Leaf Angle in Phena 1.0 (°)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	0 - 90
Unit:	Degree º

“Surface Angle Average” is the average angle of the triangles relative to the height axis. It is calculated as the weighted average of all angles formed by the normals of every face in the plant mesh.

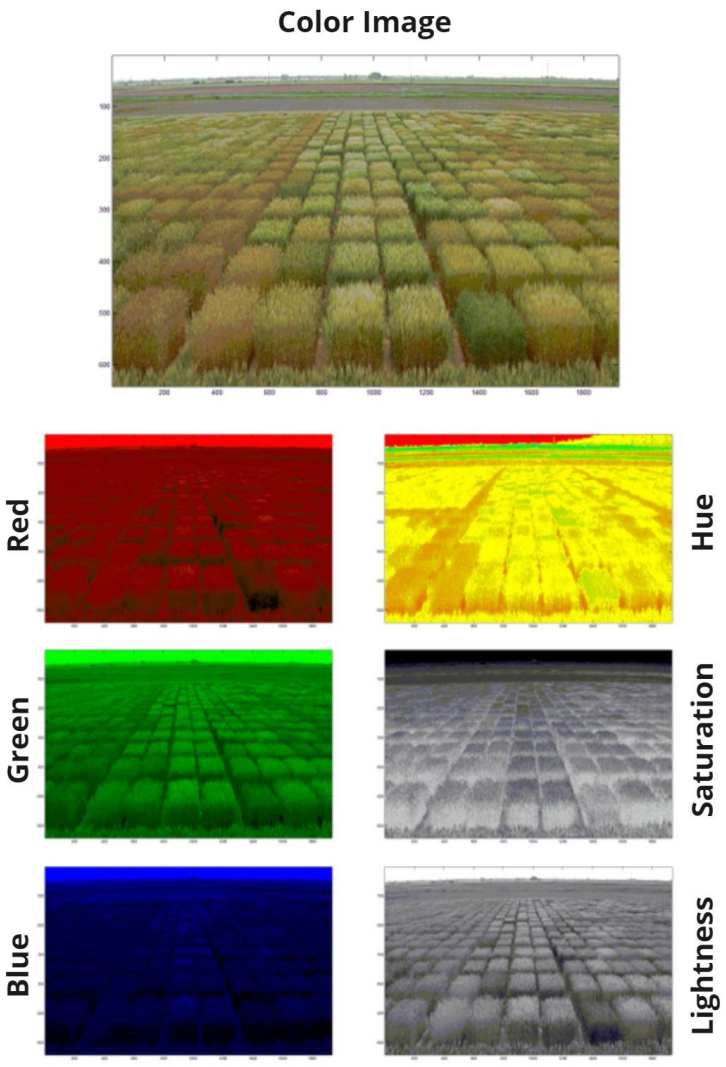
This parameter correlates with leaf angle in some plant structures and applications.



4.5. Spectral Technical Parameters

Spectral technical plant parameters, calculated using spectral data, include the plant's hue, saturation, and lightness. These parameters provide insights into the plant's color and appearance, facilitating detailed analysis of plant coloration and spectral properties.

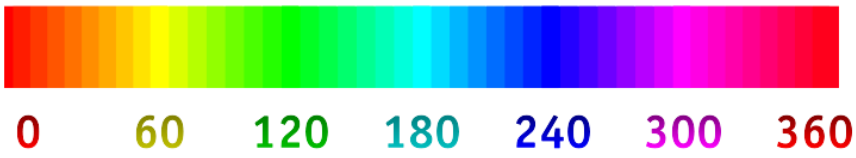
Hue, saturation, and lightness are all essential to compose a full-color image, with each parameter holding distinct information. This decomposition reveals subtle color differences that are not easily distinguishable with RGB, as seen most clearly in the hue decomposition below.



Hue average (°)

Phena 1.0 ☑	Phena 2.0 ☑
Value Range:	0 - 360
Unit:	Degree º

Hue is depicted as an angle on the color wheel, where 0° and 360° correspond to red, 120° to green, and 240° to blue.



Hue values are analyzed in two main ways:

- “Hue Average” (°): The average hue across all the 3D points in the unit
- Hue bin (%): The percentage of 3D points in a specific hue range compared to the total number of 3D points in the unit

Lightness average (%)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	0 - 100
Unit:	%

Lightness indicates the brightness of a color, spanning from 0% (dark) to 100% (bright).

Lightness values are analyzed in two main ways:

- “Lightness Average” (%): The average lightness across all the 3D points in the unit.
- Lightness bin (%): The percentage of 3D points in a specific lightness range compared to the total number of 3D points in the unit.

Saturation average (%)

Phena 1.0 ✗	Phena 2.0 ☑
Value Range:	0 - 100
Unit:	%

Saturation refers to the intensity of color, spanning from 0% (unsaturated) to 100% (saturated).

Saturation values are analyzed in two main ways:

- “Saturation Average” (%). The average saturation across all the 3D points in the unit.
- Saturation bin (%): The percentage of 3D points in a specific saturation range compared to the total number of 3D points in the unit.