

PHenOSPEx

Smart Plant Analysis

HORTCONTROL 3.5

Manual

Version 1.0 - 2020-07-13

Netherland

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.

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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.

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

HORTCONTROL 3.5 new FEATURES

For each HortControl release we aim to incorporate desired wishes and requirements of our customers. In the latest version of HortControl – 3.5, this includes addition of machine learning mode and external barcode reader. Below is a detailed list of new features. If you are already familiar with the HortControl 3.4, you can skip directly to these new features' sections.

Machine learning

With the machine learning module, we give the power of the data back to you! This mode gives you the ability to build your own model for estimating custom target features using generated PSX data. Target features could include disease quantifiers, biomass estimations, health indices, etc. Data from different experiments and growth stages can be combined to build your predictive model.

External barcode reader

With the external barcode reader feature, it is possible to assign your own block names to a system block id (3.6.1.4) and exclude the use of metal barcodes. In the experiment live module, you can control which block will be scanned next, without having to exchange metal barcodes anymore (3.3.3).

A hand-held barcode scanners can be integrated directly with TraitFinders. You can purchase one directly from Phenospex.

Other improvements

- ✕ Diskguard option for mounted shares
- ✕ Storage capacity of the shares is now visualized in the dashboard and top menu status
- ✕ When refreshing data in the data Overview module, the zoom will remain as before
- ✕ Input fields in the system layout module are adjustable
- ✕ Unit position hover is added in Experimental Setup 3D view in experiment setup
- ✕ And other minor improvements

Release notes HortControl

You can find all release notes from the previous versions on [Phenospex.helpdocs.com](https://phenospex.helpdocs.com)

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1. ABOUT THIS manual

1.1. Purpose and target group

This manual describes the use of the PHENOSPEx software HortControl 3.5. 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 3.5 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 suggested to keep 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 whereabouts of this user manual.

It is recommend 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 setup 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 3.5 is web-based software that is used to set up experiments and analyze data acquired by the Phenospex PlantEye 500 scanner(s).

With HortControl 3.5, 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 new 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 to upgrade to the latest Chrome versions prior to use.

The minimum HortControl 3.5 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

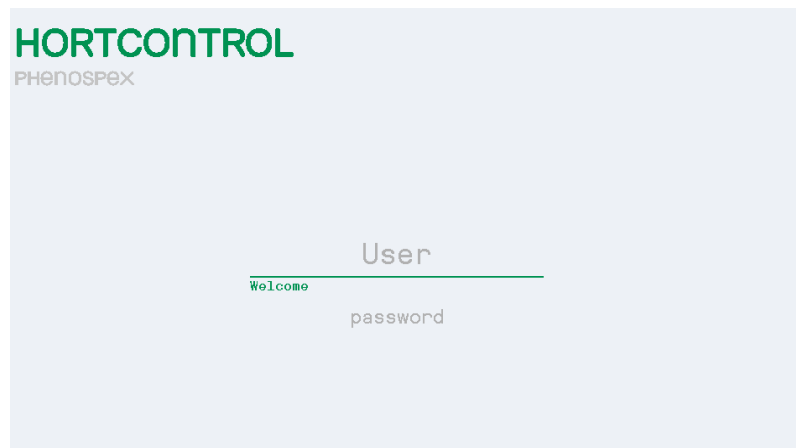
3. WORKING WITH HORTCONTROL

3.1. Access HortControl 3.5

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.

3.2. Navigating through HortControl 3.5

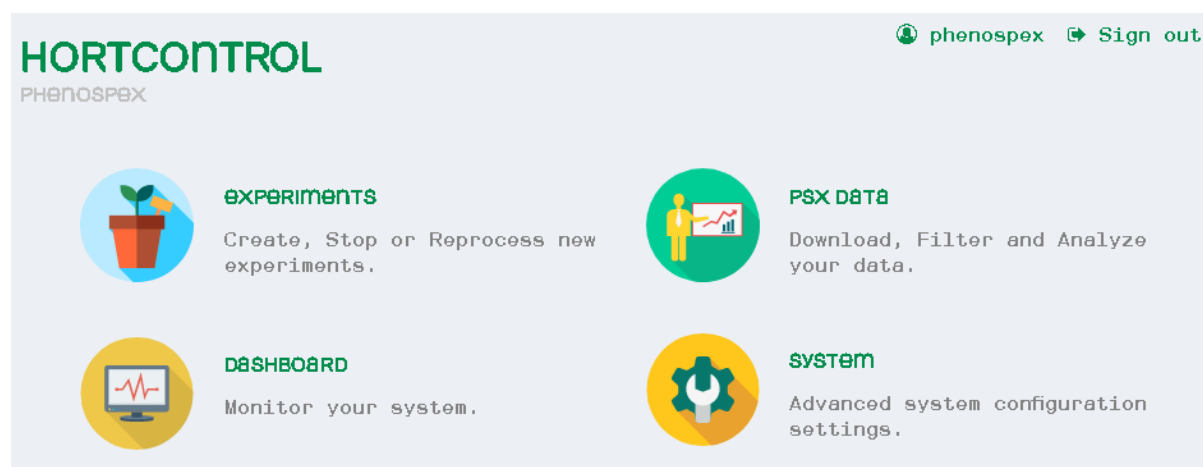
HortControl 3.5 is comprised of an initial **Homepage** and multiple **Boards**. In turn, each board combines different functionalities or **Modules**, which consist of one or more visualization options or *Views*.

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 details in section 3.4.

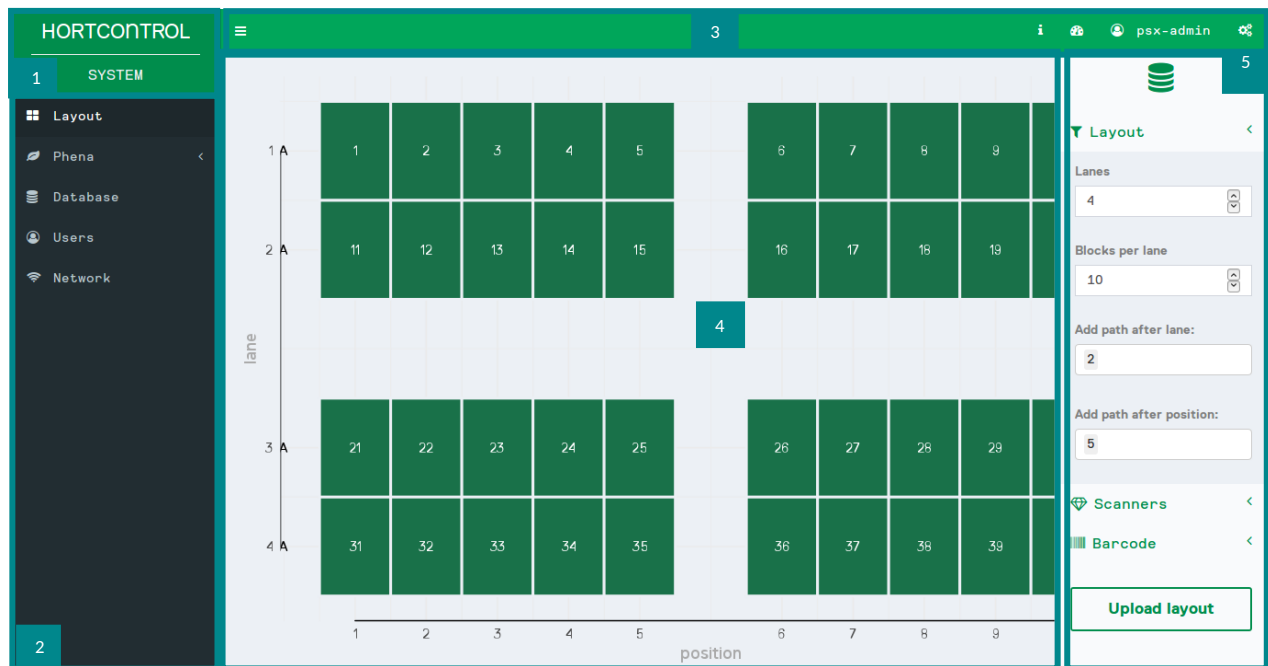
Dashboard. The dashboard acts as the control room of your system. Here you can consult the system's current state. Please refer to 3.5 for additional information.

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

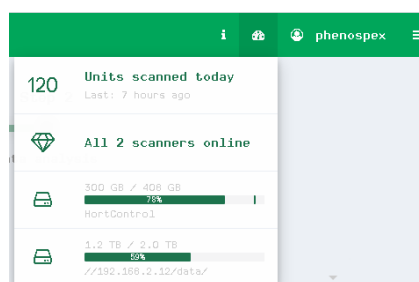
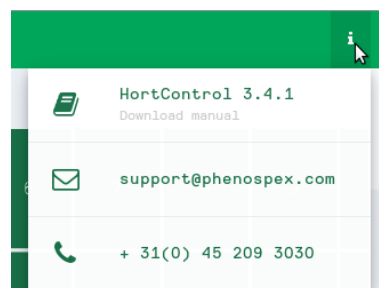
Once selected, each board has the same structural layout and consists of:

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

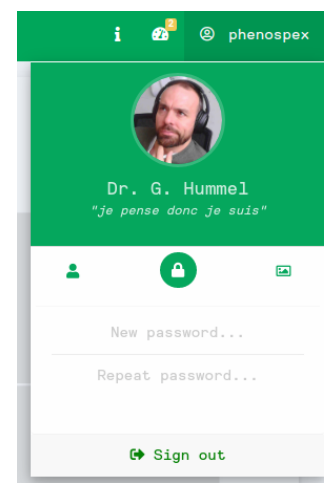


In the information bar you can:

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



Experiments Board



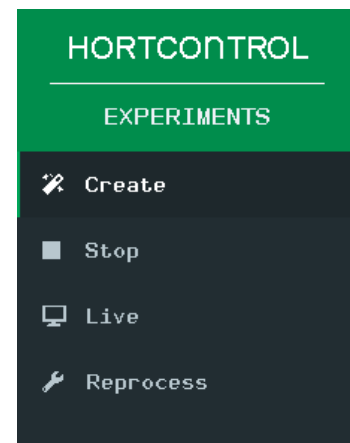
In HortControl 3.4, there can be one or multiple experiments running on your platform simultaneously, all of which can be managed independantly within the **Experiment** board. This board consists of four modules: **Create**, **Stop**, **Live** and **Reprocess**.

Create module allows user to set up and start a new experimental platform (3.3.1).

For detailed explanation on how to **Stop** your experiment please see section 3.3.2.

When using External Barcode reader (3.6.1.4), please use *Live* module to assign scanners to this mode (3.3.3).

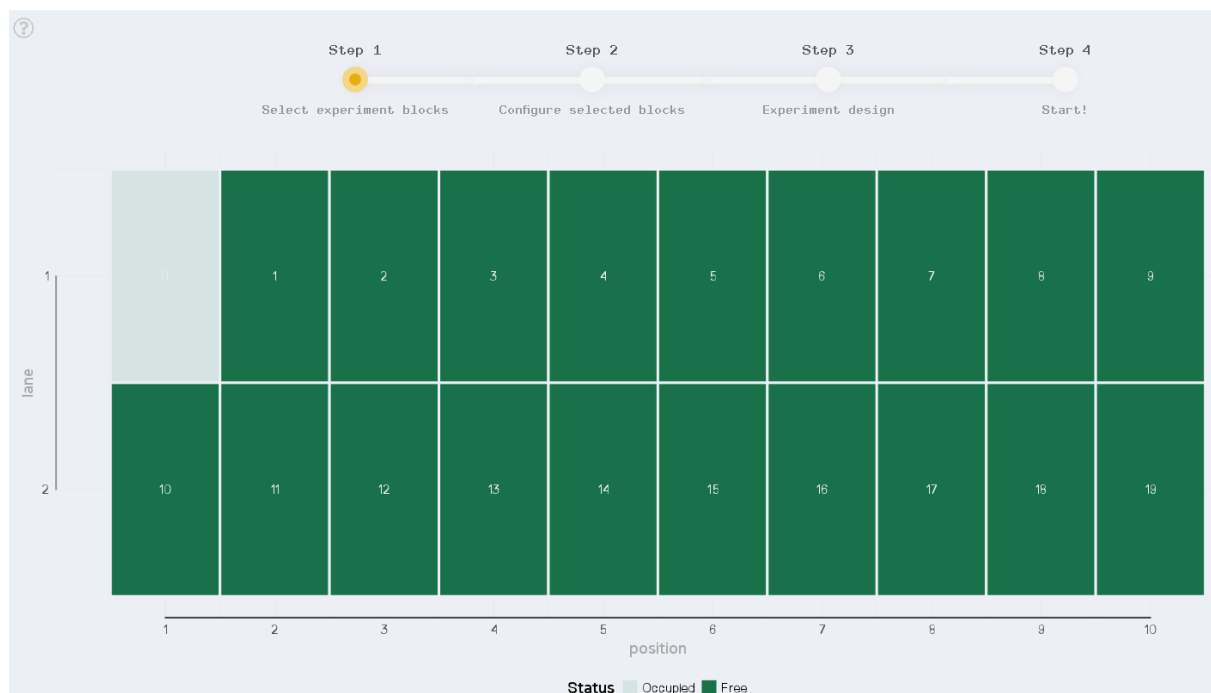
Finally, you can **Reprocess** the scans from a completed experiment(s) with new splitting and/or multispectral binning settings (3.3.4).



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 four steps (please note them on the top of the main window in the image above):

- Step 1: Reserving blocks for the experiment by selecting free (green) blocks
- Step 2: Configuring selected blocks by splitting the blocks in units

Step 3: Configuring experiment design by adding biological information (genotype and treatment) to the units

Step 4: Uploading your experiment and starting 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 unfished step highlighted in gray.

3.3.1.1. Select free 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, Step 2 becomes available in the workflow bar. Click on it to proceed to Step 2.

3.3.1.2. Configure Blocks

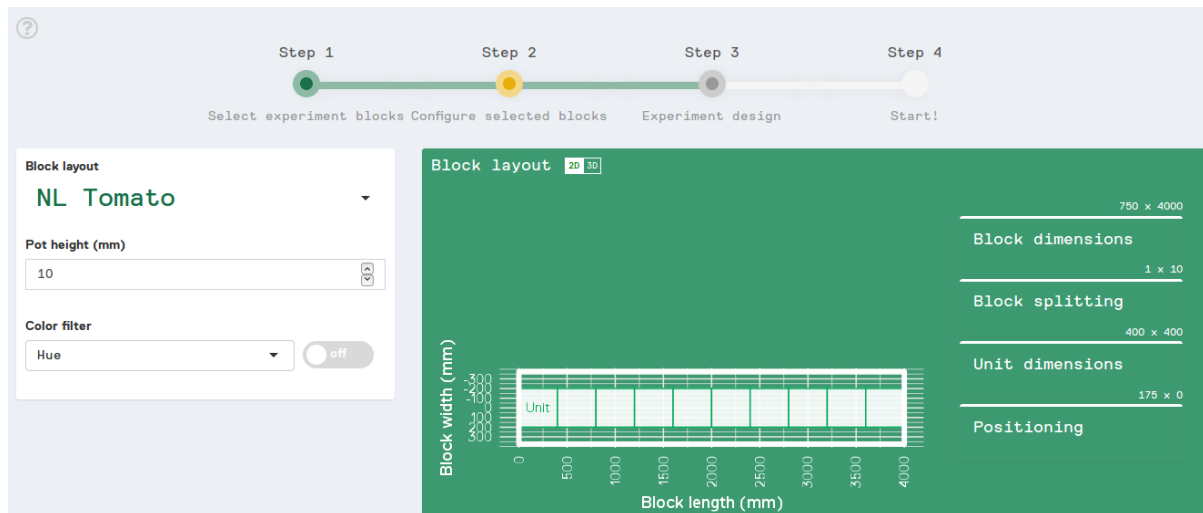
In this step the selected blocks will be subdivided into units and the height of the pot is set.

Units are the most detailed part of your platform's coordinate system. Any block can be subdivided in x by y units. It is to these units that plants and plants' information is assigned for each experiment.

IMPORTANT

This is the most crucial step for the correct setup and final results step.

Once you select/reserve a block in Step 1, and move to Step 2: Configure selected blocks, you will be prompted to the next window (shown below).



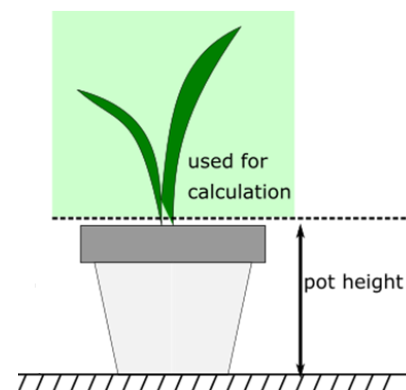
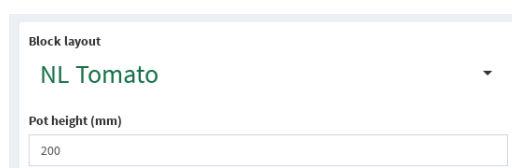
First, you define a block layout, name and save it. The saved block layouts can be reused in later experiments. To create a new block layout, you enter a new name first, e.g. *NL Tomato*. Click on the area under “Block layout” on the left side, type in the name and press “Enter”.

IMPORTANT

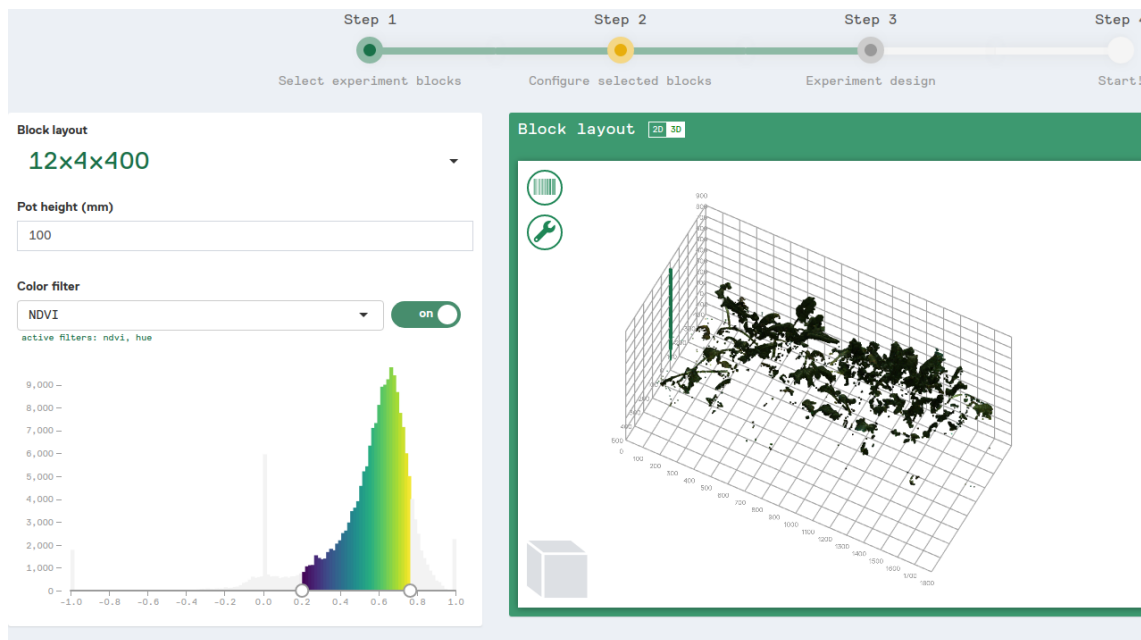
When dealing with a large system (multiple lines, hundreds of plants and/or multiple barcodes) it is advised to include barcode numbers associated with this block within your block layout name.

Next step is to define a pot height (in mm).

The pot height (shown on the right image) 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.



Optionally, you can also add a color segmentation processing step. With this step you can choose which parts of the different color indices you want to keep for calculating plant parameters. For example, 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 desired range. For an optimal color segmentation, you can use multiple color indices filters simultaneously.



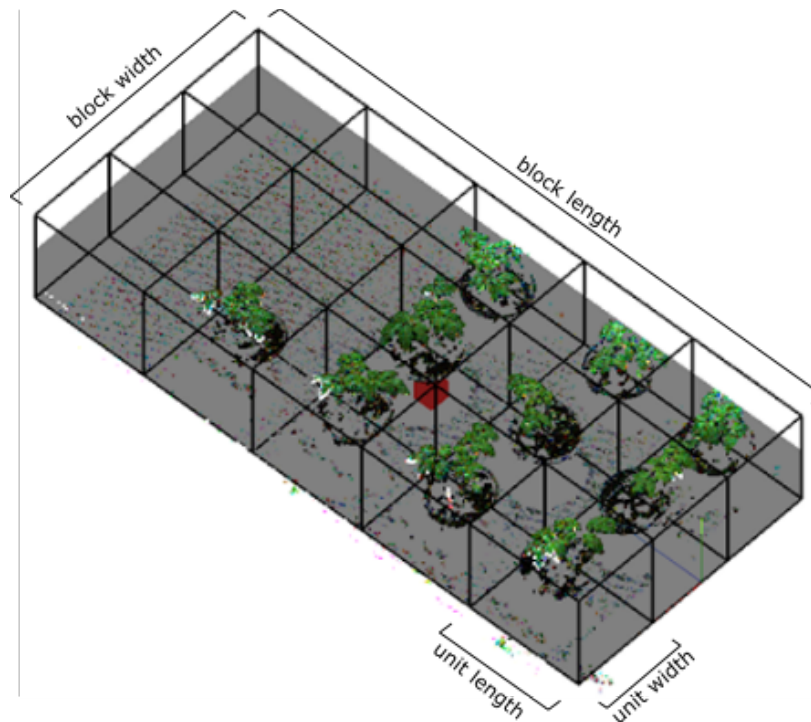
IMPORTANT

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).

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 preconfigured 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).

	1000 x 1230
Block dimensions	
	1 x 1
Block splitting	
	1000 x 1230
Unit dimensions	
	0 x 0
Positioning	



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).



Block

17 ▼



View

Boundary

yes


Resolution

low high

Color


Color

Color ▼



x Block

Select



x Boundary

Toggle 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.

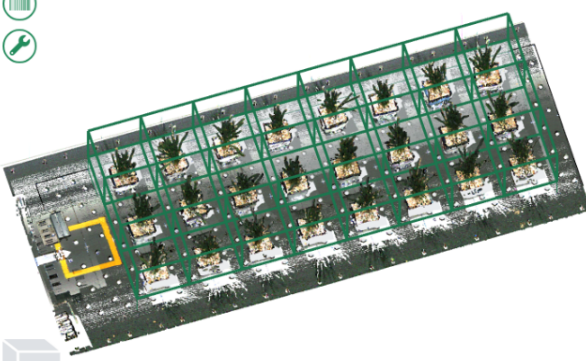
x Color

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. Experiment setup

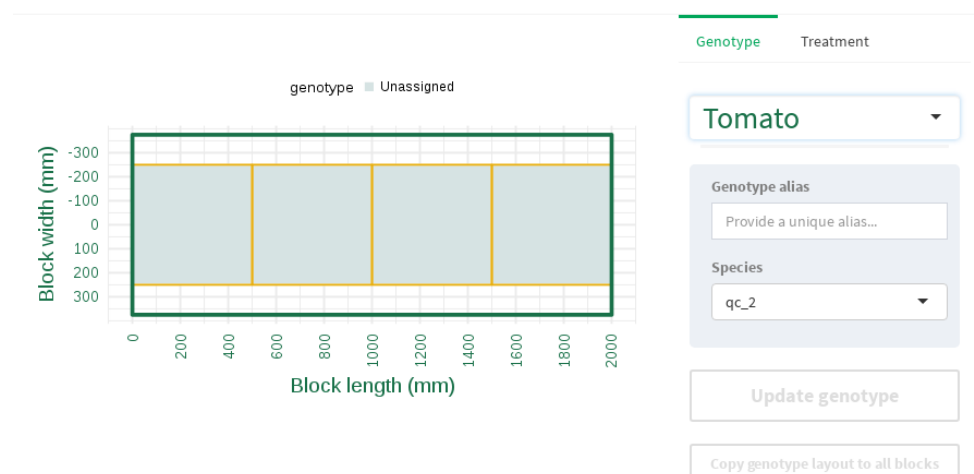
During this step biological (genotype and treatment) information is attached to the newly created units. This is a crucial step in which data is transferred from your physical world to the biological world. Once the information is assigned / uploaded, the blocks will show up in yellow (image below).



As mentioned, there are two ways to add biological information: 1) adding this information block by block using the system overview, and 2) uploading the biological information in batch using a csv file.

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 chose 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.



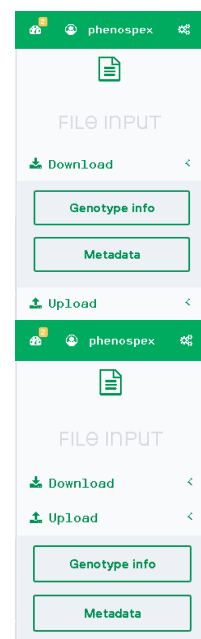
If all your selected experiment blocks need different biological information, you have to update each block separately. However, if the genotype and/or treatment pattern in all your blocks is the same, you have a simple way to copy the current block information to all other selected blocks for your experiment. 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.

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 current created experiment units (“Metadata” button).

These files can be manually updated and uploaded to HortControl repeatedly via 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.



barcode	unit column	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

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.

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 complete system update, you are ready to move to the final step.



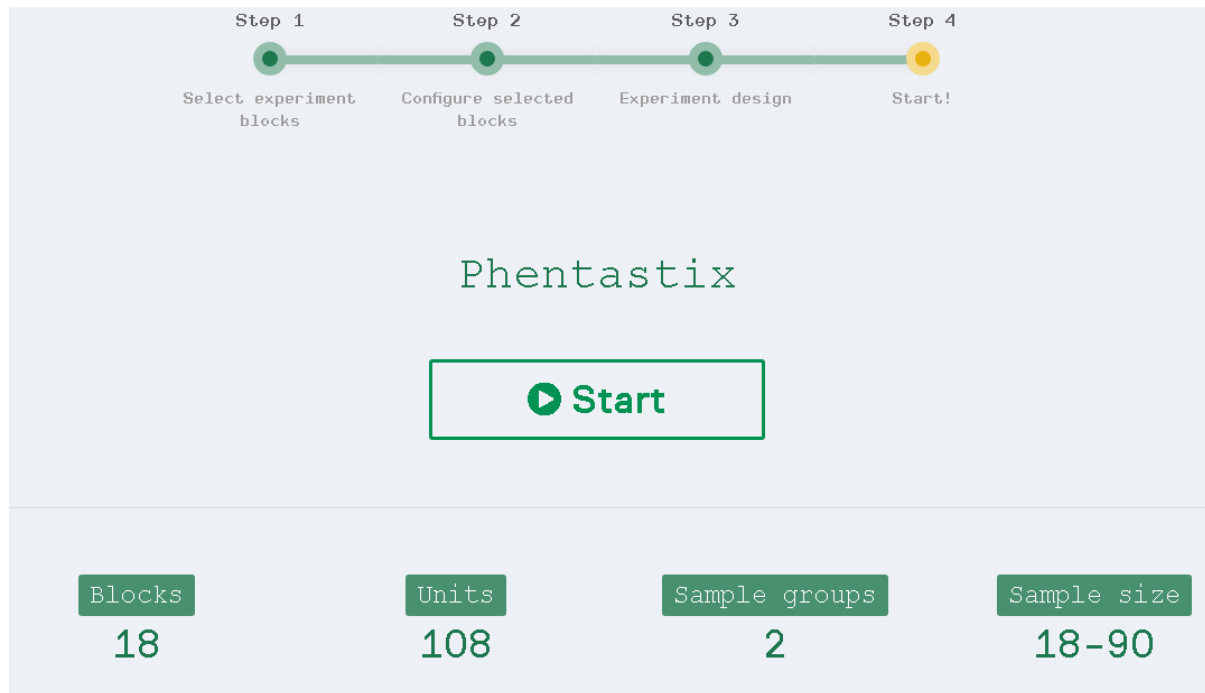
3.3.1.4. Start!

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.
- ✗ 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

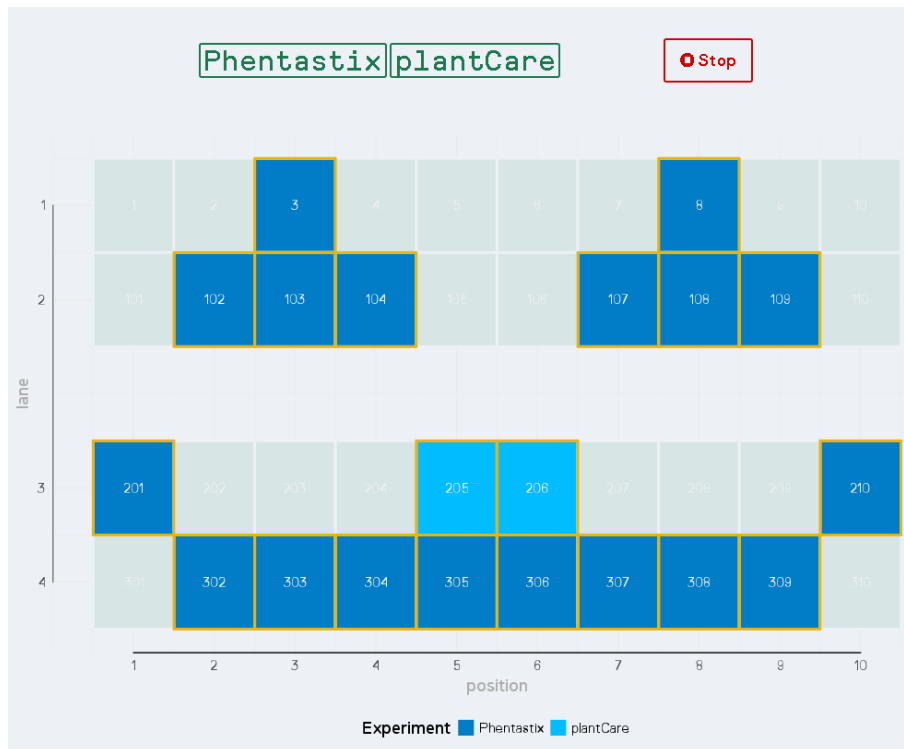
information. These errors can compromise final statistics. For more information about finding the right sample size please refer to the Wikipedia https://en.wikipedia.org/wiki/Sample_size_determination.



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. 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.



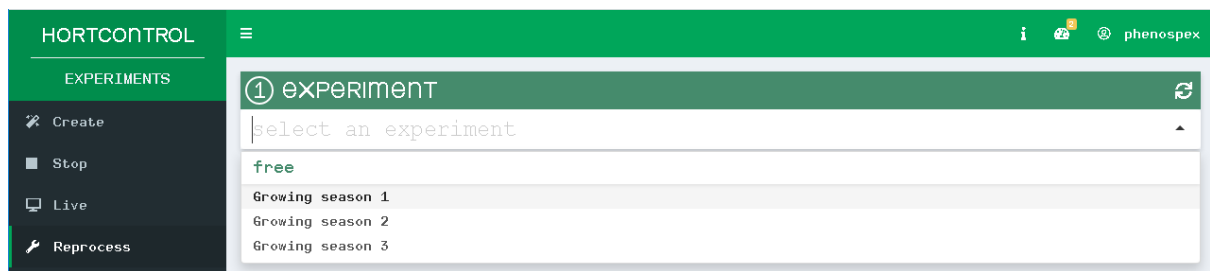
3.3.4. Reprocess Module

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 a few steps: 1) select the experiment you want to reprocess, 2) select an example scan, 3) update settings and compare old data with new data, and 4) when you are satisfied with the new settings, start the reprocessing job for your whole experiment.

3.3.4.1. 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.

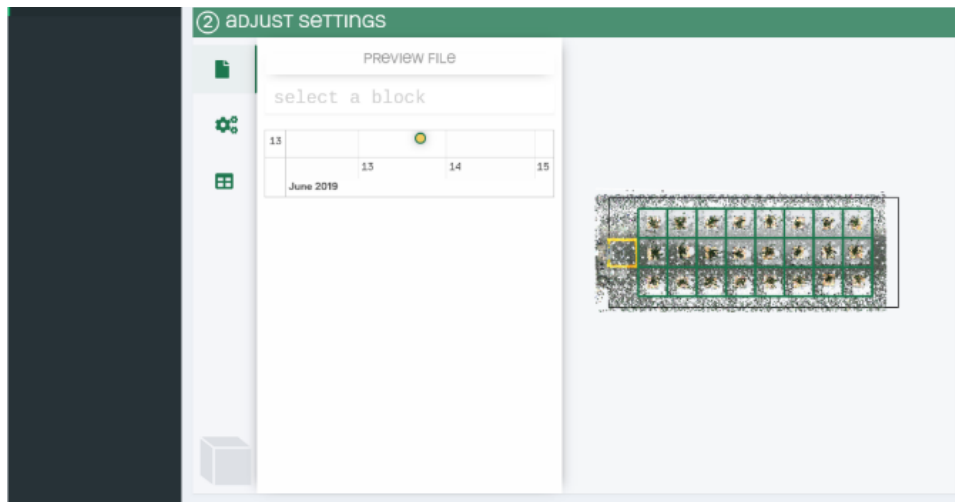
Finish. Reprocessing has been completed, but there were some errors that require corrections.

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

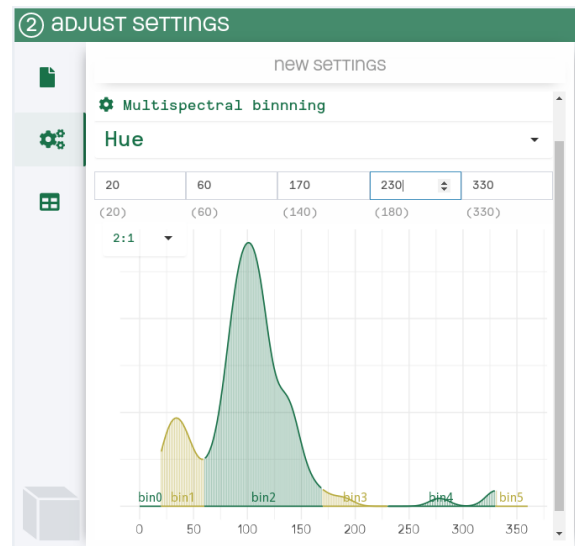
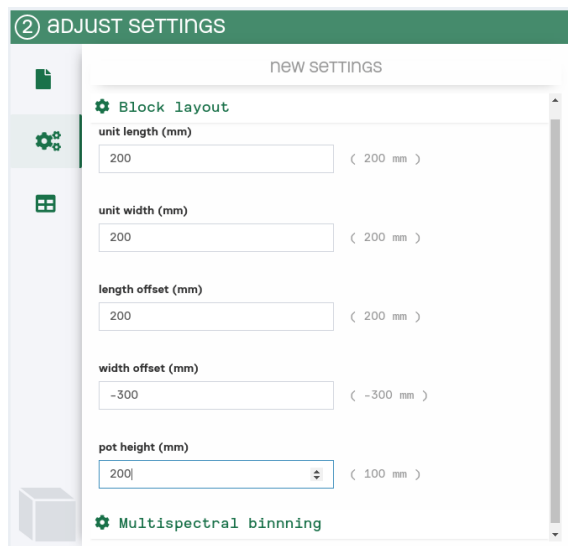
Once an experiment is free you can proceed to Step 2, where you will be able to select a scan, apply new settings and view how new setting will affect your scan images and data. When you are satisfied with the new settings, you can choose to start reprocessing, which will reprocess **all** scans for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

3.3.4.2. Change settings

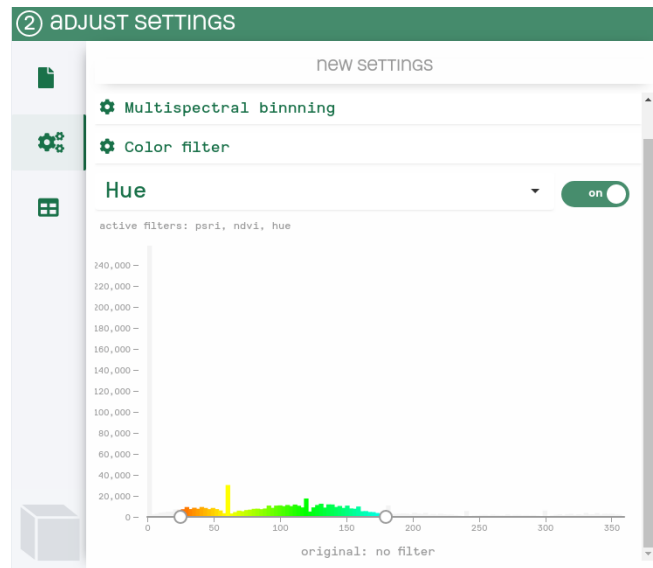
When a free experiment is selected, you will be able to select a preview scan to optimize your new settings. You can select a preview scan by selecting a block id from the preview file dropdown. This will show you all the available scans for that block. Select a scan, and a 3D view will be loaded.



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.

② ADJUST SETTINGS

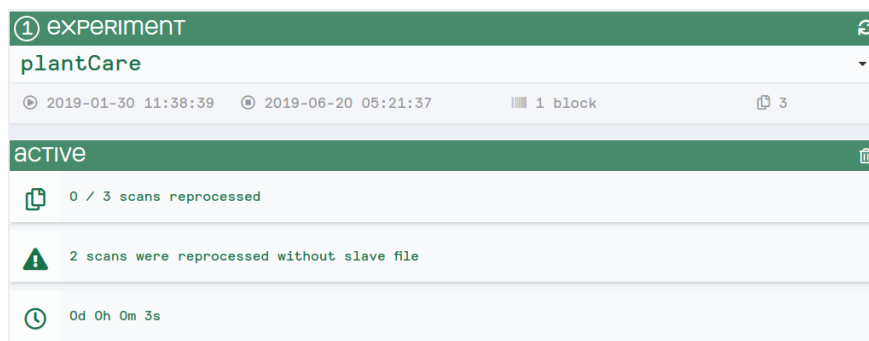
COMPARE DATA

COLUMN	ROW	VARIABLE	VALUE	new
A.		A1		
1	1	Digital biomass	297523 mm ²	7297.059 mm ²
1	1	greenness average	0.18677	0.19625
1	1	greenness bin0	0 %	0 %
1	1	greenness bin1	0 %	0 %
1	1	greenness bin2	5.773 %	3.82 %

Previous 1 2 3 4 5 - 207 Next

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.

3.4. PSX Data Board

Once the experiment is launched, and the data starts to accumulate, it becomes available in the PSX Data board. You can download either .ply files or calculated values printed in .csv document. 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**.

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.

Digital biomass (mm ³)
Morphology
Digital biomass (mm ³)
Height (mm)
Leaf angle (°)
Leaf area (mm ²)
Leaf area index (mm ² /mm ²)
Leaf area (projected) (mm ²)
Leaf inclination (mm ² /mm ²)
Light penetration depth (mm)
Hue
NDVI
Greenness
NPCI
PSRI

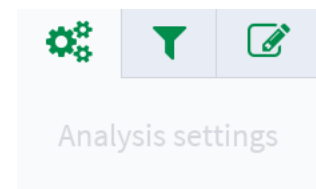
3.4.1.2. Refining data

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.



reflect current analysis



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 genotypes 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.

Filter data

Time

2017-12-04 00:00 to 2018-02-01 00:00

Treatment

Genotype

FILTER DATA

x Time
Define a time window for your dataset.

x Treatment
Select the treatment(s) you want.

x Genotype
Select the genotype(s) you want.

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, the Download button will initiate collection of the measured and calculated parameters within the .csv file.

The screenshot displays the PHENOSPEx interface. At the top, a progress bar shows 'Step 1' (Select experiment) and 'Step 2' (Data analysis). The main area shows 'Exp1' with a 'Download' button. Below this, a table lists parameters: Blocks (1), Units (7), Sample groups (1), and Sample size (7). On the right, a 'FILTER DATA' sidebar contains input fields for Time, Treatment, Genotype (G1), Genotype alias, and Species.

By default, downloaded .csv file will be comprised of all collected data. If you wish to extract information for any specific treatment, genotype, or species of dates, you can do so by apply necessary filters.

The same filters are applicable in Step 2, to view collected data points on the plot. 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 prompt to the information window.

Plant @ 16:1:1

Data File

INFO	measurement	value
<div>2020-06-08 13:03:15 TIME</div> <div>Potato GENOTYPE</div> <div>1 TREATMENT</div> <div>* Delete measurement</div>	Digital biomass	141419000 mm ³
	greenness average	0
	greenness bin0	0 %
	greenness bin1	0 %
	greenness bin2	0.1 %
	greenness bin3	4.1 %
	greenness bin4	7.4 %
	greenness bin5	88.3 %
	Height	440.5 mm
	Height Max	496.5 mm
All		All
Previous		1 2 3 4 5 Next

Once in the window, select File, and you can preview 3D image of the data point you have selected. You can also adjust viewing options, such as number of points shown.

Plant @ 16:6:1

Data File

i

↺

⚙

View

Color

Points


Point size

0.05

Maximum points

100000

⬇



Within .ply files you have an option to download *Raw* and *Transformed* files (which contain the image of the whole block), as well as *Units* files (which contain separate file for each of the units within the block).



Settings

File processing

Raw |

Transformed

Units

Compression level

0

Download

For the dual scan in the Scanner side your scanned image

Maximum compression level is value in this

Select Download download.



Settings

File processing

Raw Transformed

Scanner side

M S

Compression level

6

Download

system, please select both M and S window. Otherwise, only part of will be downloaded.

recommended download 6, but you do not have to select a window.

button to begin your 3D image

3.4.2. Overview Module

Your system generates a time series with pre-defined time intervals for every plant. Using 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.

TIME AGGREGATION

x Time points

The time point to which data should be mapped per day. You can define up to 24 time points (1 per full hour). One typical application is mapping data to the night (e.g. 0:00) and daytime (e.g. 12:00).

x Maximum range (h)

The maximum time window around the selected time blocks that is used to aggregate your data. If we take the example above and set the range to 2 hours the data at 18:00 would be discarded as it is 6 hours away from the time points 0:00 and 12:00.

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

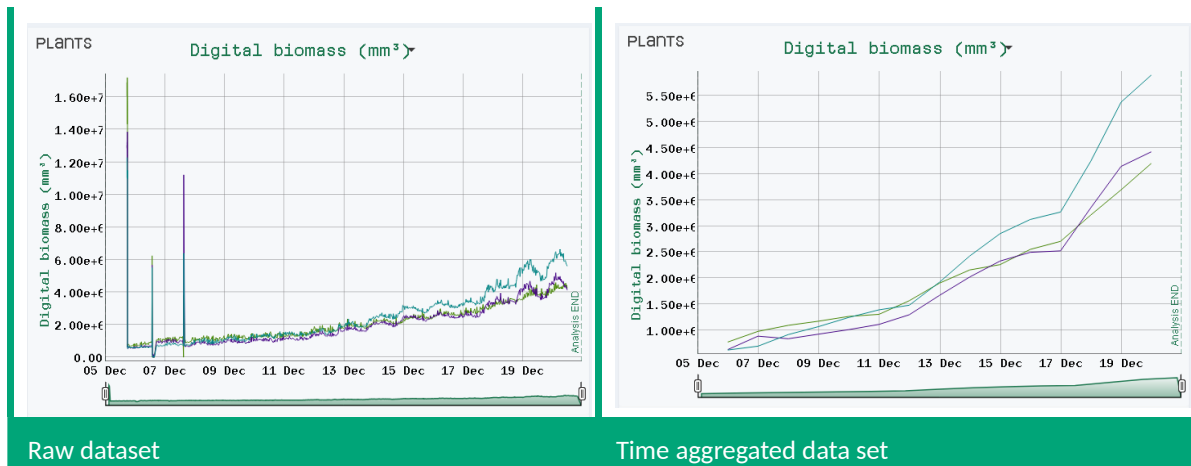
With the previous settings you define how the raw data should be mapped to discrete time points. Here, you can choose an aggregation function to combine all this mapped data to 1 value per time point. The default method is *median* which will take the median value of all data points mapped to a time 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.



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.

⚙️
🔍
✎️

Analysis settings

▼ Data <

📊 Grouping <

Sample groups

Function

median ▼

GROUPING

x Sample groups

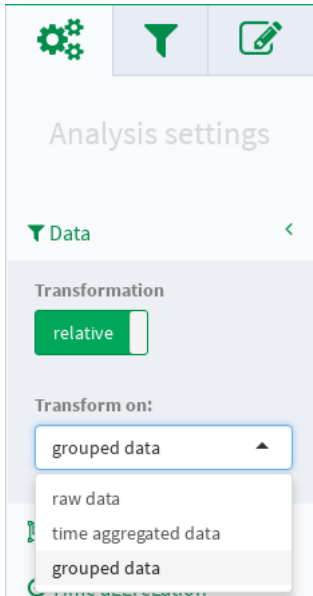
You can choose to aggregate the plants by treatment, genotypes or both.

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.



Data Relative

x Raw data
Making the data relative is done on the raw data set, i.e. on the irregular time series of every plant. The time aggregation and grouping are then performed on the resulting dataset.

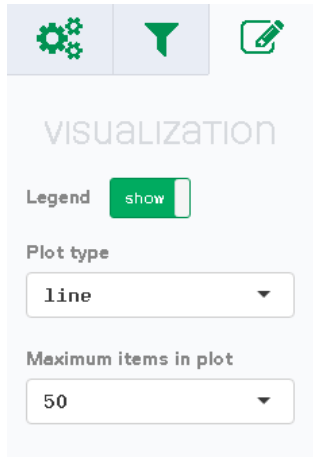
x Time aggregated data
Making data relative is done after time aggregate has been performed. I.e., on the simplified time block time series of every plant.

x Grouped data
Making data relative is done after time aggregation and grouping has been performed. I.e., on the simplified time block series of every treatment and/or genotype.

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.



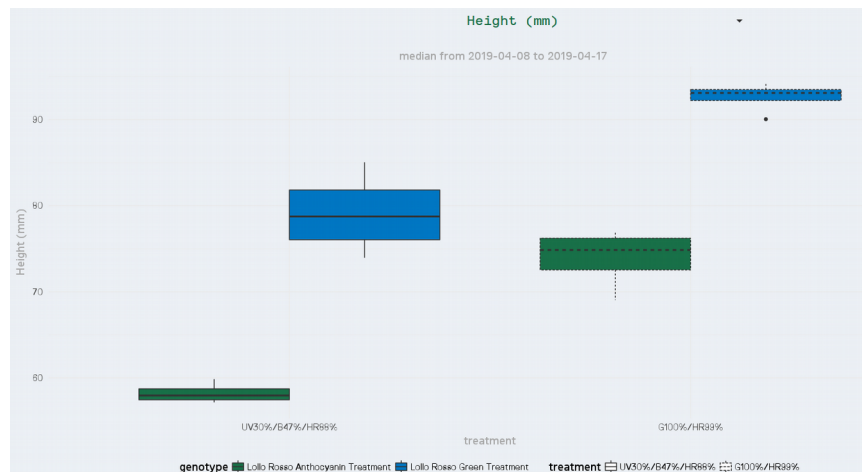
view

x Plot type
Line. Connects all measurements per plant/genotype/treatment over time and is good for visualizing the trend over time.
Stem. Shows the projection of the value on the time axis. Handy to look for missing data points or assess the scanning frequency.

x Maximum items in plot
Limits the plants/genotypes/treatments that are displayed.

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.

⚙️
🔍
✎️

analysis

⌚ Quadrant <

Quadrant type
 Treatment ▼

X variable
 PPFD 1 ▼

Y variable
 ▼

GROWTH QUADRANT SETTINGS

x Quadrant type

Treatment. Individual treatments can be compared on the axes.

Variable. Individual variables can be compared on the axes.

x X variable

The variable data that should be plotted on the X axis.

x Y variable

The variable data that should be plotted on the Y axis.

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.

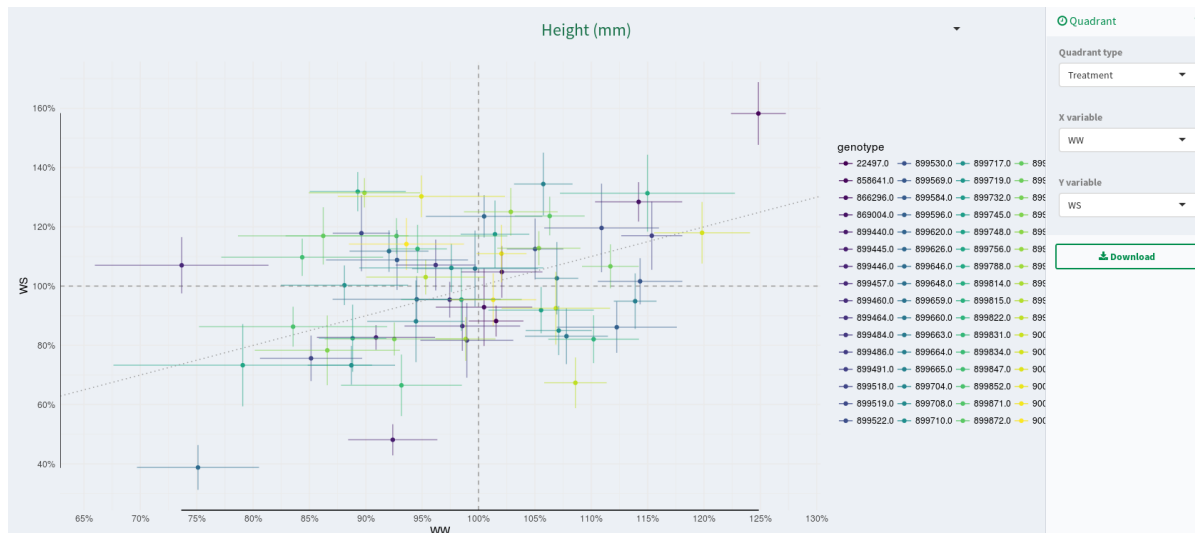
genotype: Tray 3
treatment: PPFD 1
HEIGHT
2.208
mm/day
IQR: [2.208, 2.208]
range: [2.208, 2.208]

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.

DIGITAL BIOMASS	HEIGHT
136%	121%
genotype: Tray 3	
treatment: PPFD 1	

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.

⚙️
🔍
📝

analysis

Threshold

histogram

Threshold occurrence

last

Block

15

GERMINATION SETTINGS

x Threshold

The value for which the time point should be derived.

x Threshold occurrence

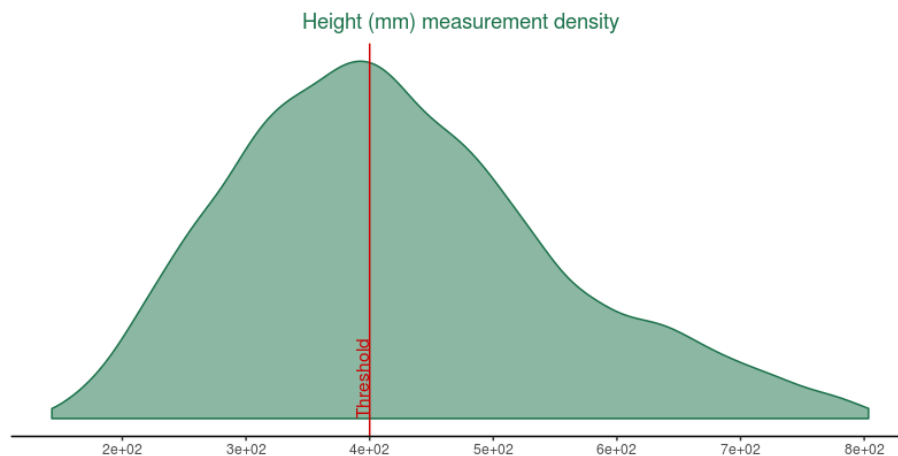
First. Takes the time point when the threshold is exceeded for the first time.

Last. Takes the time point when the threshold is exceeded for the last time.

x Block

Only available for the map view (!). Shows the unit layout of the selected block.

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.



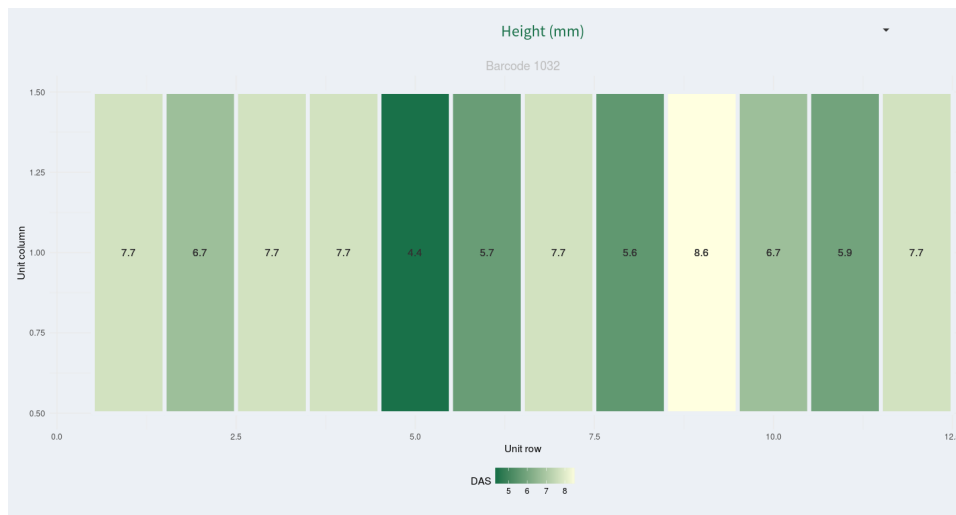
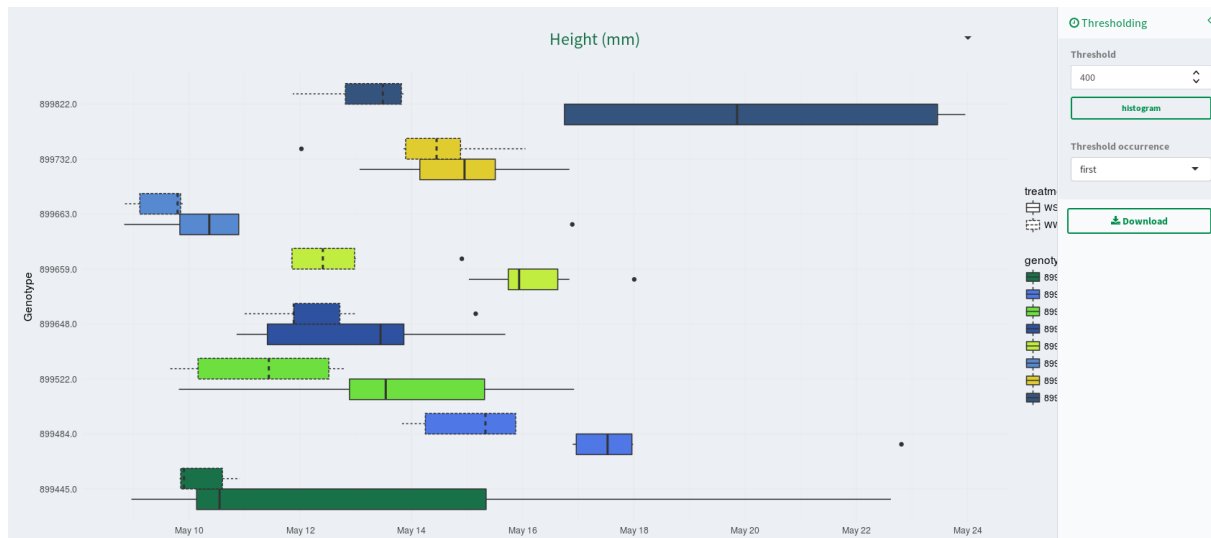
There are two views available - the boxplot view and map view.

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.

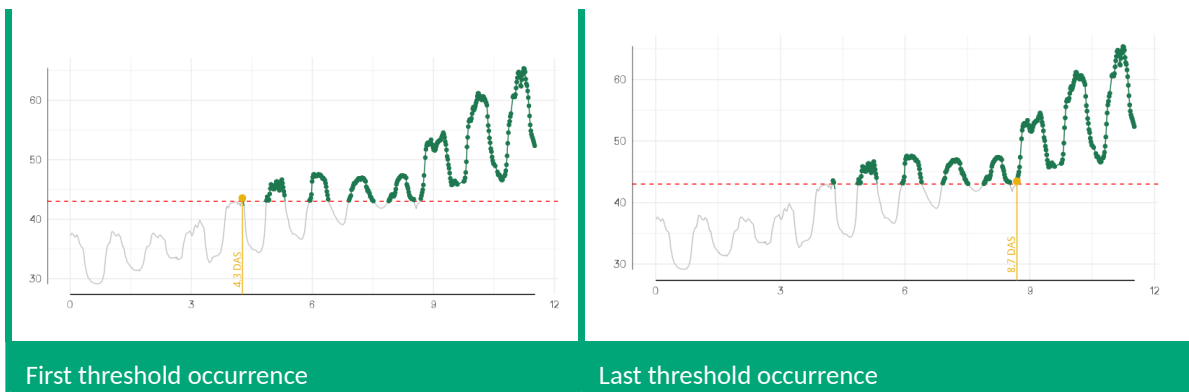
3.4.5.3. Map view

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.

GERMINATION UNIT VIEW



3.4.6. Correlation Module

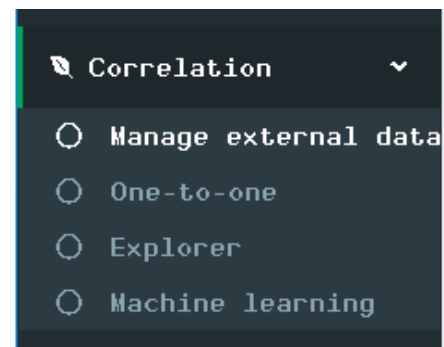
With the correlation module you can import an external dataset to the experiment and search for correlation between the PSX data (generated by your system) and your external dataset.

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 details 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






analysis

 PSX data <

Independent variable
 Leaf area

Correlation date
 2019-01-26

 External data <

Dependent variable
 plant height

Correlation date
 2018-03-16

Correlate!

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*.

external data 

No external data found for this experiment. Please upload a dataset first

 Add data
  Download data template

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 time stamp 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).

UPLOAD EXTERNAL DATA

UPLOADED UNITS

- + Unknown units
- + Missing units

UPLOADED VARIABLES

- ✓ Fresh Leaf Biomass
- + height
- ✓ Lai
- ✓ Lam
- ✓ num_leaves
- ✓ root_diameter
- ✓ root_fresh_weight

MISSING UNITS

The following units were found in your dataset, but not in the experiment. The unit names are derived from the barcode, unit column, and unit row columns as barcode:column:row.

barcode:column:row
3:4:1
3:5:1

Upload dataset

Close

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.

UPLOAD EXTERNAL DATA

UPLOADED UNITS

- + Unknown units
- + Missing units

UPLOADED VARIABLES

- ✓ Fresh Leaf Biomass
- + height
- ✓ Lai
- ✓ Lam
- ✓ num_leaves
- ✓ root_diameter
- ✓ root_fresh_weight

- FRESH LEAF BIOMASS

measurement unit
Add a unit (like mm, g, g/mm,...)

PLANT TRAIT ONTOLOGY

select a trait ontology

Upload dataset

Close

UPLOAD EXTERNAL DATA

UPLOADED UNITS

- + Unknown units
- + Missing units

UPLOADED VARIABLES

- ✓ Fresh Leaf Biomass
- + height
- ✓ Lai
- ✓ Lam
- ✓ num_leaves
- ✓ root_diameter
- ✓ root_fresh_weight

- PLANT HEIGHT

measurement unit
mm

PLANT TRAIT ONTOLOGY

plant height

Upload dataset

Close

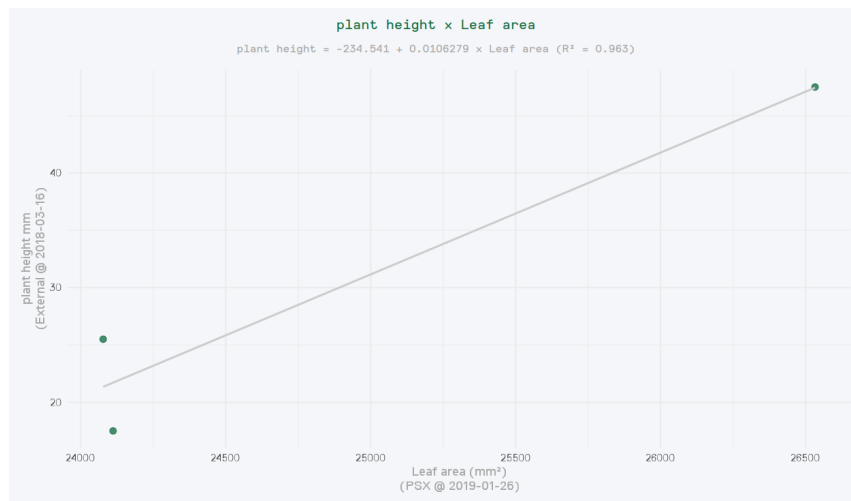
Once you have all desired matching variables on the list, you can choose to upload the external data to the database and attach it to your experiment. You can add as many or as few external data sets as you wish.

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

3.4.6.3. One-to-one mode

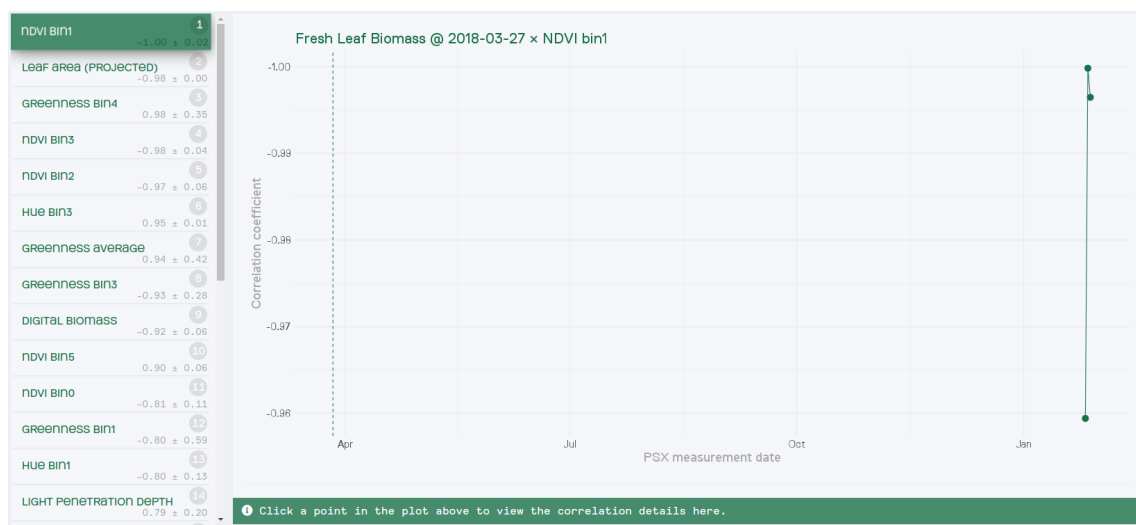
In this mode you can correlate a specific external variable to a specific PSX variable. This mode can come in handy when validating measurements. To use this mode, select necessary variables and their associated dates

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.

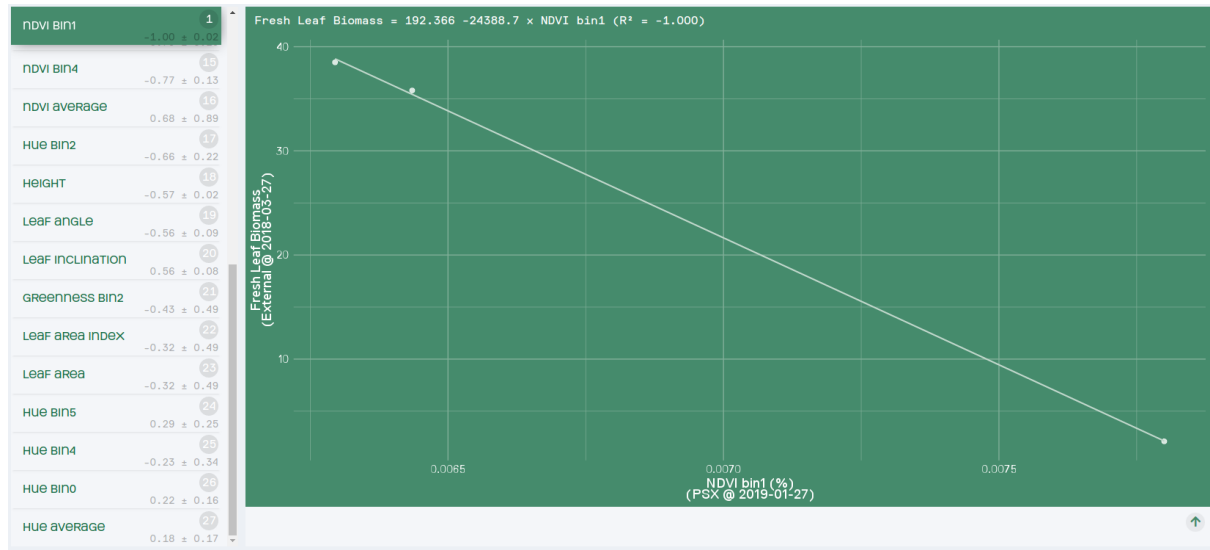


3.4.6.4. Explorer mode

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 pencil icon next to the name of your model.

model

Model for Biomass

Non-destructive biomass estimation

MODEL INFO

name

parameter

unit

description

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.

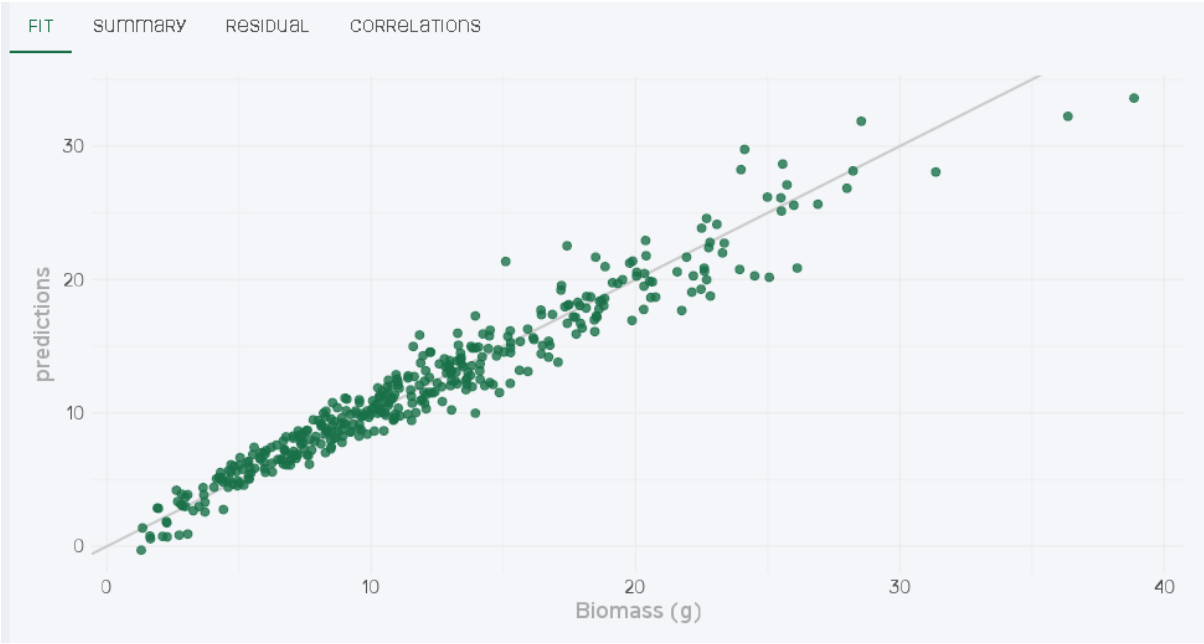
The image shows two panels of the PHENOSPEx analysis configuration interface. Both panels have a top bar with icons for settings (gears), selection (funnel), and editing (pencil). The left panel is titled 'analysis' and shows 'PSX data' selected. Below this, there is a section for 'Independent variable' with a dropdown menu set to 'all', and a 'Correlation date' field set to '2018-05-01'. The right panel is also titled 'analysis' but shows 'External data' selected. It has a 'Dependent variable' dropdown menu set to 'Biomass' and a 'Correlation date' field set to '2018-05-01'.

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.

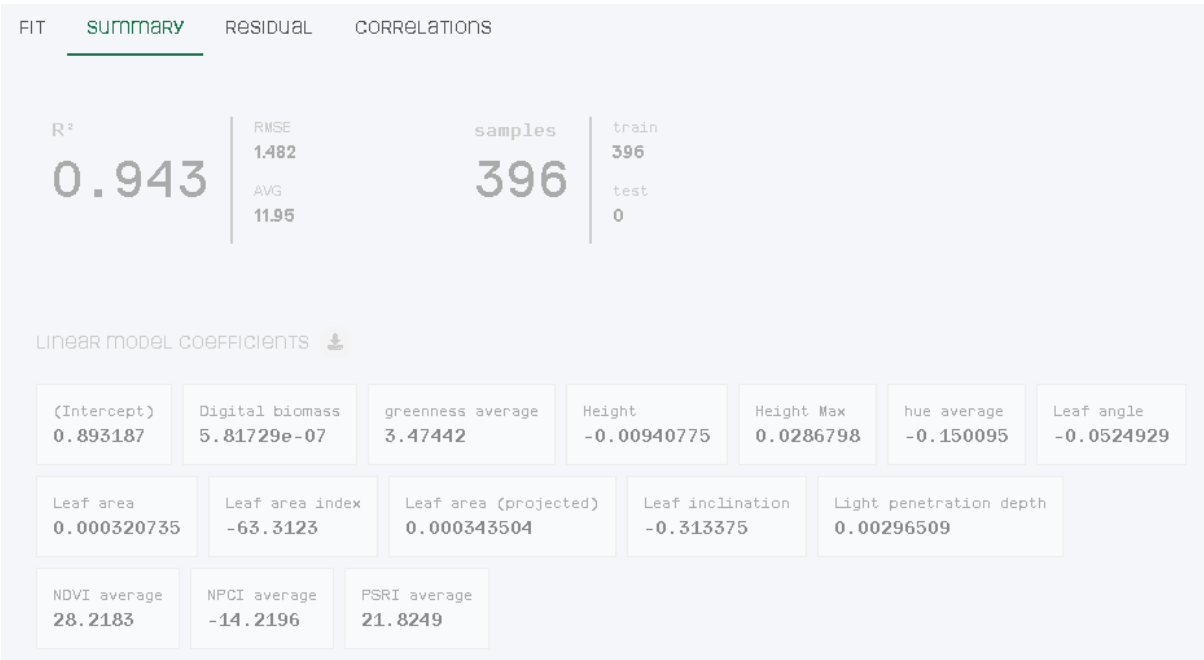
The image shows the 'DATA' section of the PHENOSPEx interface. At the top, there is a 'MODEL' dropdown menu set to 'Model for Biomass' and a '+ ' icon. Below this is the model name 'Non-destructive biomass estimation'. The 'DATA' section contains a table with two data sets. The first data set is for 'Growing season 1' and the second is for 'Growing season 2'. Each data set has columns for 'target', 'source', and 'units', along with icons for viewing and deleting the data set.

	target	source	units		
Growing season 1					
1	2018-05-01	2018-05-01	198	👁	🗑
Growing season 2					
2	2019-05-01	2019-05-01	198	👁	🗑

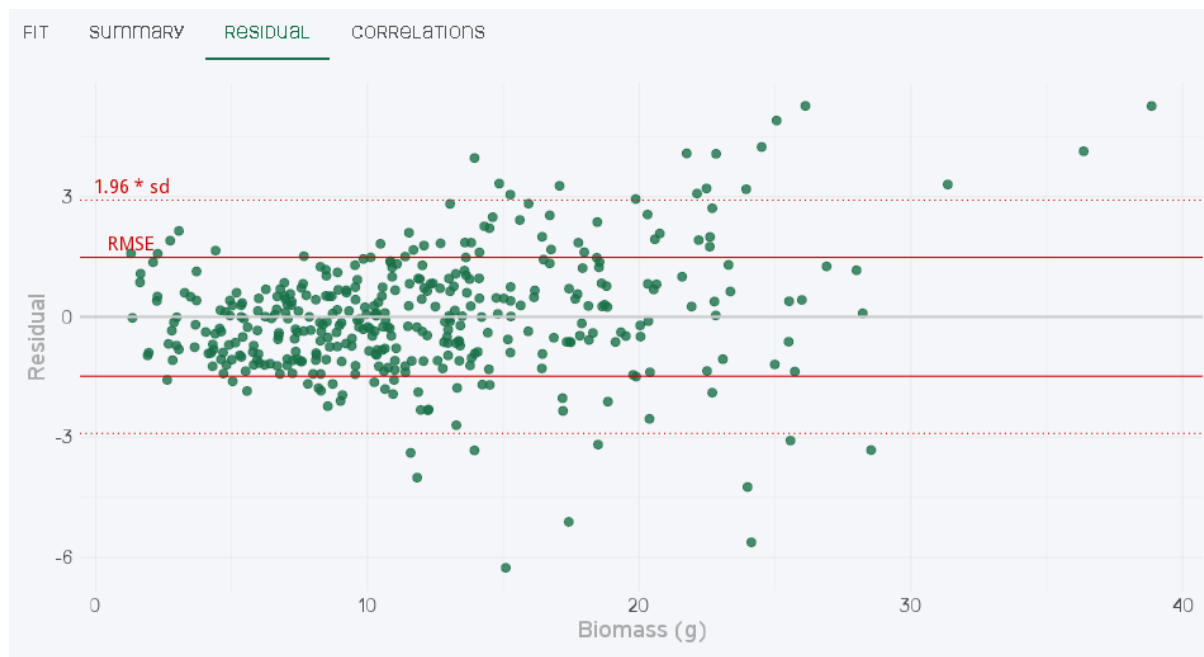
Furthermore, you can filter your data sets by time frame, treatment and genotype. For the best model fit it is advised for both PSX and external data sets to have matching days. Once you add desired data sets and select filters, you are ready to visualize data. In the FIT tab, you can view a simple prediction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



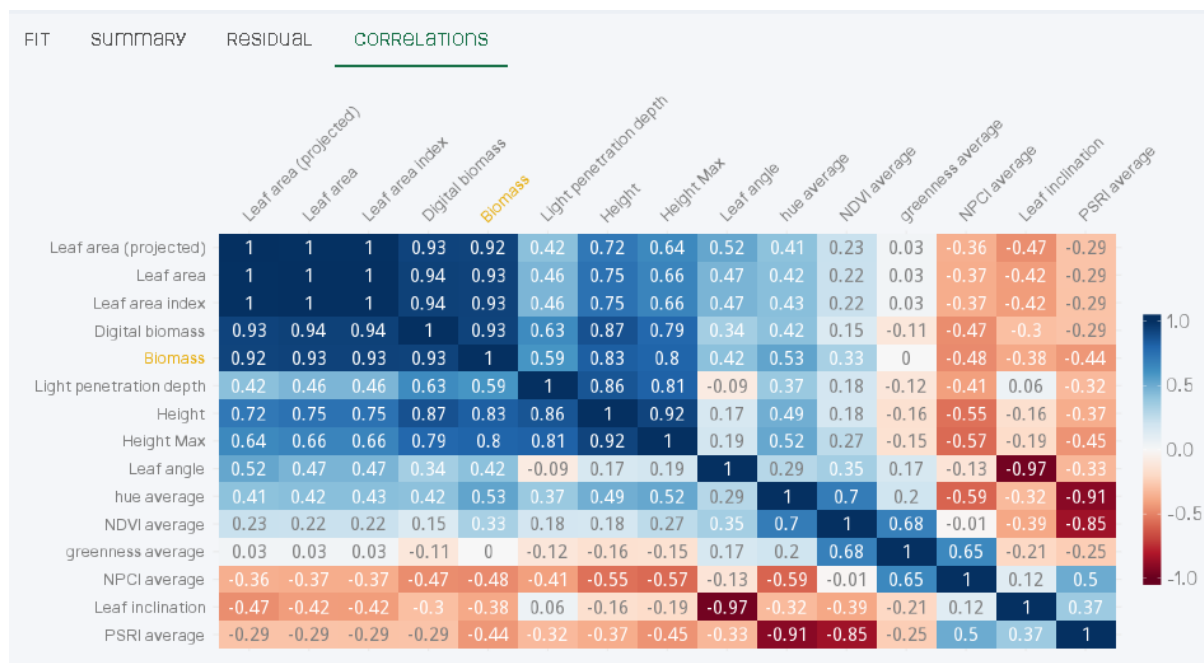
To view data, and information associated with this model, please go to SUMMARY tab. Here you can view correlation coefficients of your linear model for all selected variables. Other details of the model include R^2 , root mean squared error (RMSE), as well as sample size.



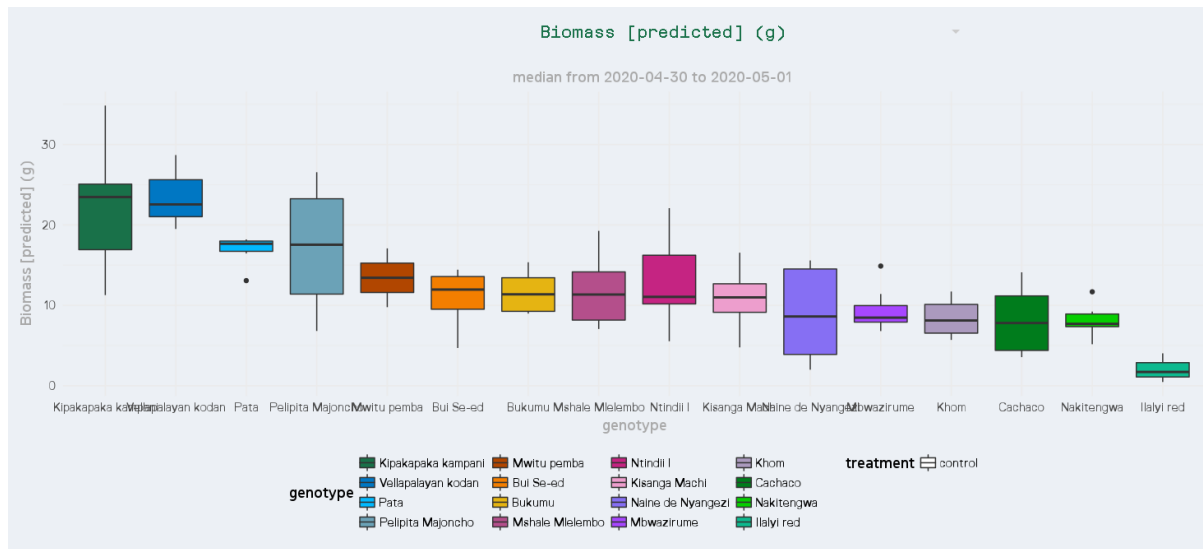
Error distribution is visualized over a range of target values in the RESIDUAL plot. It is determined based on the difference between fitted and target values.



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

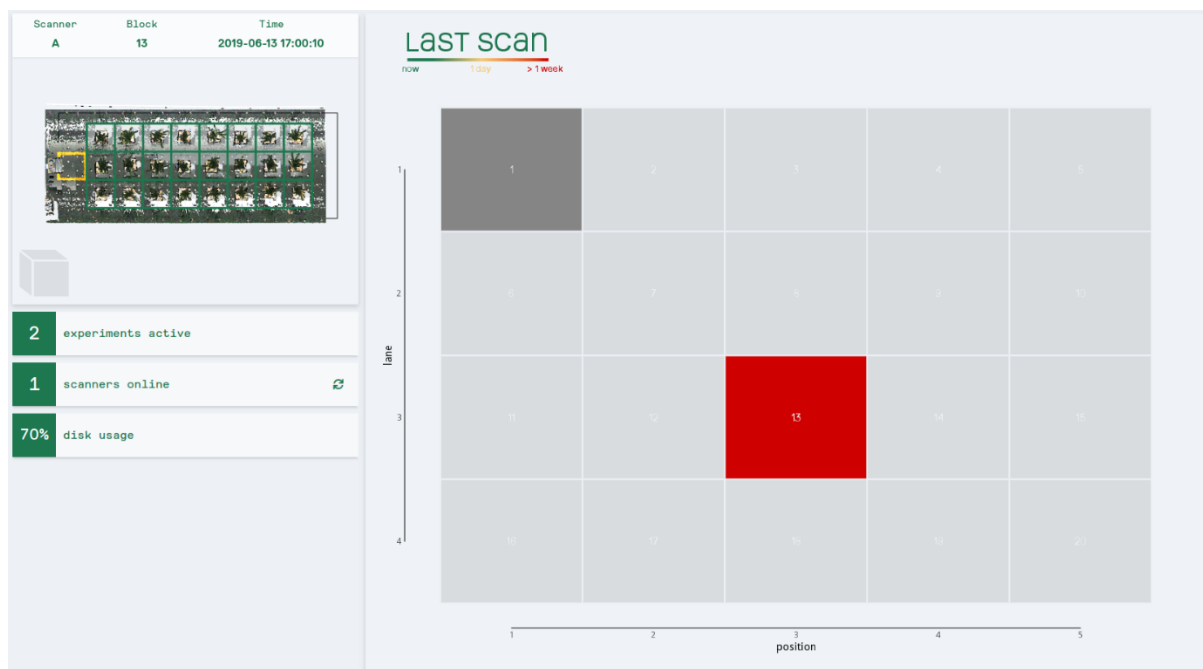


The models can later be used in other PSX Data modules. In the example below, built model is incorporated with the snapshot module. Here, the data originally collected over two growing seasons is used to estimate new features in growing season 3.

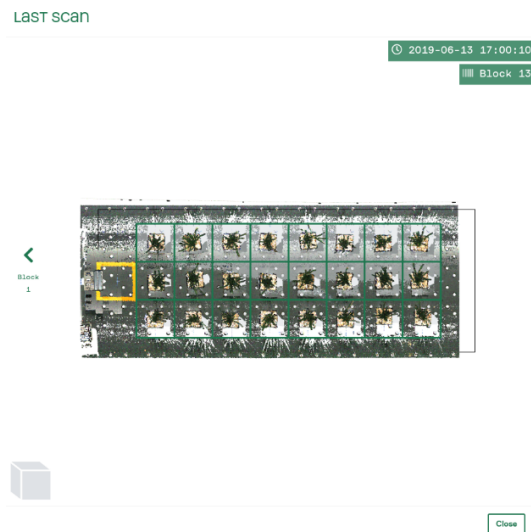


3.5. Dashboard

In the dashboard you can monitor the state of your system. 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. The overview module also provides a system overview on the right with the active blocks color-coded based on the 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.

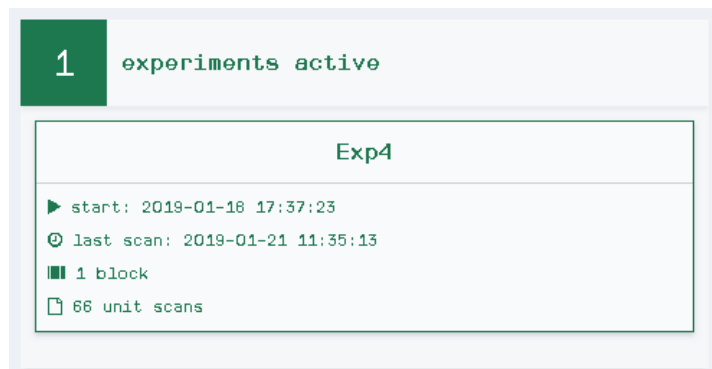


You can click any of the active blocks in the overview to visualize the last scan that was made for that block. Clicking left or right from the visualization will easily allow you to go to the latest scan of the previous or next active block.

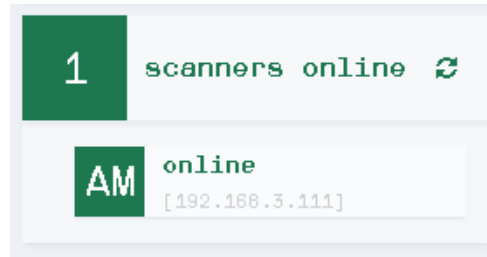


On the left you will find collapsible panels with information on the experiments, scanners, and the file system. You can open the experiments and scanners tab for more detailed information.

Experiments active. In the active experiments panel, you can find a summary for all active experiments. It shows you when you started the experiment, when the last scan for that experiment was made, how many blocks are reserved for that experiment and it gives you the cumulative number of units that have been scanned since the start of the experiment.



Scanners online. This tab can be expanded to give you details on the scanners that are online and offline. It will give you the name and IP address of the scanner along with its status. The scanner status is queried every minute, but you can always choose to poll them sooner by pressing the “refresh” button.

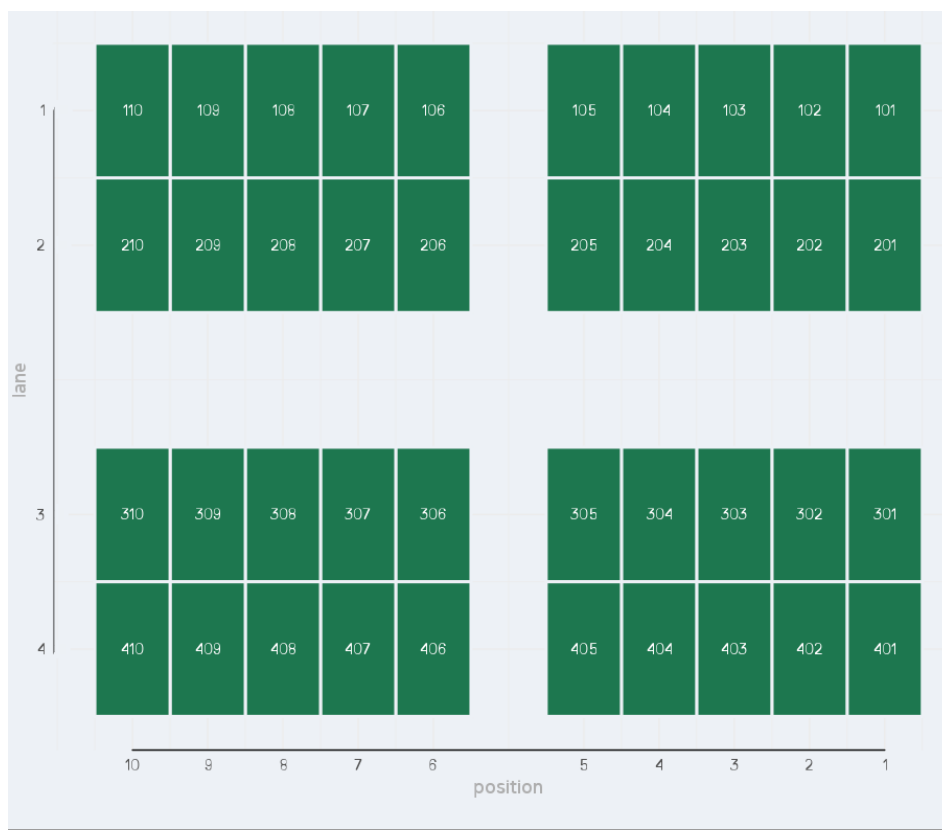



3.6. System Board

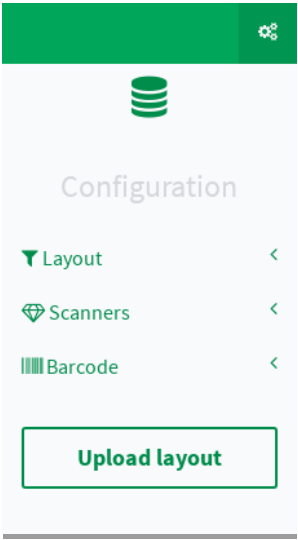
The system board is only accessible by users with an admin role. It allows you to manage and configure the systems to your specific needs. The board consist of 4 modules: Layout, PHENA, database and users.

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. 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.



CONFIGURATION

x Layout
Arrange the scan area in lanes and blocks.


x Scanners
Assign scanners to lanes.

x Barcode
Assign barcode numbers to individual blocks.

x Upload layout
Save your new layout

3.6.1.1. Layout configuration

The first step involves sub-dividing 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.



LAYOUT

x Lanes
Lanes define the different tracks for a scanner. They are the first level to split the scan area.

x Blocks per lane
Blocks are a subdivision inside a lane. They correspond to a barcode or an RFID chip, which serves as a reference point for the PlantEye. If the blocks in your system are not ordered in a matrix, e.g. when using a gantry system or mobile device, you can use the lanes and blocks to organize your barcodes.

x Paths
Can be added after a lane or block position to mimick the physical layout. They generally represent walkways across your platform.



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.

Configuration

Layout <

Scanners <

Select scanner

A
▼

Select scanner lanes

123456789

▼

Barcode <

Upload layout

scanners

x Select scanner

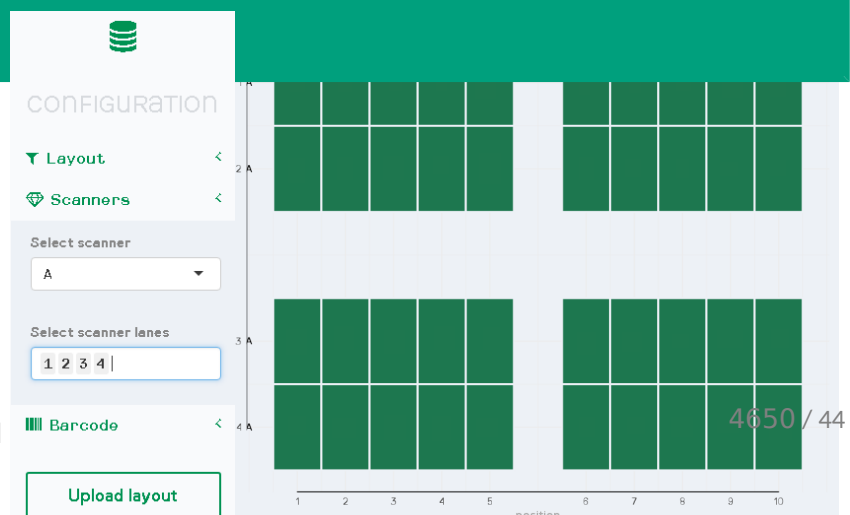
In this dropdown you select the scanner that you wish to assign lanes to.

x Select scanner lanes

Once you have selected the scanner, you can select the lanes this scanner should be assigned to.

If you have more scanners, you will need to repeat the process for every scanner.

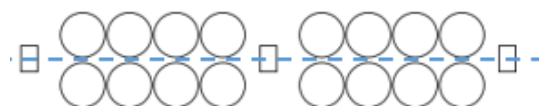
In the example on the right, we assign all 4 created lanes to a single scanner A.



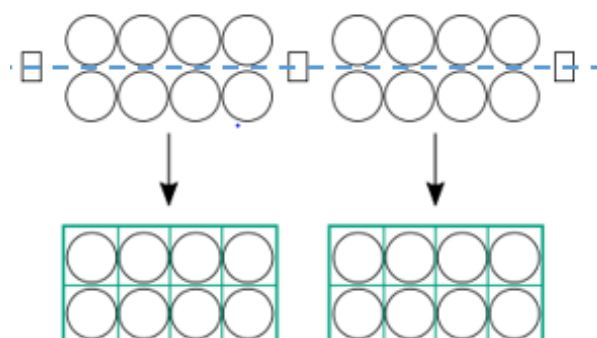
3.6.1.3. Barcode assignment

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) with RFID chips.

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-dividing it as shown on the image below (blocks represent barcodes, circles – plants, and blue dashed line – PlantEye path).

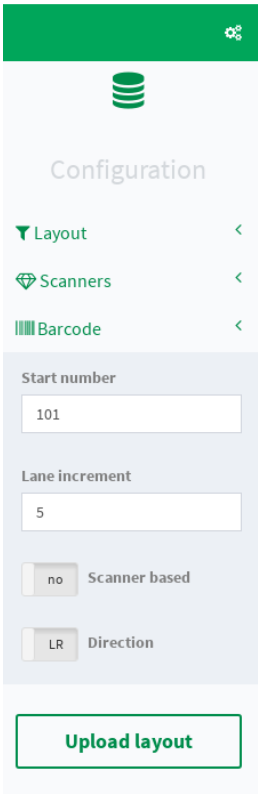


The above example should be translated into HortControl in the Experiments Board as follows (with each of the plants occupying its own block):



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 position of the initial barcode with respect to the direction of the PlantEye.



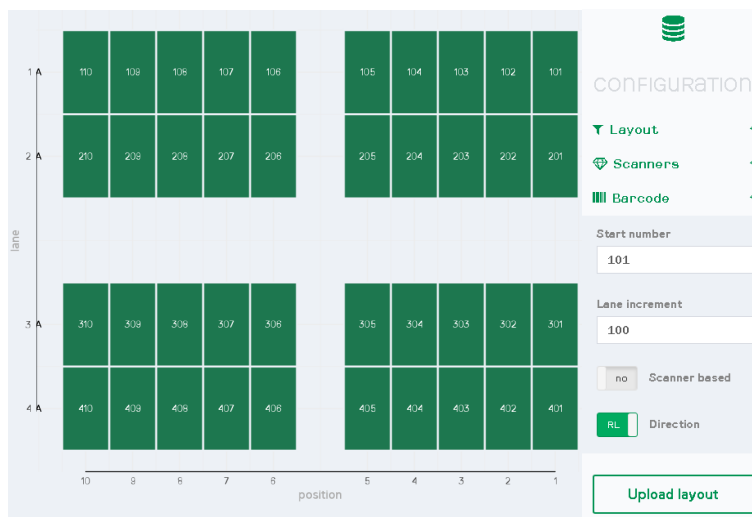
Barcode

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 setup 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

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.

The screenshot shows a web interface titled "Scanner Block ID mode". It contains two dropdown menus: "Mode" and "Scanners". The "Mode" dropdown is currently set to "ID 0". The "Scanners" dropdown is currently set to "A". To the right of the "Scanners" dropdown is a green "update" button.

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

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 customer 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 chose 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.

SCANNER BLOCK ID MODE

Mode: External Scanners: A update

EXTERNAL ID	BLOCK ID
All	All
1	1
2	2
block for Arabidopsis	3
sample 1 to 6	4
sample 7 to 12	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14

Showing 1 to 14 of 50 entries

Previous 1 2 3 4 Next

Upload table Download table Set as default

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.

3.6.2. 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 details 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. As a result, the following parameters are provided:

- ✕ 3D Leaf Area, Leaf Area Index and Projected Leaf Area
- ✕ Leaf inclination and Leaf Angle
- ✕ Digital Biomass and Height
- ✕ Multispectral parameters: NDVI, NPCI, PSRI, Hue and Greenness


For a complete list and detailed description please refer to [Plant Parameters](#) helpdocs.

3.6.3. Database Module

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

3.6.3.1. Remove experiments / block layout

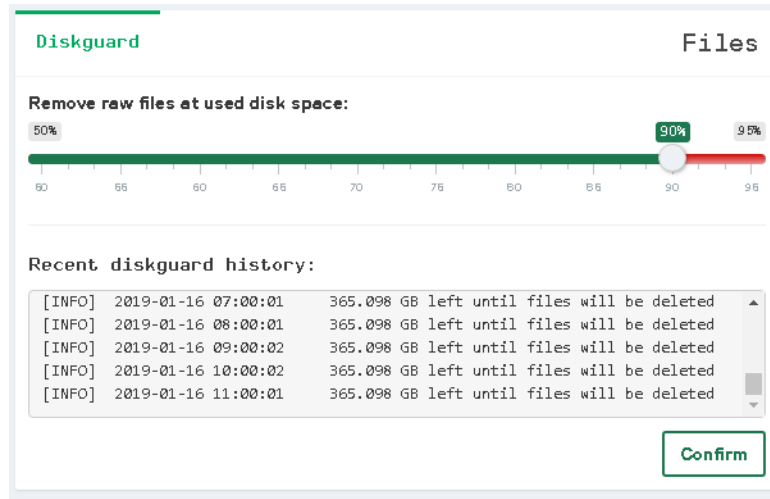
You can either remove experiments or block layouts by clicking the corresponding tab and pressing the button.

 **Remove** This is commonly done to remove unwanted experiment 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.

3.6.3.2. DiskGuard

DiskGuard is a safety feature in HortControl that will remove the oldest 3D files when the filesystem is close to be 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.

3.6.4. 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.

CREATE NEW USER

☐ no **Admin rights**

Register

ADJUST USER SETTINGS

User

psx-admin

Last seen: 2019-01-15 17:50:37

Email: NA

Reset password

Remove as Admin

Remove

3.6.5. 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: <ip:1612/device/network/confirm>. When anything fails during this process or if the new IP cannot be

HORTCONTROL

SYSTEM

Layout
Phena
Database
Users
Network
Operations & Support

NETWORK CONFIGURATION

Current IP: 192.168.1.127

Static network method
☐ no

HORTCONTROL

SYSTEM

Layout
Phena
Database
Users
Network
Operations & Support

NETWORK CONFIGURATION

Current IP: 192.168.1.127

Static network method
☒ yes

New IP
192.168.1.50

Netmask
255.255.252.0

Gateway
192.168.1.1

DNS server
8.8.8.8
192.168.1.5

+

Update

confirmed within 20 minutes, the network settings will be restored to

the previous settings.