

DSI FinePointe™ Cough Site Application Manual

011580-001 Rev 04

Table of Contents

Welcome 3
Introduction 3
The Cough and the Whole Body Plethysmograph 4
Configuring Apparatus for Cough 8
Cough Study 14
Create Cough Study Wizard 15
Selecting Cough Algorithm Profile 21
Creating Groups 23
Creating Reports 28
Calibrating 31
Acquiring Data 33
Launching FinePointe™ Station 33
Assigning Subject IDs 35
Configuring Views for the First Time 36
Walking Through the Task Sequence 40
End the session 42
Cough Detection 44
Multi-cough Event 44
Guinea Pig and Rat Analysis 45
Parameters Reported for Guinea Pig 47
Mouse Analysis 47
Parameters Reported for Mouse 47
Spike Detection 48
References 50
Data Sciences International (DSI) 51
DSI Technical Support—North America 51
DSI Technical Support—Europe 51

©2023 Data Sciences International

Welcome

This manual highlights the use of DSI's FinePointe™ Cough Site for Mouse, Rat, and Guinea Pig studies. The purpose of this document is to provide an overview of the methods used to measure coughs, as well as to describe the process required to configure the FinePointe™ Whole Body Plethysmography system and FinePointe™ software for successful measurements.

Introduction

The FinePointe™ System provides support for research that requires counting of coughs and comparison of these cough counts under varying conditions. Traditionally, this type of experiment was performed by trying a technician to watch and listen to a single guinea pig and subjectively make a determination one each expelling event if it is a cough, sneeze or some other event. These researchers have usually only been interested in coughs, so they would increment a counter on each cough event. They would monitor the subject for a couple fixed intervals of time following a cough stimulation challenge.

Due to the subjective nature of this method of evaluating cough, it is known that the results are determined to some degree by the technician. Training of the technician is critical, and some suggest that it is best of have the same technician evaluating the data for all the subjects within a study. Certainly, if only one technician can perform the cough counting, this will severely limit the throughput and so the number of experimental conditions that can be evaluated.

The FinePointe™ system provide analysis which automates this counting and introduces much needed objectivity. The approach that FinePointe™ uses to count coughs is not the same. That is, FinePointe™ employs an Unrestrained Whole Body chamber to measure box flow data to assess coughs, rather than visual observation and listening for the characteristic sounds. This box flow signal is a function of two components: the change of pressure within the lung, and temperature and humidity conditioning of the air passing in and out of the animal.

FinePointe™ supports cough detection on guinea pigs and mice. Each uses a distinctly different algorithm. Both algorithms use a very similar approach to detecting an expelling event, but they differ in how they categorize that event as a cough or something else.

The guinea pig categorization was developed using a fuzzy logic algorithm by comparing a great deal of manually scored data with parameters derived from each event. Categorization for rat uses the same logic as the guinea pig algorithm. Since it is very difficult for a technician to assess a cough based on sound, the mouse categorization simply codes the shape of the event as a number. The meanings of reported parameters are not the same for each species.

In this document, the background of the application, which describes what a cough is, and a typical cough protocol is described. Following that, the apparatus is briefly described which and covers some special calibration options which may need to be set. Finally, each algorithm for each species is described separately.

©2023 Data Sciences International

The Cough and the Whole Body Plethysmograph

A cough begins with an inspiration of air into the lung. Next, the air is compressed against a closed glottis (compressive phase), and then finally released through the glottis (expulsive phase).

The unrestrained whole body plethysmograph measures air expansions and contractions that take place within the chamber. The animal is not restrained or instrumented in any way, and since the animal's breathing is responsible for most of the air expansions and contractions within the chamber, using Boyle's law and some assumptions about the lung mechanics, the animal's ventilation can be inferred.

The inspiration of air prior to a cough is not necessarily any different from a normal inspiration, though it can be faster or deeper than it typically is during a normal breath. When air is inspired into the lungs, the air is transferred from outside the lung to inside the lung, and in doing so, it is heated and humidified (conditioned). In addition, in order to force the air into the lung, the diaphragm causes a slight negative pressure in the lung. So during inspiration, the heating, humidification, and the slight negative airway pressure cause the air drawn into the lung to expand. In normal healthy breathing, the air expands by roughly 10%. The additional expanded volume is forced out of the plethysmograph through the pneumotach located in the side of the plethysmograph. The rate of flow out of or into the plethysmograph is measured by a pressure transducer (calibrated as a flow[1]) and presented to the user as Box Flow. low. Again, this box flow is typically about 10% of the airflow that the animal is actually breathing.

During a normal expiration, the process is a little more complex but similar to the reverse of inspiration. The animal recovers some of the heat added to the air it breathed in, but not. Also, if the animal is suffering from airway constriction, a possible compressive pressure may be exerted in the lung in order to force the air out. Both the reclaiming of heat and humidity in the expired air and the possible compression cause air to be drawn back into the plethysmograph. And once again, the flow of air drawn into the plethysmograph through the pneumotach is measured.

[1] The pressure transducer can be calibrated as a flow since the design of the pneumotach ensures a linear relationship between the pressure across the pneumotach and the flow rate through the pneumotach.

©2023 Data Sciences International

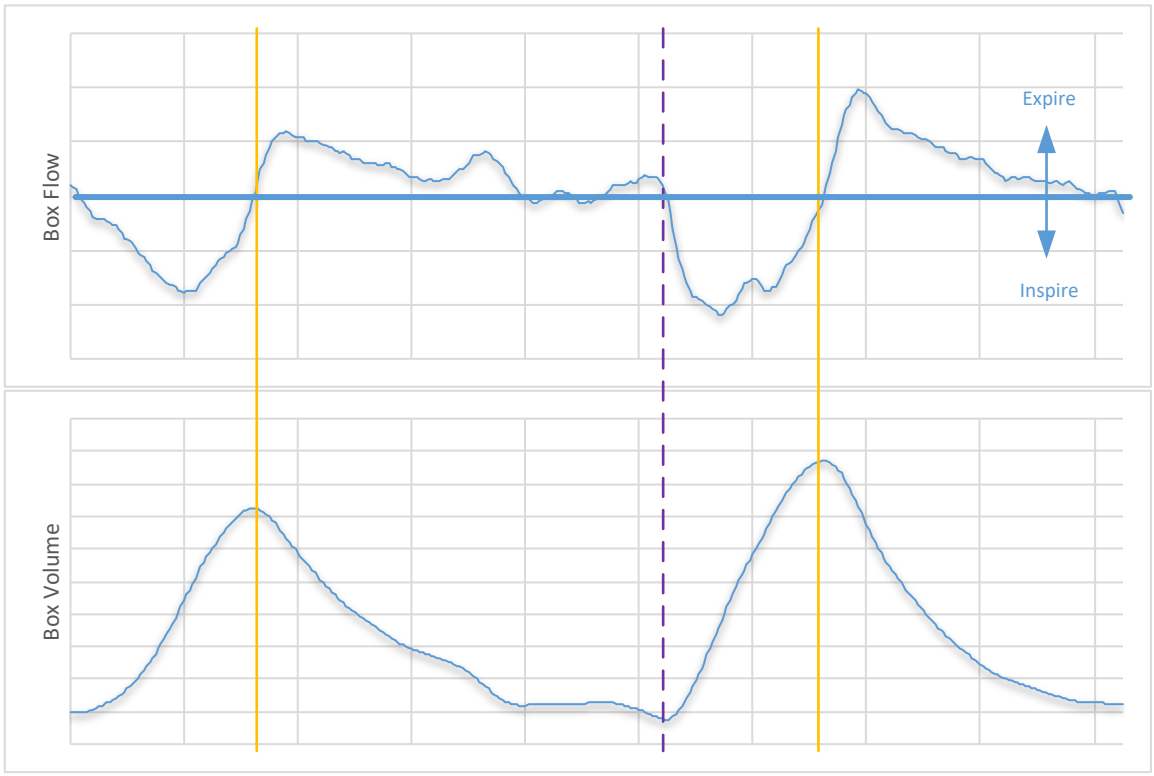


Figure 1. Box flow and box volume during normal respiration. Box flows above the thick zero line occur when the animal is expiring. The dashed line shows where the animal is transitioning from expiration to inspiration of the next breath.

To illustrate this, Figure 1 shows the relationships between box flow and box volume (the integrated form of box flow). The dashed line indicates when the lung volume is at FRC, at the end of expiration. The box volume peaks occur when the animal switches from inspiration to expiration.

The compressive phase of a cough occurs immediately after the inspiration of air into the lung. The glottis is blocked, and the diaphragm compresses the air in the lungs against the glottis. The compressed air in the lung causes air to be drawn into the chamber, even though no air flows in or out of the animal.

©2023 Data Sciences International

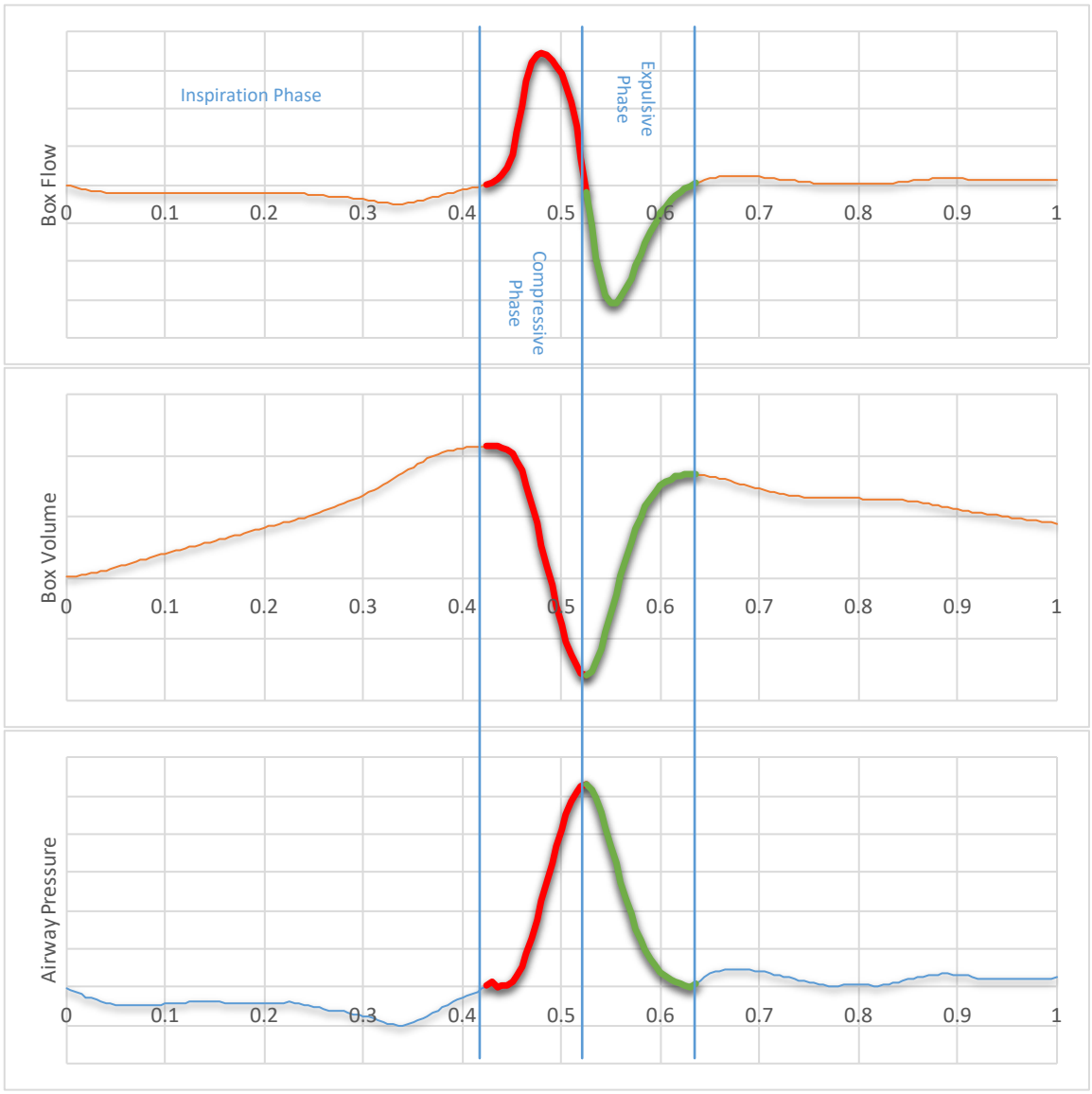


Figure 2. This shows a close-up look at a cough, its phases, and how they are reflected in box flow, box volume, and airway pressure. The red portion of the trace shows the Compressive Phase. The green portion shows the Expulsive Phase.

In Figure 2 the compressive phase is shown in red. Immediately following the inspiration phase, there is a massive buildup in pressure shown in red on the Airway Pressure chart. That build up in pressure forces the air in the lungs to compress and air is drawn into the chamber as shown on the box flow and box volume signals (in red).

At some point, the animal opens the closed glottis and the pressure in the lung is released in the following expulsive phase of the cough. As air rushes past the glottis, it produces a characteristic hoarse cough sound. Pressure is relieved and returns to normal levels at the end of the expulsive phase.

©2023 Data Sciences International

In Figure 2 illustrates the expulsive phase in green. Notice that although air is rushing out of the animal in this phase, the box flow signal moves seem to show air flow in the inspiratory direction. This is due to the expansion of the compressed air overwhelming any affects due to conditioning. In fact, if you were to remove the compressive and expulsive phases from the box flow and box volume signals, the result would appear to be something like a sigh.

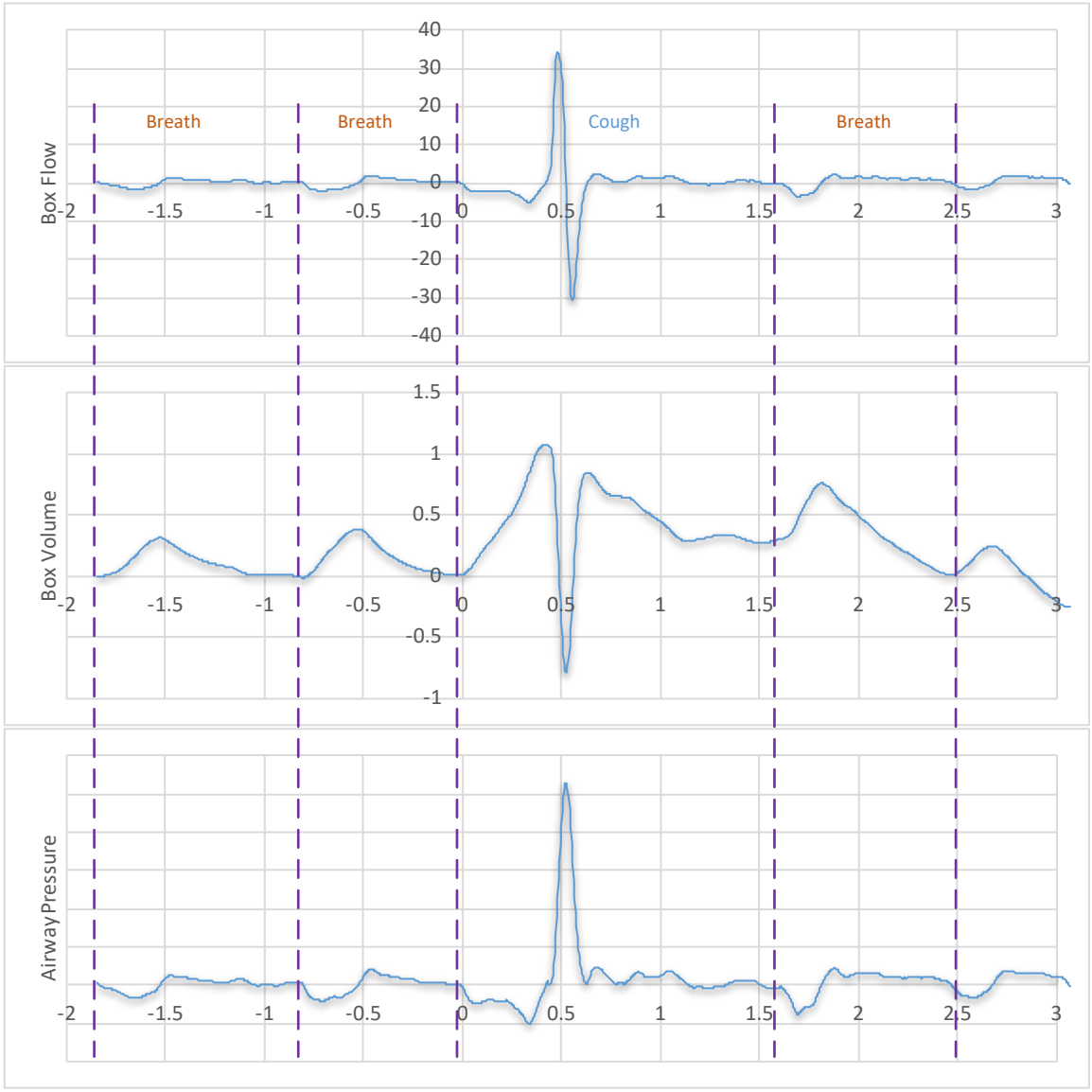


Figure 3. These graphs illustrate the relationship between box flow, box volume, and airway pressure during normal breathing and a cough. The Box Flow shows the flow in and out of the plethysmograph. Negative flows mean air is leaving the plethysmograph, and positive flows are air entering the plethysmograph. During inspiration, air leaves the plethysmograph (negative flow).

Figure 3 shows a cough event surrounded by normal breaths. This illustrates the magnitude differences between the various signals to give you some idea how a cough might relate to a normal breath.

©2023 Data Sciences International

Configuring Apparatus for Cough

Note: If you are utilizing the FinePointe™ WBP controller or the QT 1000, then no special configuration is necessary.

However, if you are using a MAX II with MAX2270 or MAX2275 preamplifiers, then you will need to set an option in the hardware configuration so that the box flow will be calibrated with a lower sensitivity. This is necessary since the flow box rates during the compressive and expulsive phases will saturate a normal calibration.

The following section describes how you create a hardware configuration for the MAX II preamplifiers.

In FinePointe™, the apparatus is configured by using the FinePointe™ Control panel to create or edit a hardware configuration. Begin by running the FinePointe™ Control Panel. You will need Windows administrator account credentials to log in.

Once you have logged in, click the ***Hardware Configuration*** button from the main page.

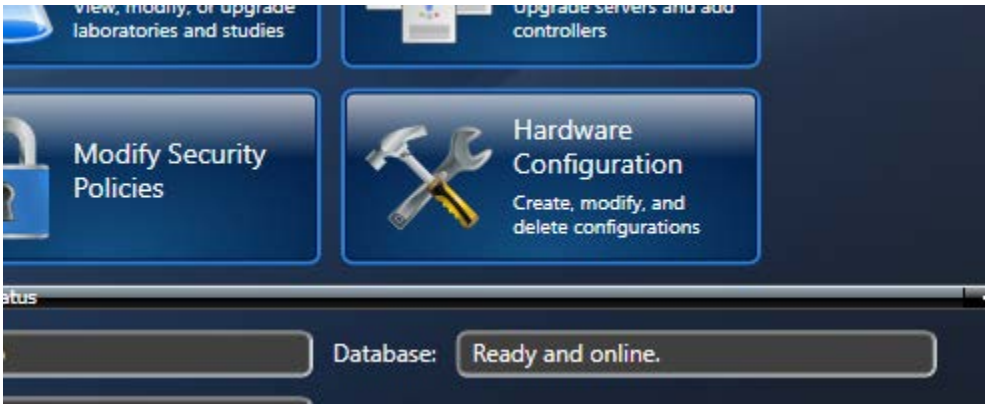


Figure 4. The Hardware Configuration button on the FinePointe™ Control Panel main page.

Clicking this button will bring you to the hardware configurations page.

©2023 Data Sciences International

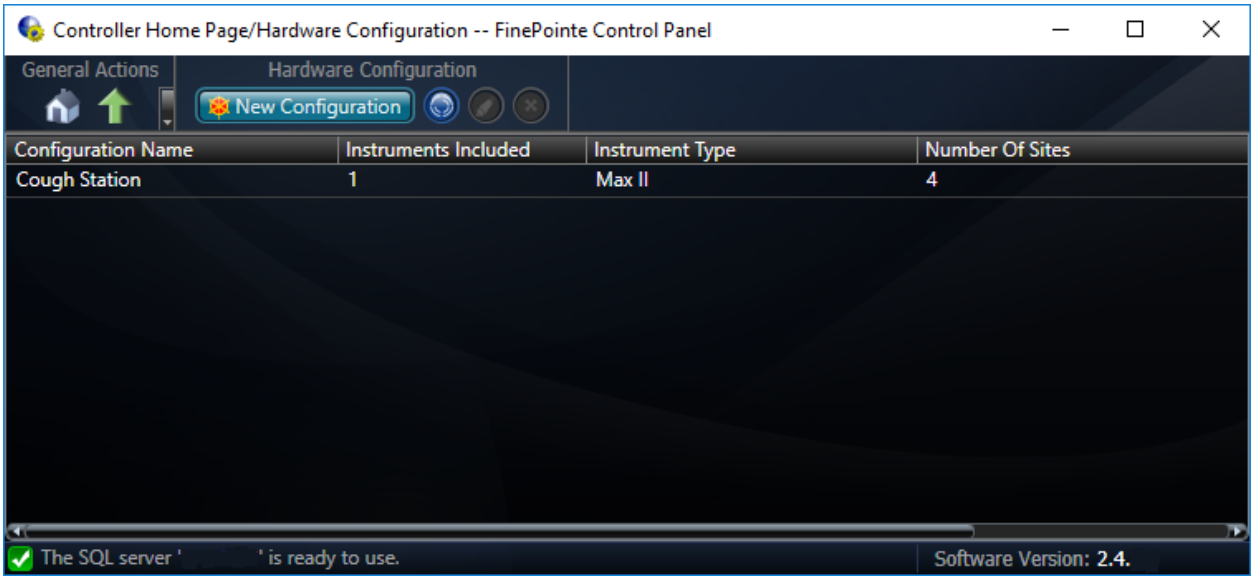


Figure 5. The Hardware Configuration page in the FinePointe™ Control panel. This image shows that there is already one hardware configuration (named "Cough Station").

From the hardware configurations page, you can either create a new hardware configuration, or you can edit an existing one. To create a new one, click the ***New Configuration*** button. To edit an existing one, choose the configuration you want to edit and click on the amber button between the blue and the red buttons.

When you create a new configuration, FinePointe™ walks you through a wizard to help you set it up. Editing an existing configuration is the same process except the wizard is populated with the selections you saved previously.

The first page of the wizard asks you to name the configuration and select the hardware that you will use with this configuration. The name is the name you will see in FinePointe™ Review when you want to acquire data or calibrate.

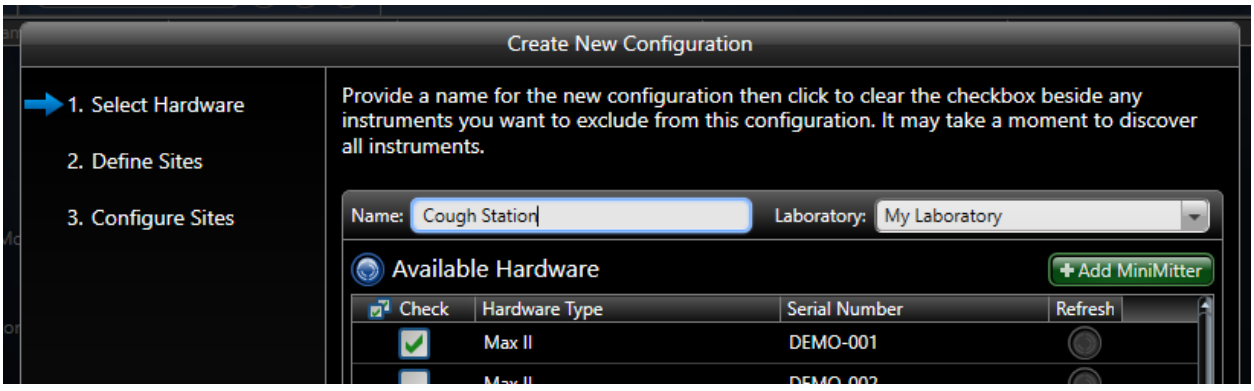


Figure 6. The first page of the Hardware Configuration Wizard.

©2023 Data Sciences International

The name must be unique from all the other configurations you have, and if you are editing an existing one, you can assume the name does not need to be changed. Uncheck the hardware you are not using and make sure the hardware you want to use is checked. In this case you should have one Max II instrument checked. Click ***Next***.

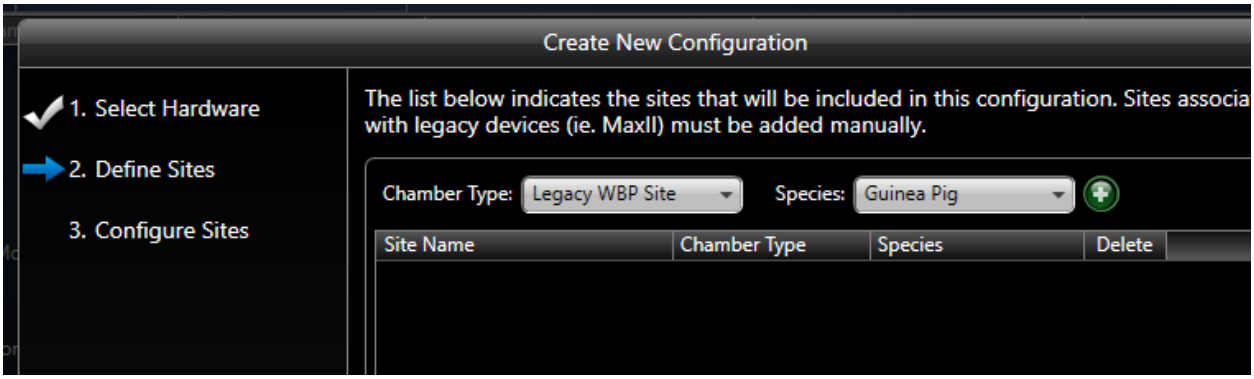


Figure 7. The second page of the Hardware Configuration wizard. On this page, you define the sites you have. A site is apparatus for acquiring data for a single subject.

Next you have to define the sites you have. A site is apparatus for acquiring data for a single subject. Here you should select the Chamber Type as Legacy WBP Site and the species you will run with. Shown in Figure 7 Guinea Pig is selected. Next you need to click the **+** button once for each site.

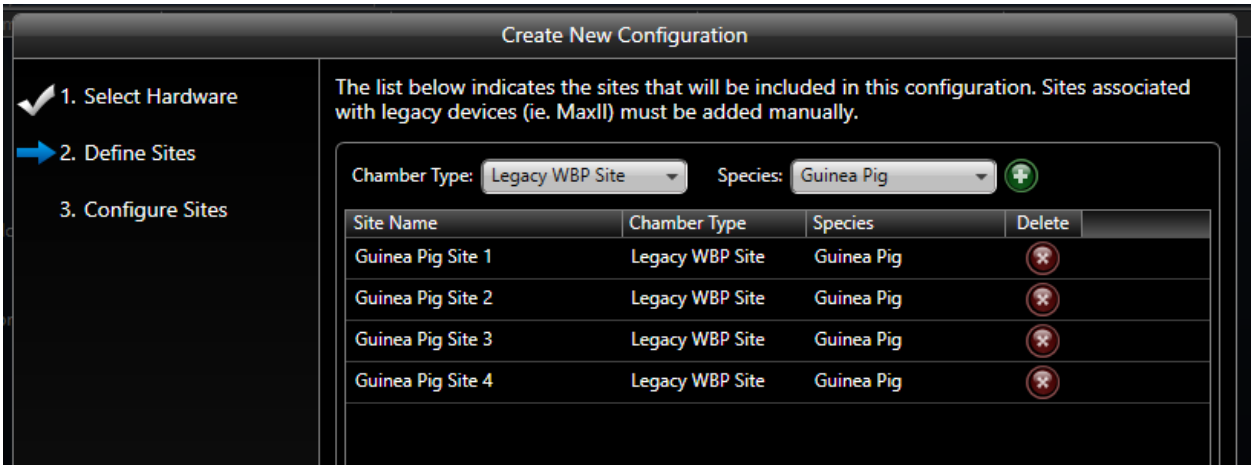


Figure 8. The second page of the Hardware Configuration wizard after 4 guinea pig sites have been added.

Click ***Next***.

©2023 Data Sciences International

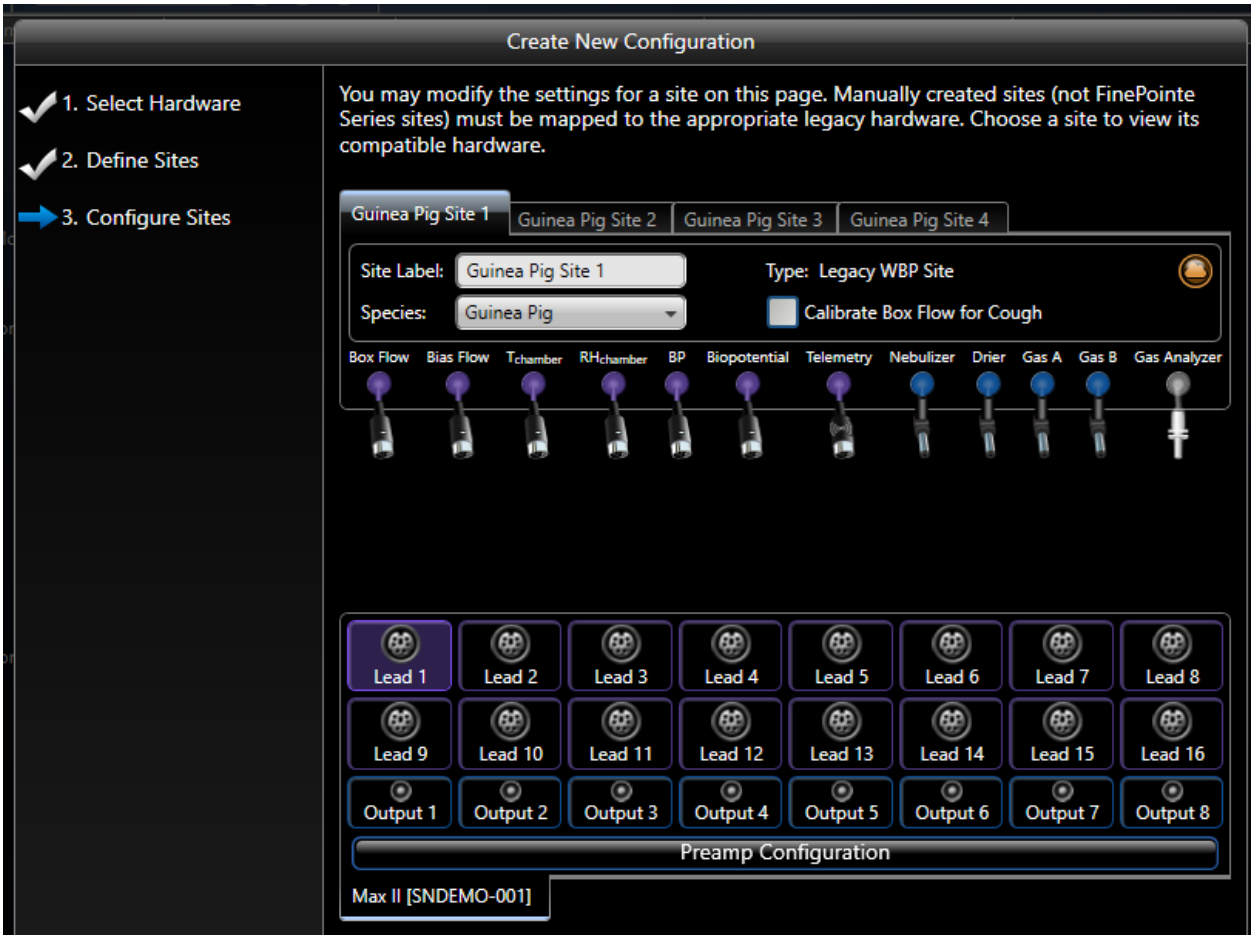


Figure 9. The final page of the Hardware Configuration wizard. This page allows you to connect the hardware you selected on the first page to the sites you declared on the second page.

On the final page of the Hardware Configuration wizard, you need to connect the inputs of the site to the instrument preamplifiers that the site is physically connected to.

This page is divided into two parts. The upper part shows the sites you defined on the second page of the wizard, and the lower part shows the instruments you selected on the first page of the wizard. There is one tab on the upper side for each site, and one tab on the lower side for each instrument. You will need to make sure each site is connected up properly to the instruments on the lower part of the page.

For each site, you will need to connect the **Box Flow** signal to one of the leads on an instrument. The other signals should be left disconnected. Also, you must make sure that the ***Calibrate Box Flow for Cough*** button is checked. This checkbox tells FinePointe™ to reduce the sensitivity of the calibration so that it is suitable for the cough detection.

On the first site, you will want to connect the nebulizer and drier digital control lines to outputs on the Max II. This is necessary so that the task sequence on the first site can control the nebulizer to deliver the irritant.

©2023 Data Sciences International

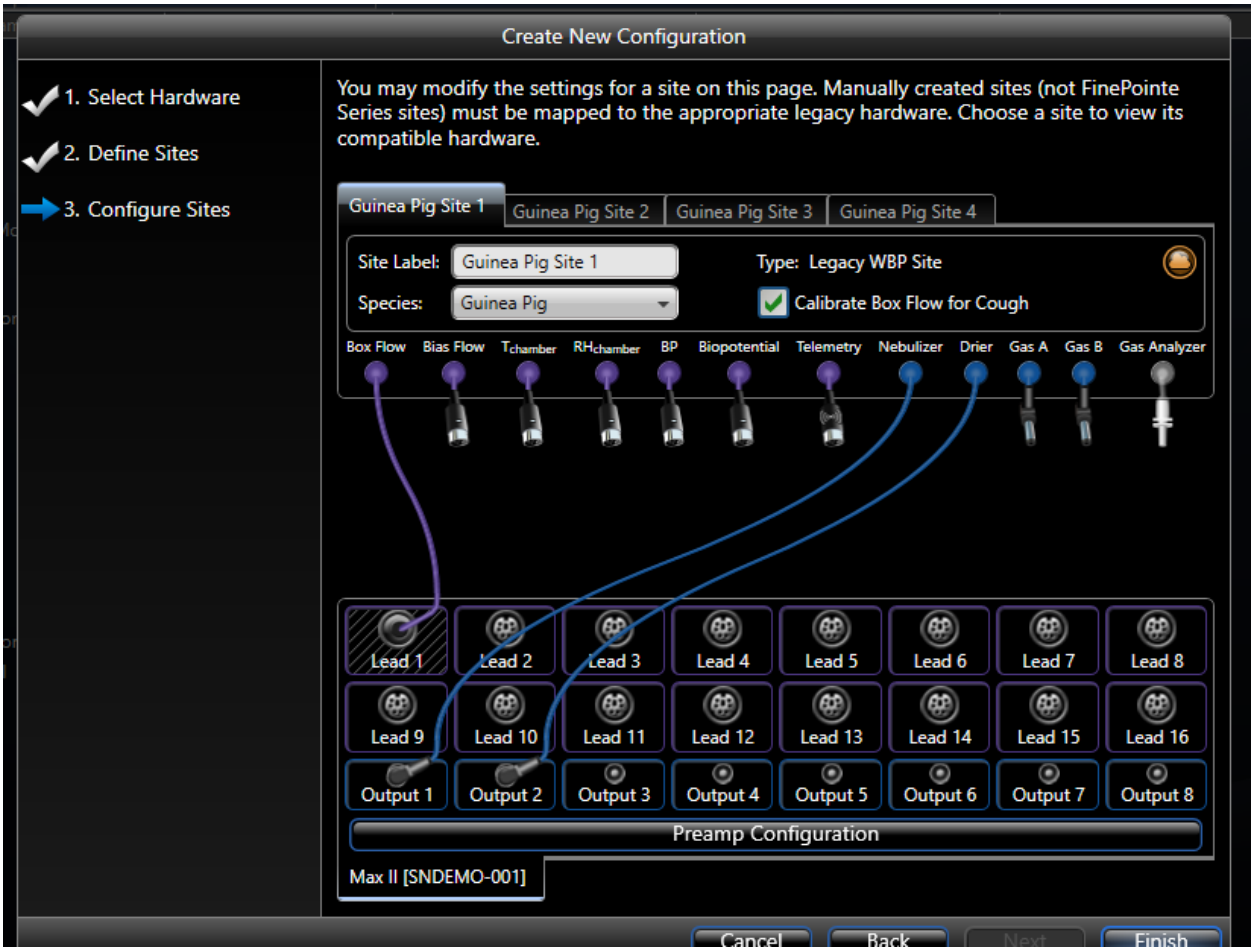


Figure 10. Typical connections for the first site of a hardware configuration.

The second site (and each site after) would look similar to Figure 11 except that the **Box Flow** input would be connected to its own lead, and there is no need to connect the **Nebulizer** and **Drier** output lines.

©2023 Data Sciences International

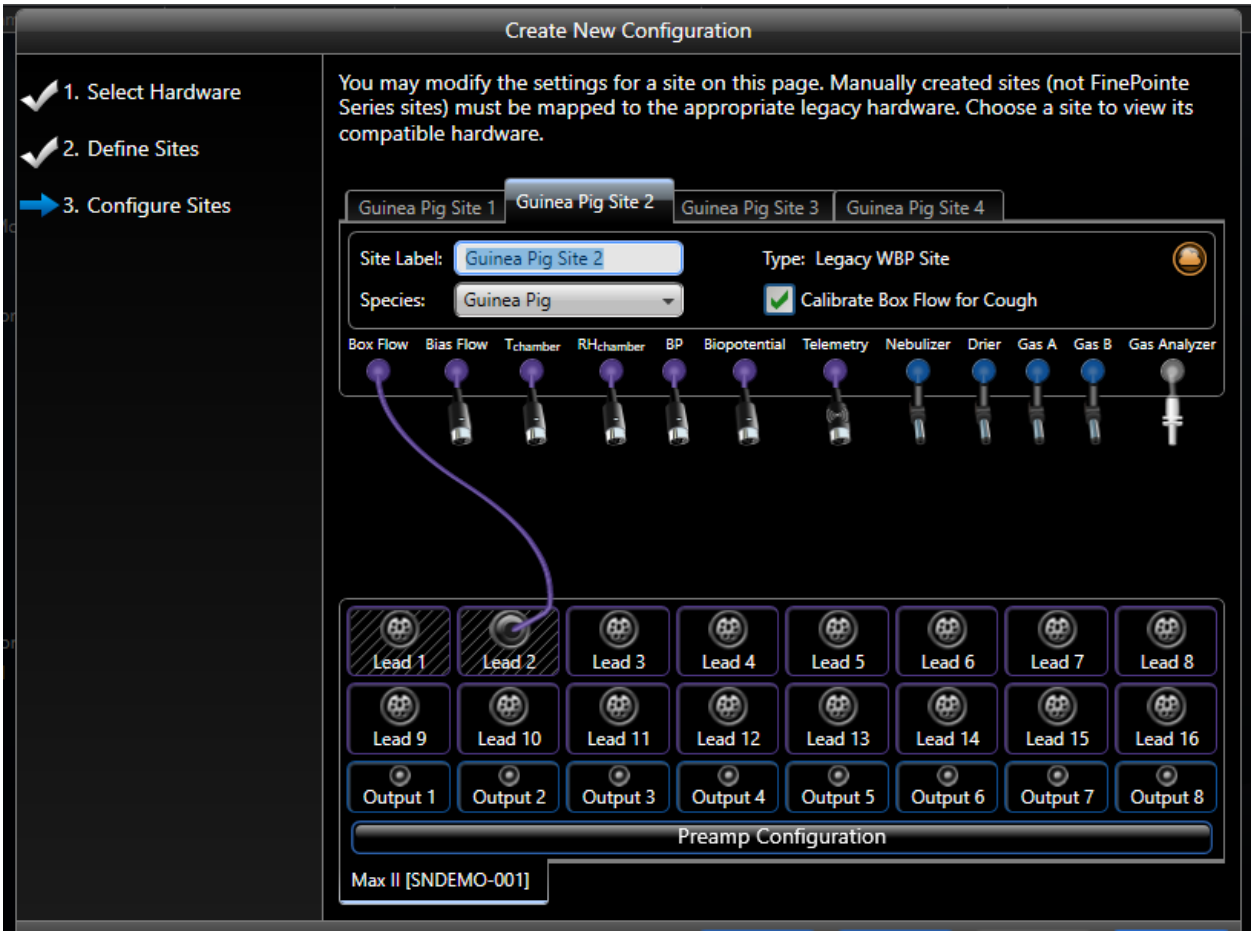


Figure 11. Setup for the second site, and subsequent sites.

Next you should click on the ***Preamp Configuration*** button so that you can tell FinePointe™ what kind of preamplifiers you are using. This setting helps FinePointe™ configure the calibration wizard to provide instructions explicitly defined for your hardware.

©2023 Data Sciences International

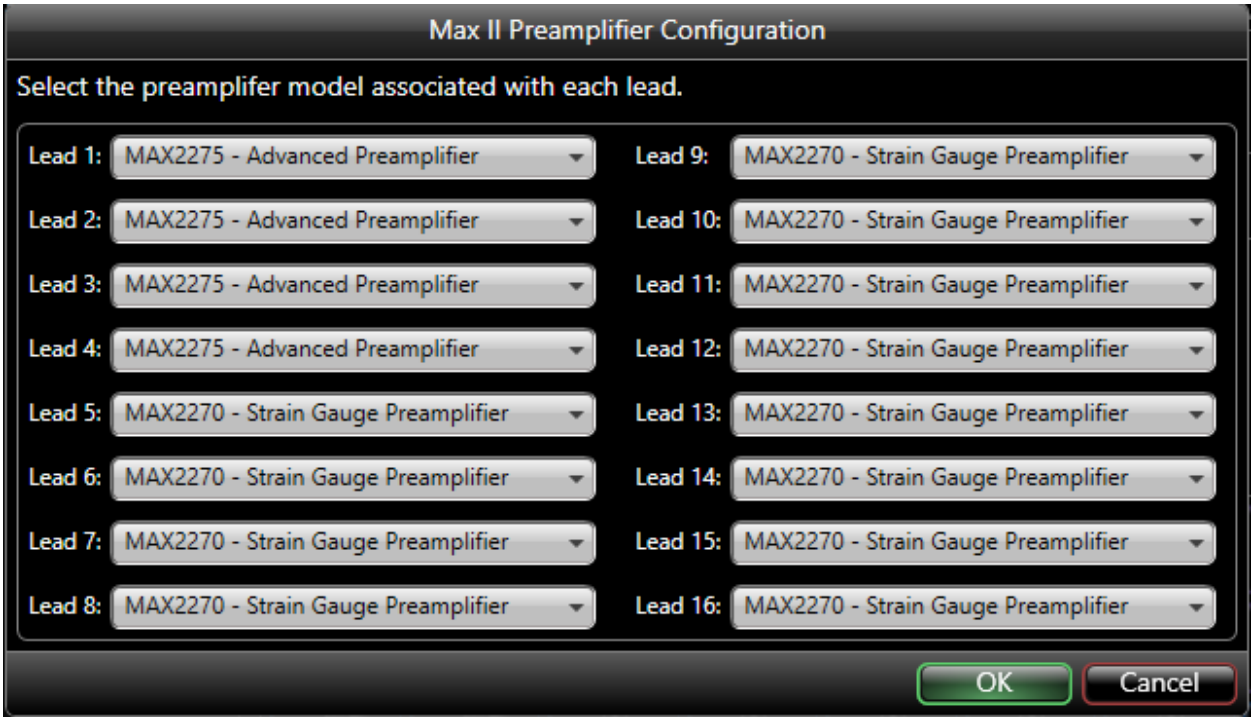


Figure 12. Preamp Configuration form. Pictured here, lead 1, 2, 3 and 4 are configured to have the MAX2275 preamplifier modules.

Click ***Finish***.

Cough Study

In FinePointe™ a cough study allows you to acquire data from multiple subjects and summarize that data in subject groups as you choose. Cough data collection sequences all follow the following procedure:

1. Acclimate the subject for a period of time. This allows the subject to settle down in the WBP plethysmograph. During this time, data is acquired and stored, but not used for reporting.
2. Start to nebulize the irritant (typically citric acid or capsaicin)
3. Acquire data during the nebulization of the irritant, typically 20 mins. A measurement interval is automatically placed for this entire period.
4. Saline or water is nebulized to clean out the nebulizer head.

This data collection procedure is performed identically for each subject. The procedure results with a single measurement named “Main” placed for each subject. This measurement can be summarized in the reports as a whole or subdivided into defined intervals as you choose. A typical cough study report will subdivide the measurement into 2 subintervals, 10 minutes each, and reporting the following expression: [Cough:IsCought].Sum.

©2023 Data Sciences International

When you create your study, you will need to do the following:

- Complete the Create Cough Study wizard
- Select the Cough Algorithm Profile

Everything else you can do as you go along. For example:

- Adding or modifying subject groups
- Adding subject IDs
- Adding or modifying reports

Create Cough Study Wizard

To create a cough study, find the FinePointe™ button under the Create Study Options on the Laboratory view.

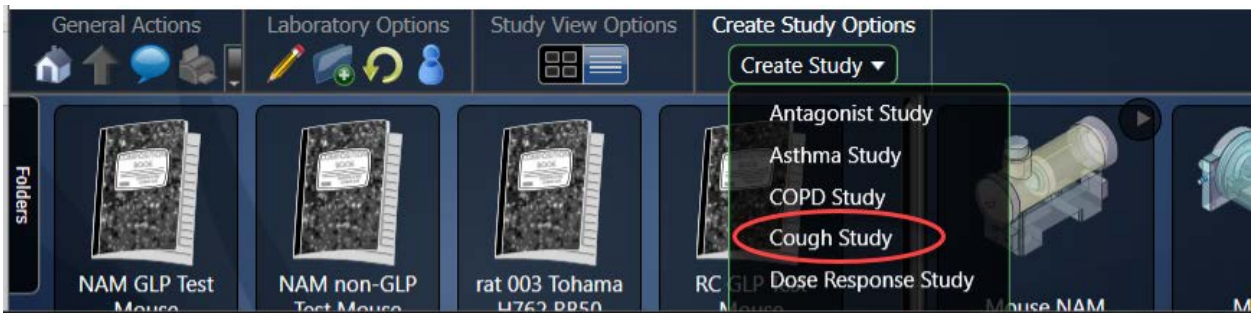


Figure 13. The Laboratory page in FinePointe™ Review. The Create Study button is indicated by the red oval.

Select ***Create Study*** from the available studies you can create. This will launch the Create Cough Study wizard.

©2023 Data Sciences International

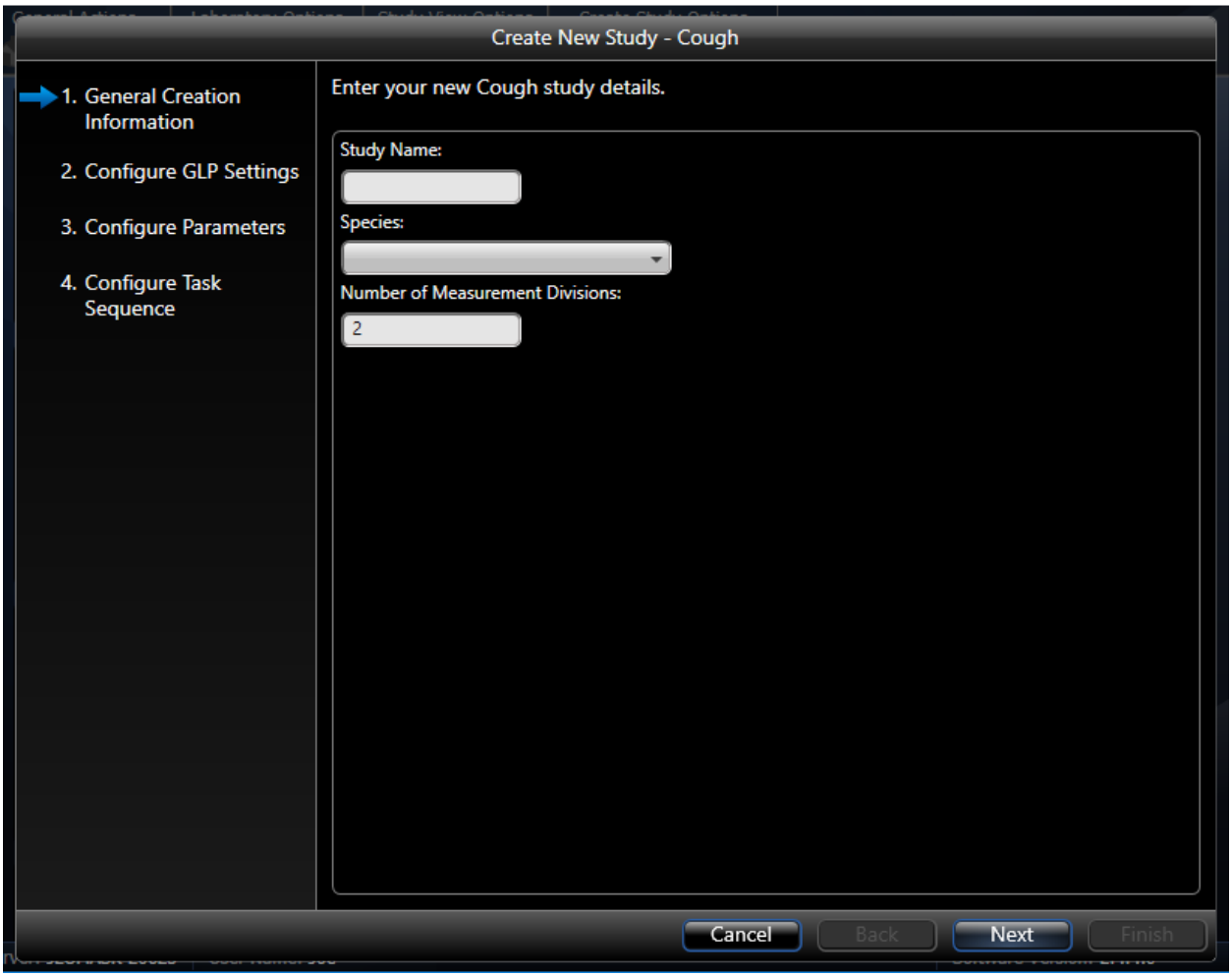


Figure 14. The first page of the Create Cough Study wizard.

On the first page of the wizard, you need to specify a unique study name and the species you intend to acquire. You can choose between rat, guinea pig, hamster and mouse.

Finally, you can enter the number of subdivisions you want in your first report. This value can be changed later and only applies to the first report which is created automatically when you create the study.

Click ***Next***.

©2023 Data Sciences International

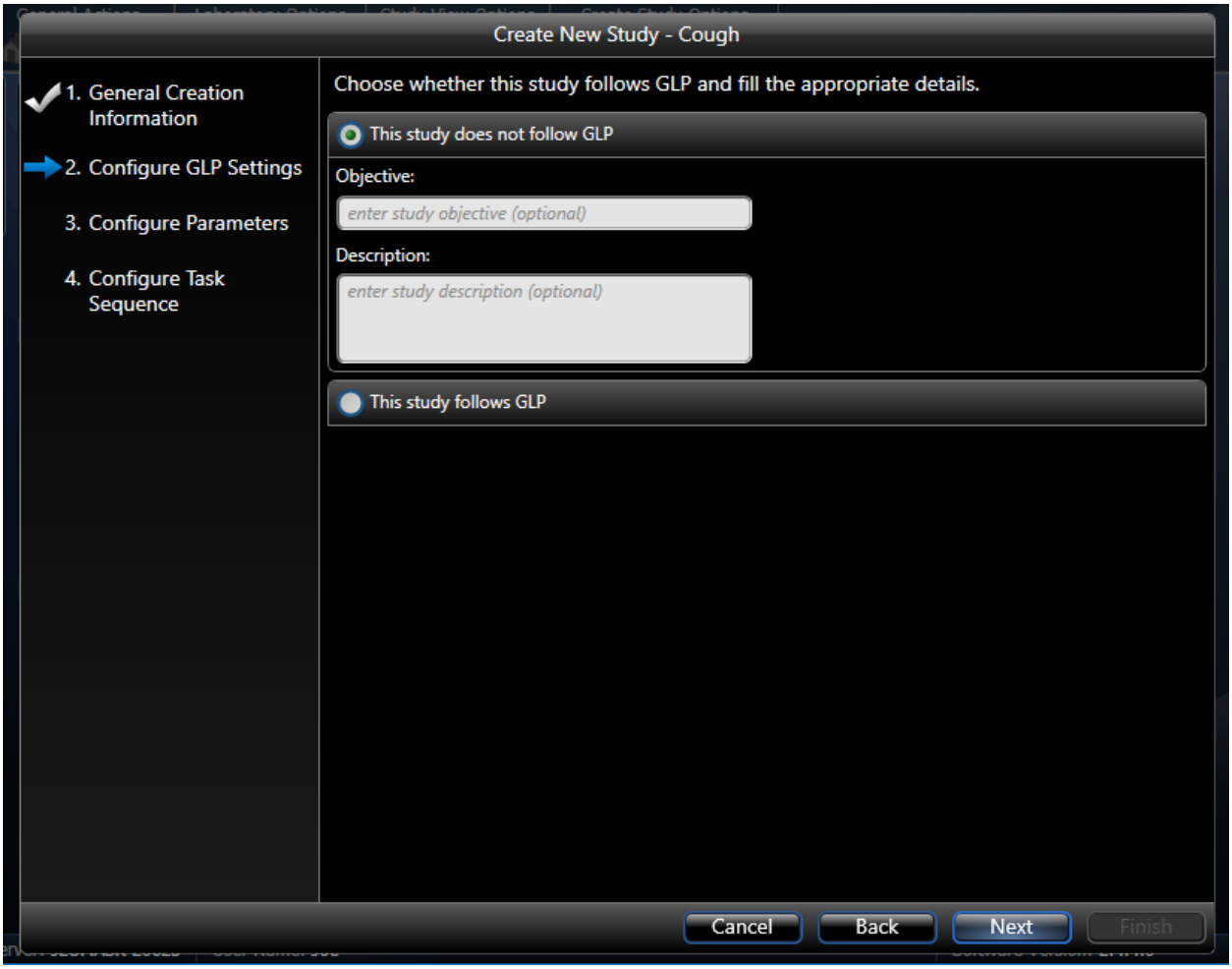


Figure 15. The second page of the Create Cough Study Wizard.

The second page of the wizard allows you to provide some descriptive information. This content is optional and can be edited later.

Click ***Next***.

©2023 Data Sciences International



Figure 16. The third page of the Create Cough Study wizard.

The third page of the wizard allows you to tell FinePointe™ what parameter or expression you want summarized in your initial report. This information can be changed later.

To create the parameter, click the ***New Parameter*** button:

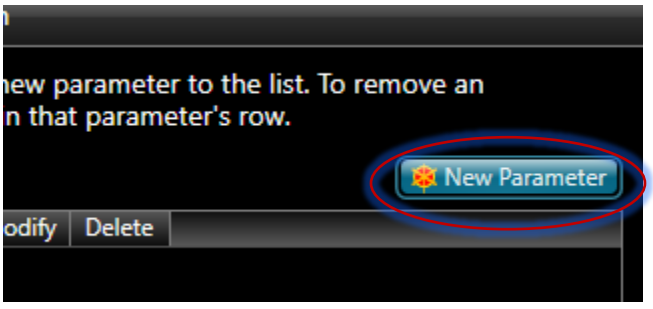


Figure 17. The yellow oval highlights the New Parameter button that you need to click to specify the summarization expression.

©2023 Data Sciences International

This button will present the Parameter Builder form.

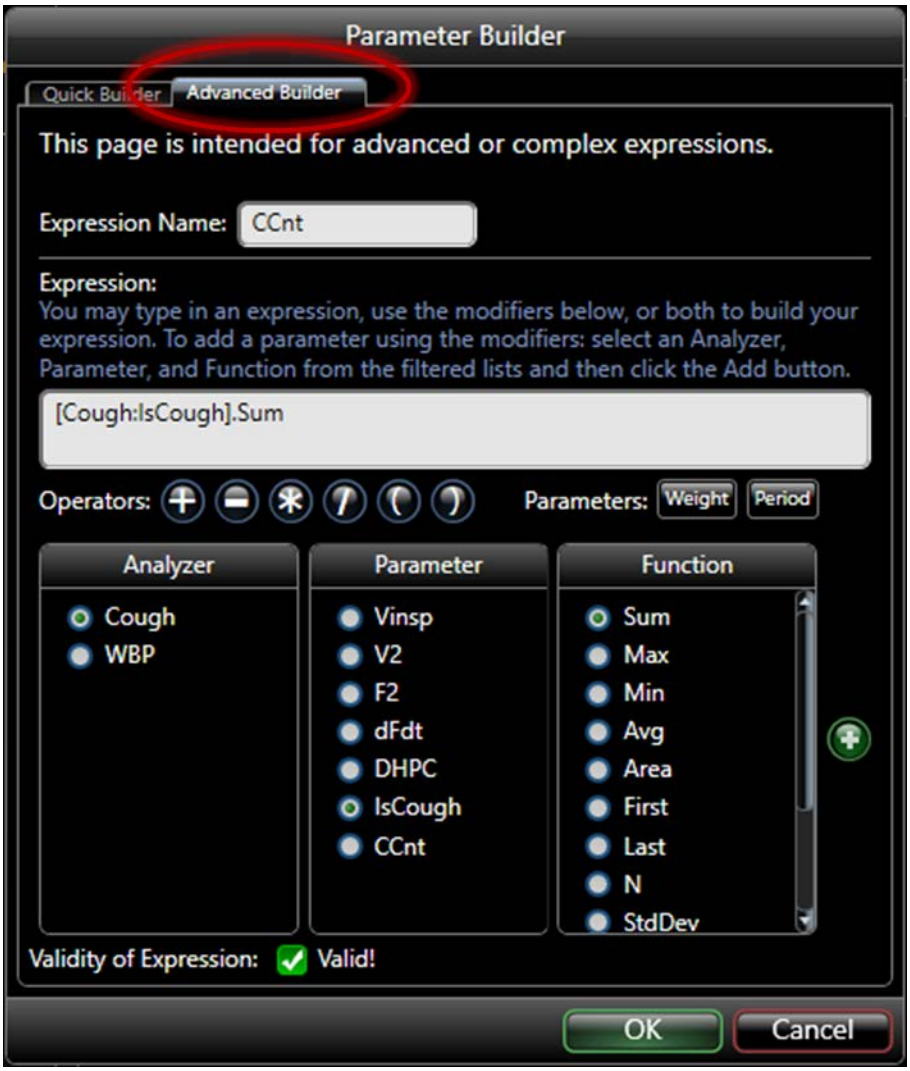


Figure 18. This shows the parameter builder form.

The Parameter Builder form has 2 tabs. The Quick Builder tab can be used for most reports, but in this case, you will need to use the Advanced Builder tab. Click on the Advanced Builder tab (as highlighted in Figure 18).

Next, fill in the Expression Name field. In the example above, "CCnt" is specified.

Finally specify the expression in the large expression edit box. In the example above, the following expression is specified: "[Cough:IsCough].Sum".

©2023 Data Sciences International

After you specify that, if you did so without any errors, the Validity of Expression should indicate Valid as it does above. Otherwise, it will describe the problem which you can use to determine what the computer does not understand.

Click ***OK***.

The wizard will return you to the third page of the wizard.

Click ***Next***.

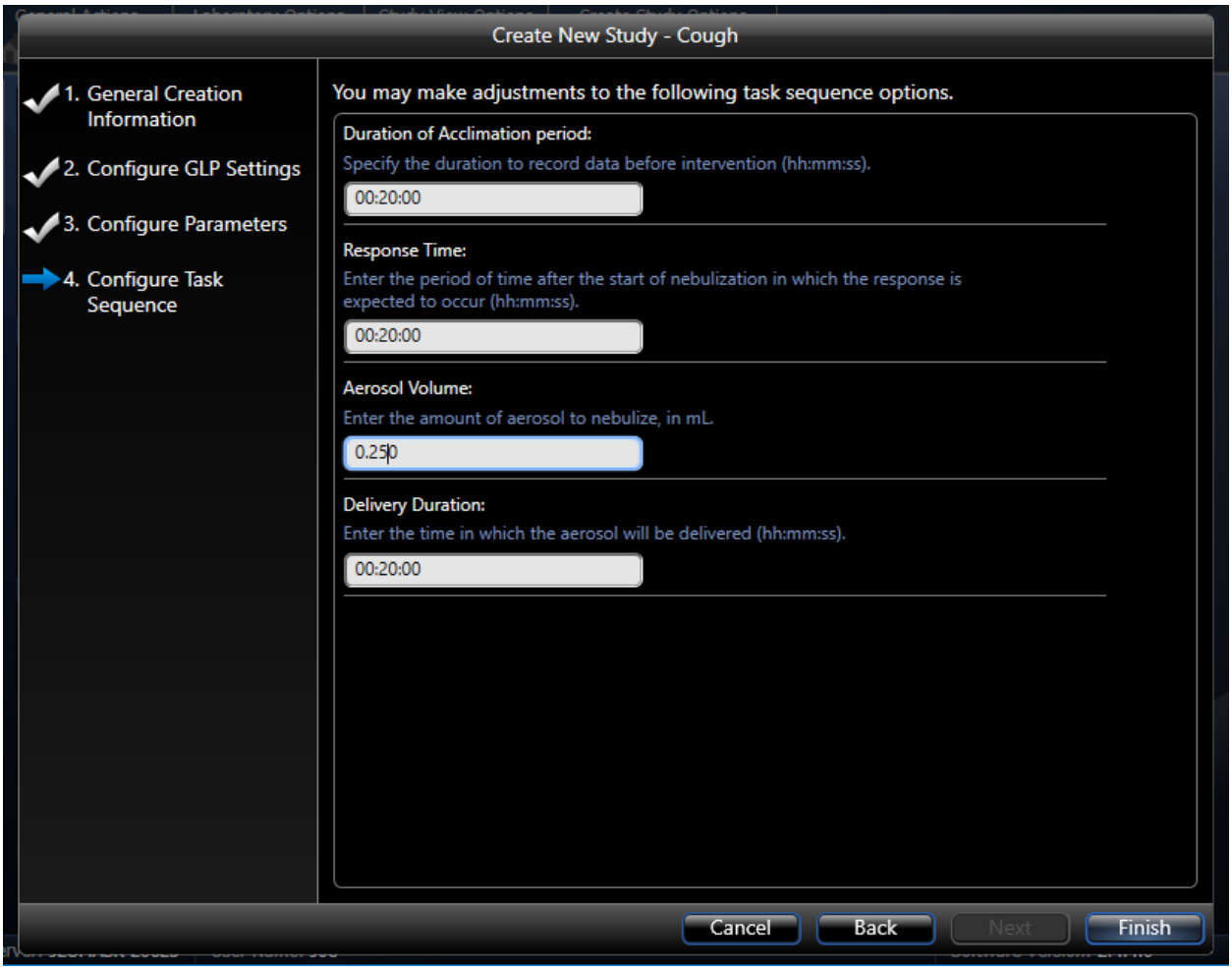


Figure 19. The final page of the Create Cough Study wizard.

On the final page of the wizard, you can specify parameters that will help you acquire data in a uniform way.

All these parameters can be changed later, but it is a good idea to settle on their values before you begin acquiring data for the first subject in the study.

©2023 Data Sciences International

The **Acclimation Period** defines the amount of data to record while the subject is getting used to its surroundings in the plethysmograph. This period can be manually ended as you wish during data collection. Any period between 5 minutes and 20 minutes is recommended.

The **Response Time** is probably the most important parameter you set up here. This duration defines how long to record the data for once you begin nebulizing the irritant. For guinea pig, a 20-minute recording is typical.

The **Aerosol Volume** tells the system the volume of irritant you will load into the nebulizer head prior to running. This value is important when you are using this system with the FinePointe™ WBP controller or the QT interface and nebulizers. But it is not used with the legacy nebulization apparatus. When using this with the FinePointe™ WBP controller or the QT interface, you should probably add a little more material than you specify here since you want the nebulization to continue throughout the Response period.

Delivery Duration specifies how long to nebulize for. Some data collection procedures may require that nebulization of irritant only takes place during the first part of the measurement period. Here you can specify a duration less than the Response Time if you want part of the measurement to be taken without the presence of the irritant.

Click ***Finish***.

FinePointe™ will create and open your new cough study.

Selecting Cough Algorithm Profile

Next you need to select a cough algorithm profile. It is important that this is done before you begin acquiring data. The profile you select determines the sensitivity that the system applies based on the expected size of the animal, and it also determines how you want to treat multi-cough events (see Multi-cough Event below).

Sometimes a cough does not occur as a single cough, but instead could be a series of coughs rapidly following one after another (a multi-cough event). You may want to treat the whole event as a single cough. Or you may want to count them each separately.

The following are the profiles you can choose from:

Species	Profile Name	Weight Range	Multi Cough Treatment
Guinea Pig or Rat	Normal, Each	200g-400g	Each multi-cough event is treated as a single cough.
Guinea Pig or Rat	Normal, Multiple	200g-400g	Each cough in a multi-cough event is treated as its own cough. But the full cough criteria are only applied to the first cough. Subsequent coughs only need to meet threshold conditions.
Guinea Pig or Rat	Normal, Single	200g-400g	Each cough in a multi-cough event is treated and counted independently. The full cough criteria are applied to each cough within the event.
Guinea Pig or Rat	Large, Each	350g-700g	Each multi-cough event is treated as a single cough.

©2023 Data Sciences International

Species	Profile Name	Weight Range	Multi Cough Treatment
Guinea Pig or Rat	Large, Multiple	350g-700g	Each cough in a multi-cough event is treated as its own cough. But the full cough criteria are only applied to the first cough. Subsequent coughs only need to meet threshold conditions.
Guinea Pig or Rat	Large, Single	350g-700g	Each cough in a multi-cough event is treated and counted independently. The full cough criteria are applied to each cough within the event.
Mouse	Normal, Each	<30g	Each multi-cough event is treated as a single cough.
Mouse	Normal, Multiple	<30g	Each cough in a multi-cough event is treated as its own cough. The full cough criteria are only applied to the first cough. Subsequent coughs only need to meet threshold conditions.

To select the profile, go to the main study page of your cough study. Find the ***Acquisition Algorithm Settings*** button on the top button menu.



Figure 20. This highlights the Acquisition Algorithm Settings button that appears on the main study page. The button is shown within the yellow oval.

Click on the ***Acquisition Algorithm Settings*** button. The Algorithm Setting form is presented. On this form you can select how you want the cough data logged and on a separate tab, how the WBP data is logged.

©2023 Data Sciences International

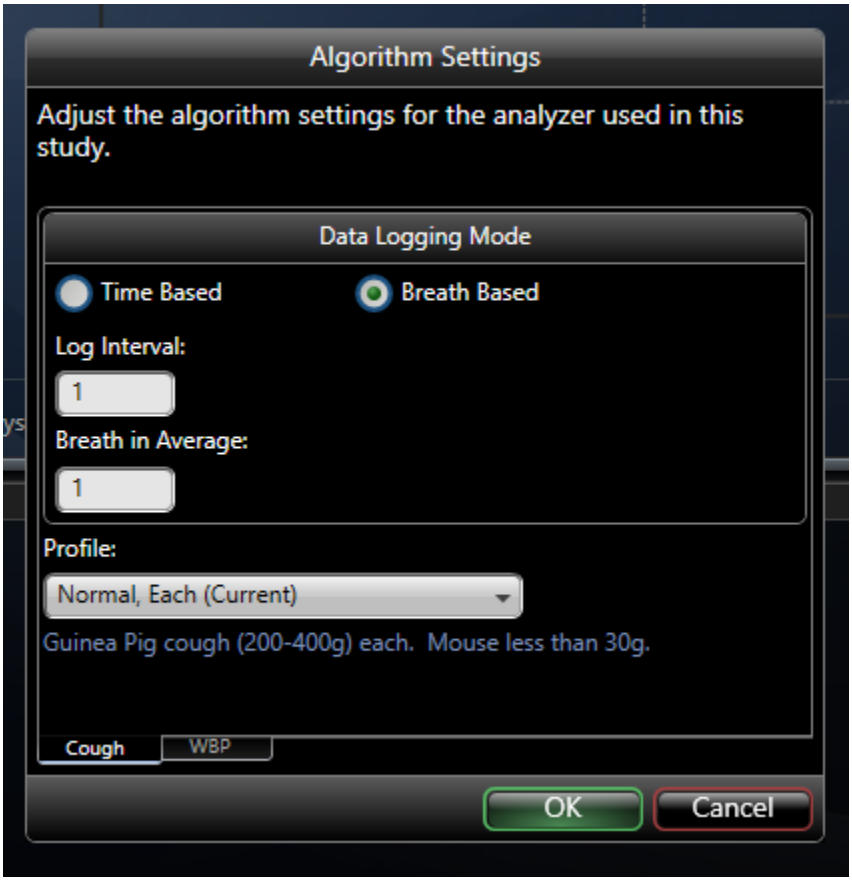


Figure 21. This is an image of the Algorithm Settings form. The Cough analysis tab is selected. If you select the WBP tab, then you can configure the algorithm settings for the WBP respiratory analysis.

Refer to table above to determine which algorithm profile best suits your needs.

Creating Groups

FinePointe™ provides a powerful reporting engine which allows you to get grouped reports which are complete enough for many users reporting needs. In addition to saving time and eliminating mistakes, making use of the built-in reporting features provides you with fully annotated and traceable dataset.

One major part of the reporting features is the facility to create subject groups. You can create as many groups as you want and have as many subjects in each group as you want. Also, subjects can belong to multiple groups, and you can add and remove subjects from groups at any time. When you define a report, you specify 3 key pieces of information: the groups to include in the report, the parameters (or parameter expressions) to summarize, and the measurements to use to select the data.

This section describes setting up groups. Keep in mind that you can set up these groups at any time, whether you've not started collecting your data, or even after all your data has been collected.

From the main study page, click the ***Manage Groups and Subjects*** button. It is shown in Figure 22.

©2023 Data Sciences International

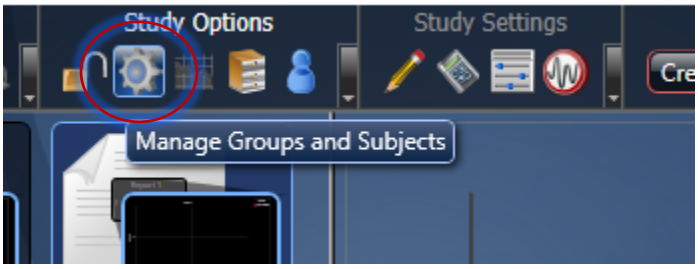


Figure 22. This shows the Manage Groups and Subjects button on the main study page.

The Groups and Subjects page is presented. This page shows you the groups and subjects that are currently defined in your study database.

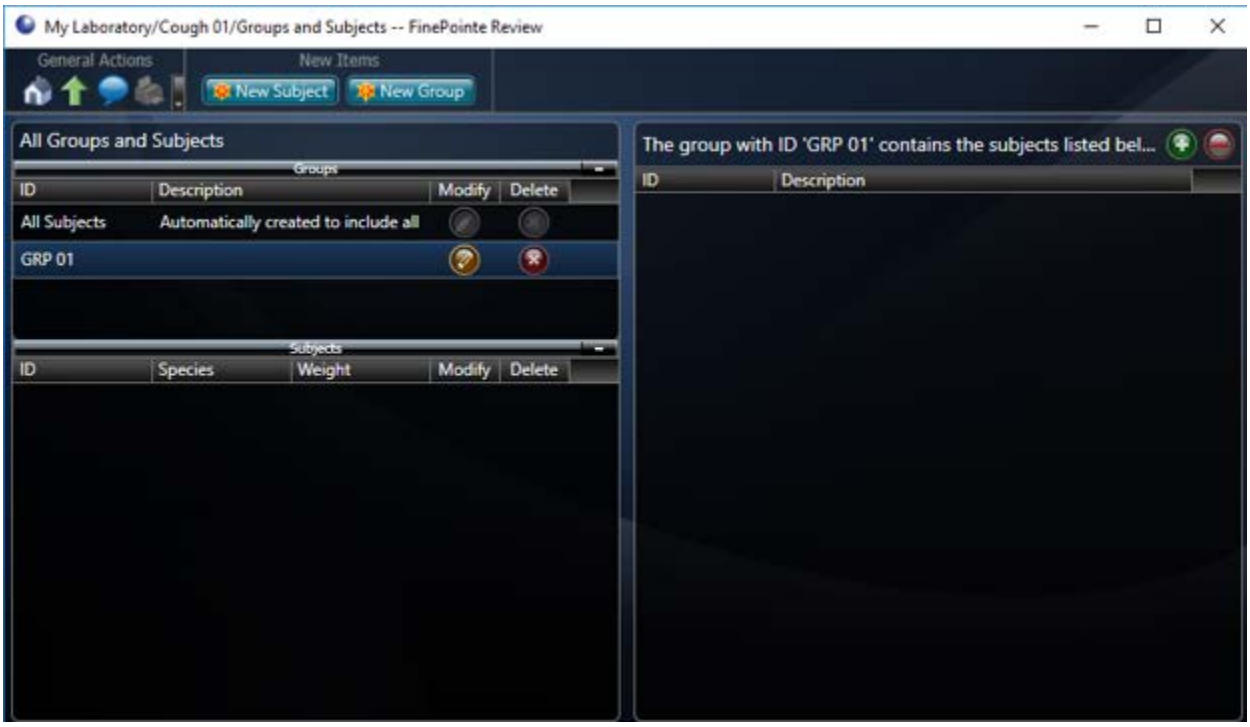


Figure 23. This shows the Groups and Subjects page.

From this page you can edit the subjects and groups which are already defined, or you can create new ones. Keep in mind that you can also create subjects on-the-fly as you acquire your data, so doing it here is not required.

To create a new group, click the ***New Group*** button located under New Items at the top of the page.

©2023 Data Sciences International

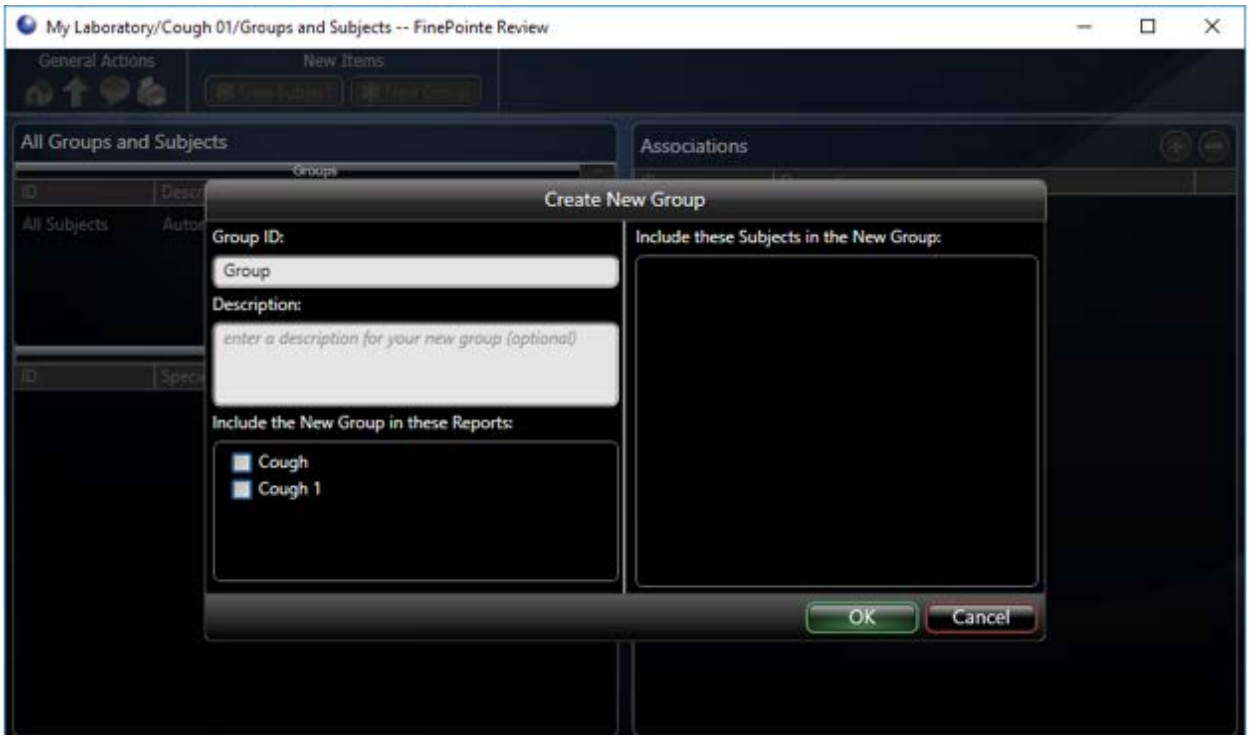


Figure 24. This shows the dialog box presented when you click the New Group button. Shown here the subjects list is empty because no subjects have been defined in the study yet. As you define the subjects you can add them to this group and other groups as necessary.

A dialog box like the one show in Figure 24 is presented. The Group ID is a text identifier you will use to refer to this group in your reports. Choose an ID which is meaningful to you and unique from all the other groups. Description is optional.

The list on the right shows all the subjects currently defined in your study. In the example above, this list is empty since no subjects are currently defined. If subjects were present, you could place a check by each subject you wanted to be part of this group.

There is also a list of reports located under the description. You can place a check by the reports that you want to include this group. You can change this also by editing the report.

Click ***OK***. The dialog box will disappear, and the new group will be created.

If a group is already defined, you can click on it in the Groups and Subjects page and the list on the right half of the page will be populated with the subjects that are members of that group. You can quickly change the membership by selecting the group and clicking the ***+*** button above the list on the right.

©2023 Data Sciences International

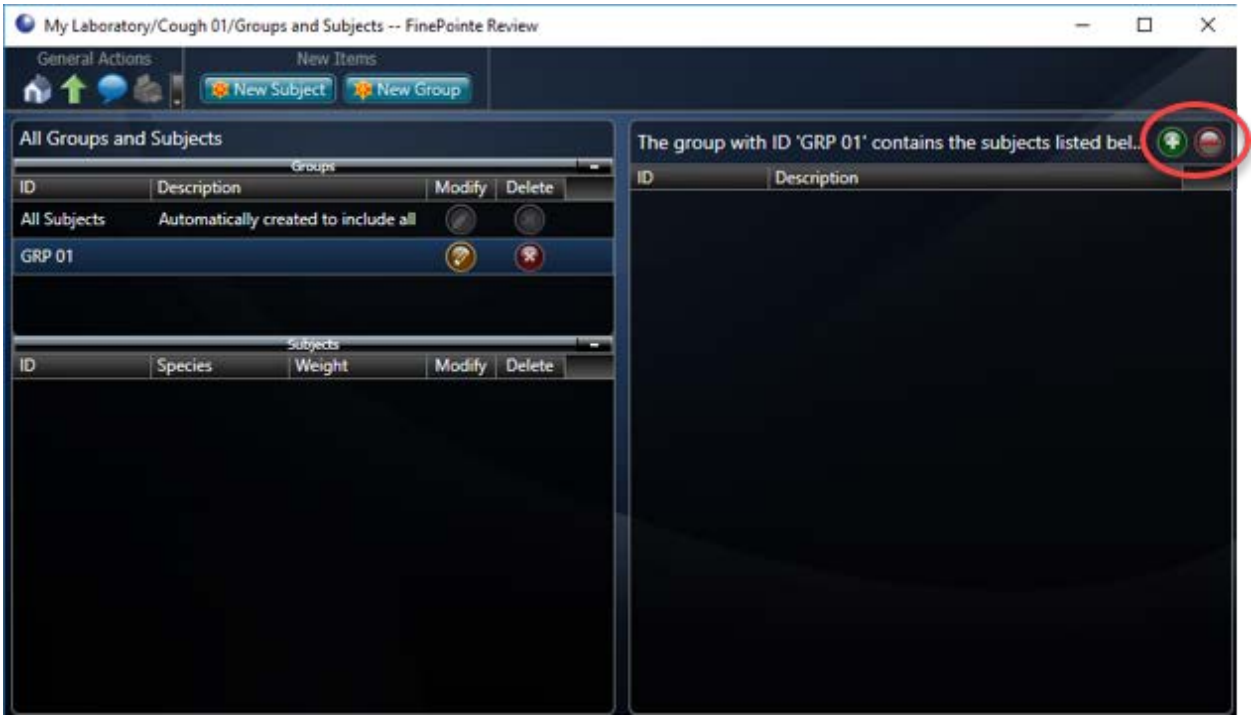


Figure 25. The Groups and Subjects page. Shown here, GRP 01 is selected, and the list on the right shows the subjects which are members of that group (there are none). The + button is highlighted. Click this to change the membership of the group.

When you click the **+** button, a dialog box is presented that allows you to change the membership.

©2023 Data Sciences International

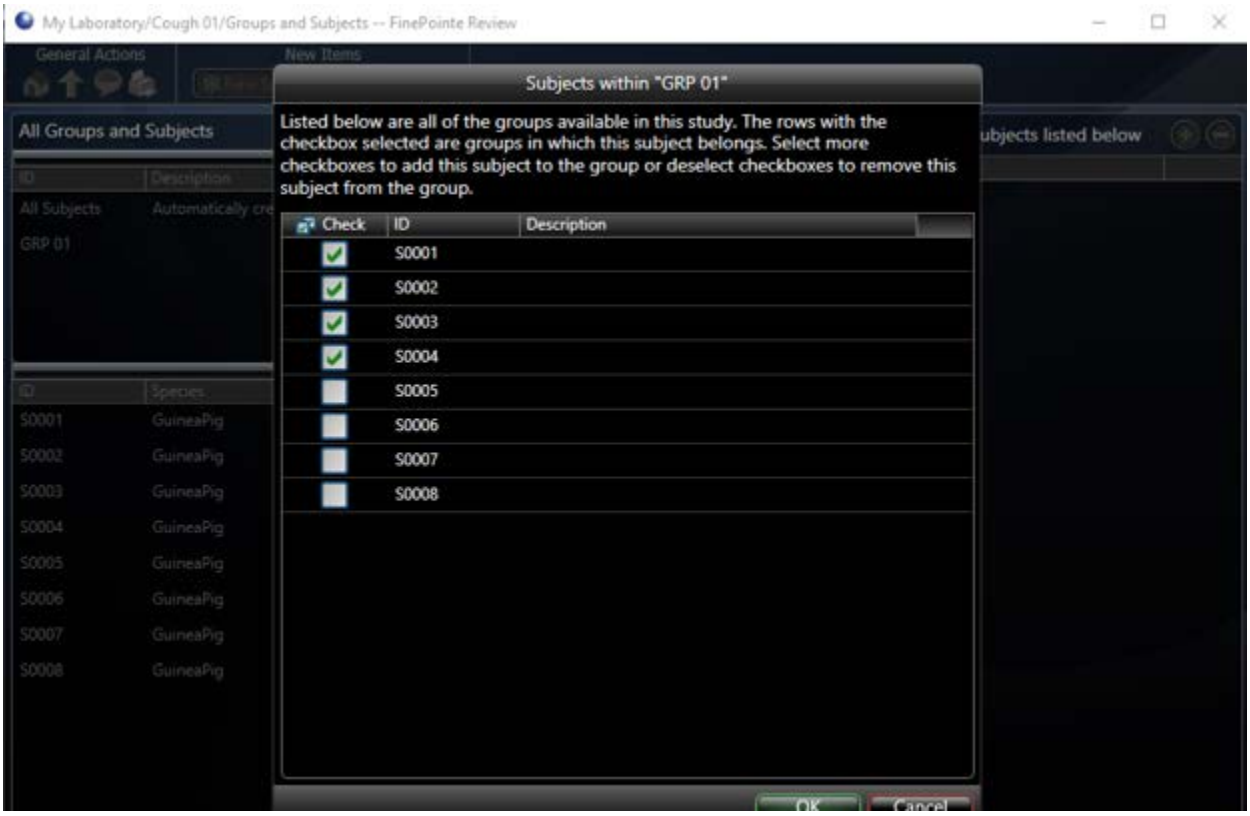


Figure 26. This shows the dialog box that allows you to change the subjects which are members of the group. Place a check by each subject which should be part of the group.

Select the subjects and click the ***OK*** button.

©2023 Data Sciences International

Creating Reports

To create a cough report, begin navigating to the main study page of your cough study, and click the ***Create Report*** button located at the top of the page. This will launch the Create Report dropdown.

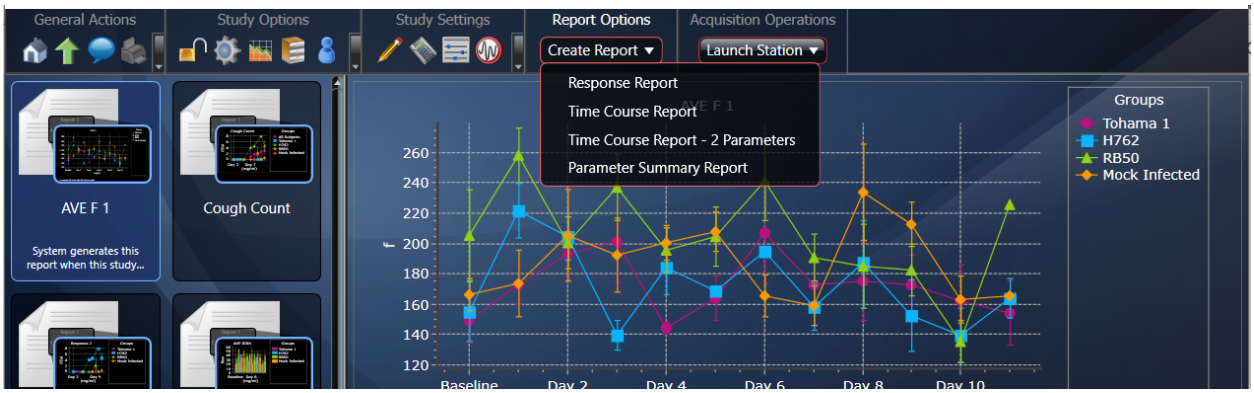


Figure 27. The first page of the Create Report wizard.

Report Type	Description
Response Report (Dose)	Summarizes one or two expressions for multiple measurements and multiple groups.
Time Course	Summarizes an expression for multiple measurements, each subdivided into fixed intervals (specified by you) and multiple groups.
Time Course- 2 Parameter	Summarizes two expressions for multiple measurements, each subdivided into fixed intervals (specified by you) and multiple groups.
Parameter Summary	Summarizes many expressions for a single measurement and multiple groups. The processing of this report is the same as that of Dose Response but permits many expressions.

These reports are described in detail in the WBP Application Manual. Below is an example of how to create a Time Course Report.

The first page of the wizard asks you to provide a name of the report, and optional description, and indicate the number of divisions to report in the response interval. The report name must be unique within the study.

The number of divisions to report allows you to have the recorded interval following the irritant to be subdivided into equal time intervals. If you specified a 20-minute response duration in the task sequence configuration, and 2 divisions, then the report will summarize the data as 2 consecutive 10-minute intervals.

Click ***Next***.

©2023 Data Sciences International

On the second page of the wizard, you specify the parameter or the parameter expression you want summarized.



Figure 28. The second page of the Create Time Course Report wizard. Here you can specify one parameter expression to summarize.

Click ***New Parameter*** to define your parameter. This button presents a dialog box which will help you build the parameter expression you want.

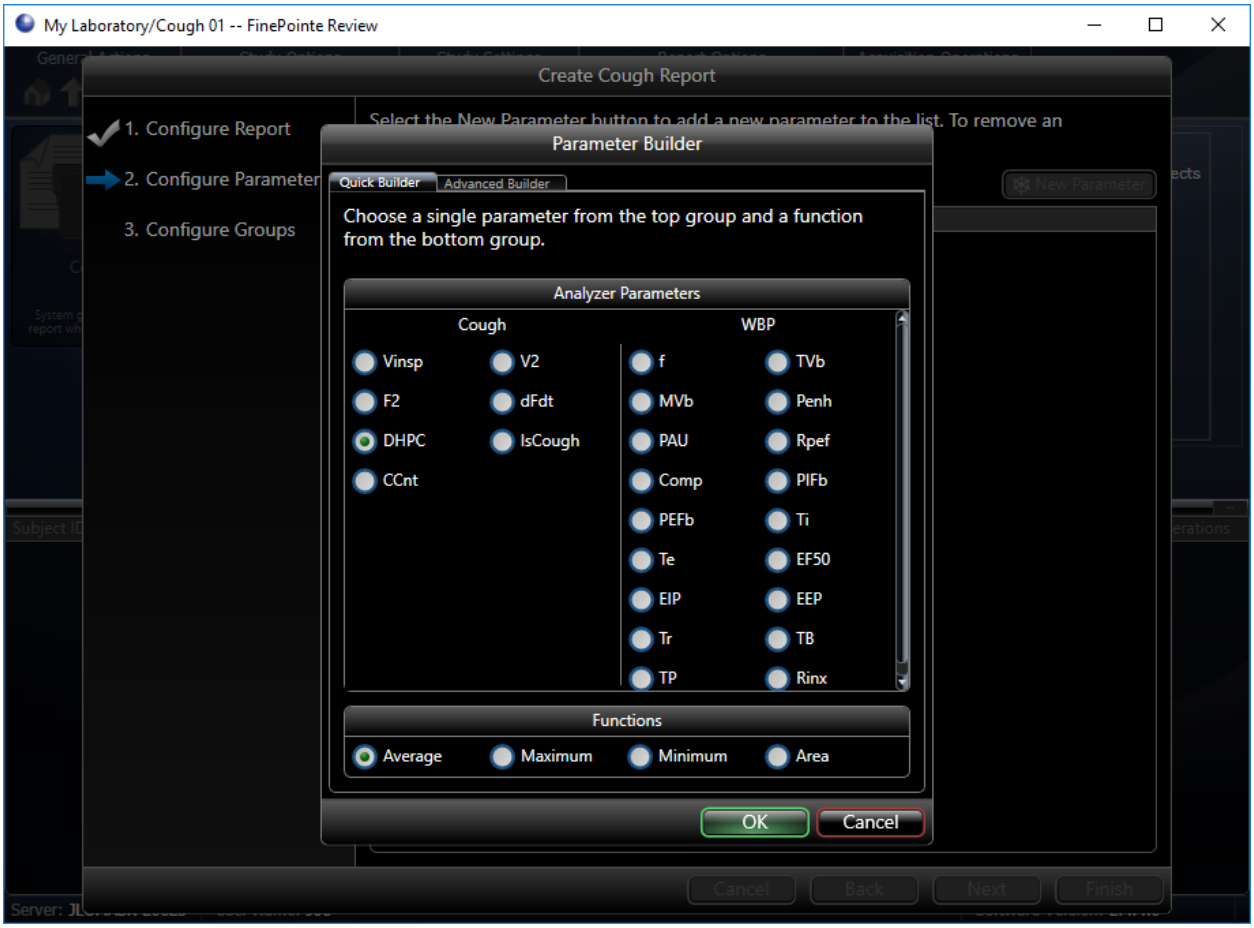


Figure 29. This is an image of the Parameter Builder which is presented when you click the New Parameter button.

©2023 Data Sciences International

The parameter builder has two tabs: Quick Builder and Advanced Builder. The Quick Builder tab allow you to make a couple simple selections and it will create the expression for you. This can be used for many common expressions, especially expressions which are based on one parameter.

The Advanced builder allows you to build more complex algebraic combinations of parameters and functions.

Using the Quick Builder, you can select one parameter from the available parameters derived on the site and one of the common functions to compute on that parameter. For example, if you wanted the average respiratory rate, click the "f" parameter under WBP and the Average function.

Once you are satisfied with your selection, click ***OK***.

You will return to the Configure Parameters wizard page. Click ***Next***.



Figure 30. The final page of the Create Time Course Report wizard. This page allows you to select which groups to summarize for this report.

On the final page of the Create Time Course Report wizard, you can select the groups to summarize in the report. All Subjects is a built-in group which automatically holds all subjects.

©2023 Data Sciences International

Click ***Finish***. When you click finish, FinePointe™ creates the report and computes the results.

You can change all these settings at any time by opening the report and clicking the ***Modify Report Settings*** button. This button will launch this same wizard again.

Calibrating

Once your hardware configuration and study are created, you will need to calibrate before you can begin to acquire data. To do so, return to the laboratory page.

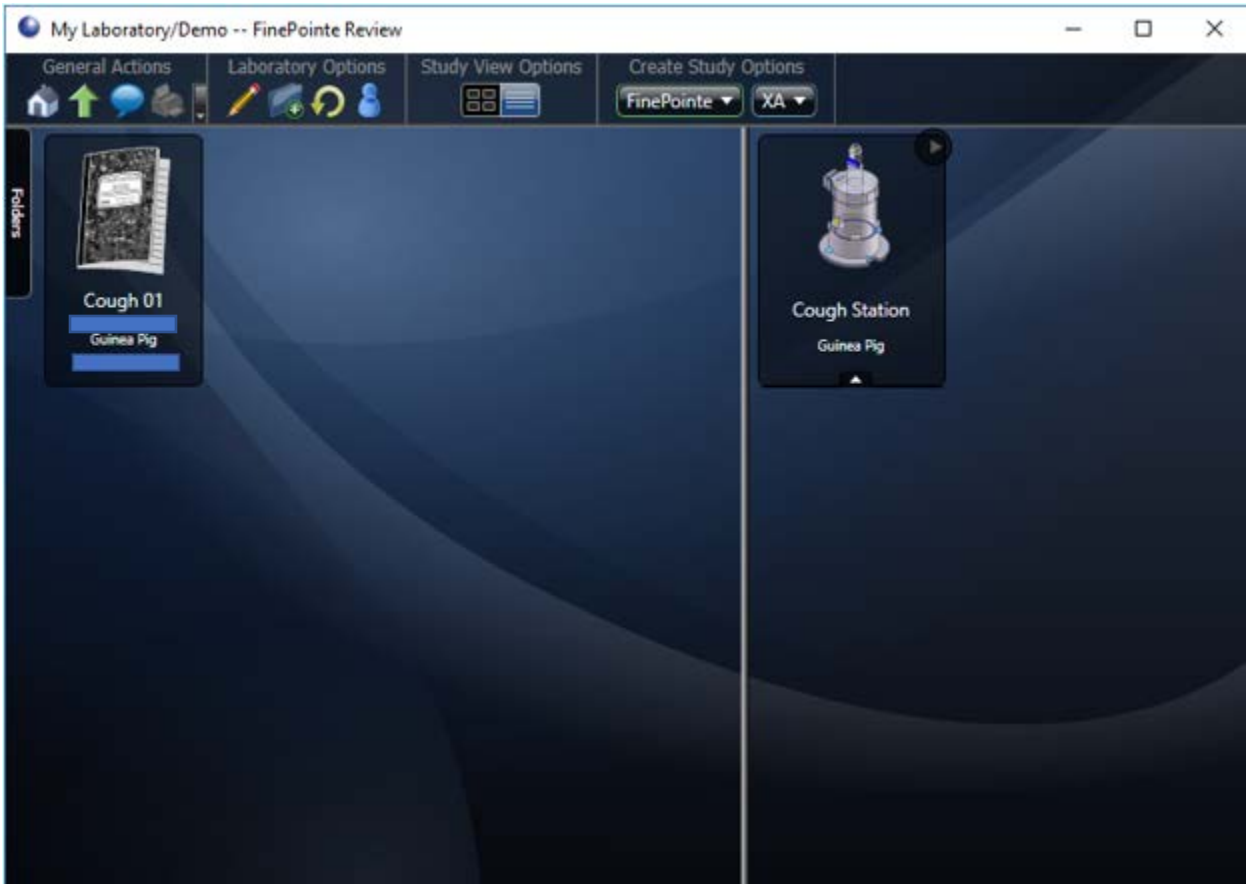


Figure 31. This shows what your Laboratory page may look like once you have created a cough study and a hardware configuration. Study databases are represented as notebooks on the left of the page, and Stations (hardware configurations) are presented on the right.

©2023 Data Sciences International

When you hover the mouse over the station, a button bar slides into view as show in the next figure.



Figure 32. This shows the buttons on the bottom of the station which slide into view when you hover the mouse over it.

Click on the amber wrench button (labeled Calibrate) to launch the calibration page.



Figure 33. This shows the calibrate page you use to calibrate the Box Flow signals.

Click the ***Calibrate*** button to launch the calibration wizard for each Box Flow signal. The Calibrate Button launches a calibration wizard which steps you through the steps necessary to calibrate the signal.

©2023 Data Sciences International

Acquiring Data

One of the greatest benefits of FinePointe™ software is the integration with reporting. FinePointe™ is aware of the types of reports you want to produce, so it is able to assist you with data acquisition in a way unmatched by any other system available.

In assisting your data collection, it helps ensure consistency of the data, freeing your hands up and your mind from details so that you can be more aware of other aspects of the experiment that may also impact consistency. As you acquire data, FinePointe™ automatically annotates the data so that you have a complete documented record of what took place and it also places measurements which will be used for your reports.

Once you are done acquiring data for a subject, typically you only need to add that subject to its associated groups (if you have not already done so by creating subjects and groups ahead of time). FinePointe™ automatically imports the new data into your study and updates your reports.

In addition to all this automation, FinePointe™ allows you to annotate your data yourself, or operate totally manually, if you need to for some reason. FinePointe™ Station is designed to offer automation where it helps and stay out of your way if you do not need it.

To acquire data, you will do the following:

- Launch FinePointe™ Station for the study where you will store the data
- Assign subject IDs to sites
- If running for the first time, you will set up your views.
- Acquire your data using the Task Sequence which walks you through your data collection procedure.
- End the session, which starts the upload to the database.

Launching FinePointe™ Station

To acquire data, launch FinePointe™ Station for the study on the station you want to run on. There are 2 ways to do this, and they are both functionally equivalent.

To launch FinePointe™ Station using the “Drag-and-Drop” method, navigate to the laboratory page showing both the study you want to acquire data into and the Station configuration on the same view. Drag the study you want to store the data into and drop it on the station you want to acquire with. Figure 34 illustrates how this is done.

©2023 Data Sciences International



Figure 34. This illustrates how to launch FinePointe™ Station using the Drag-and-Drop method. Simply use the mouse to select and drag the study and drop it on the Station configuration.

An alternate way to launch FinePointe™ Station is to open the study you want to acquire to and select the ***Launch Station*** button on the command bar of the Study page. Only station configurations which are compatible with the study are listed.

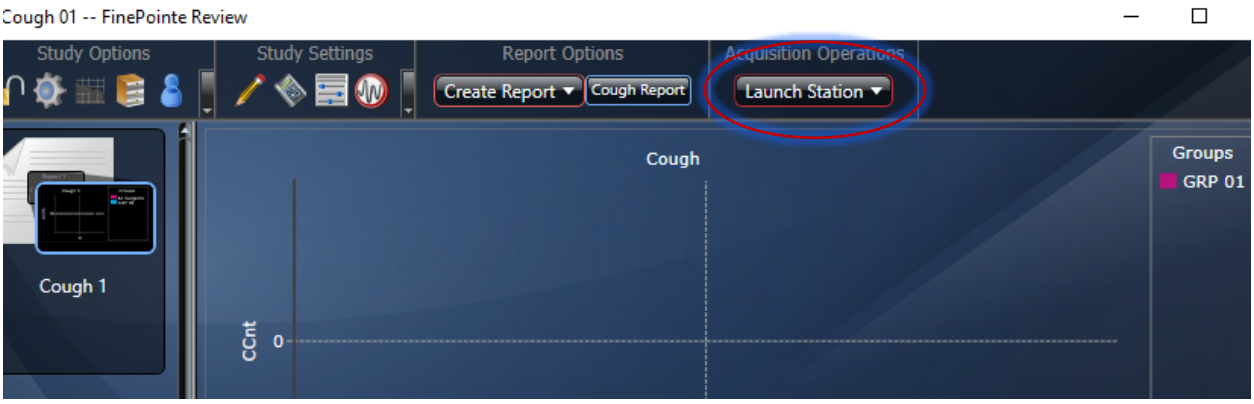


Figure 35. This illustrates where you can find the Launch Station button on the main Study page.

©2023 Data Sciences International

Assigning Subject IDs

After you launch acquisition, FinePointe™ Station opens the Assign Subject IDs page. In this page you identify the subjects that you place in each site of the station configuration. The subject ID can be almost any nonblank text.

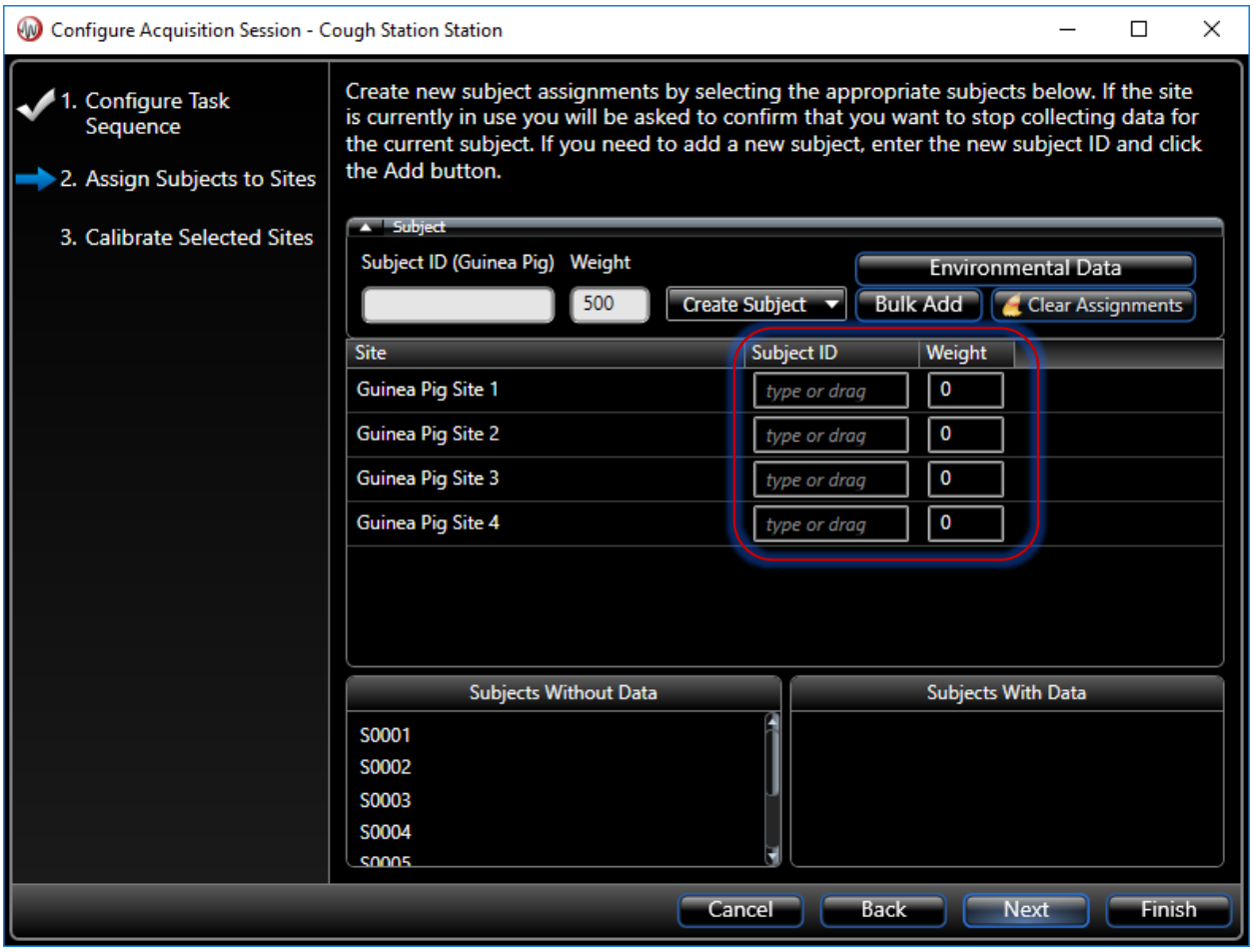


Figure 36. This shows the Assign Subject IDs page for a 4-site guinea pig apparatus. The area marked with the yellow box indicates where you need to assign the subject IDs.

In Figure 36 the yellow box marks the area where you need to assign the subject IDs. The list below labeled "Subjects Without Data" are subject IDs that you have already created in your study but have not yet acquired data for them. If you have something in this list, then you created the subject IDs in the Groups and Subjects Page described earlier in this document. The list labeled "Subjects With Data" are subject IDs that already exist in your study, but there are already recordings in the study associated with them.

You can use the subject IDs in either of these bottom lists by dragging them and dropping them on the appropriate site.

Alternatively, you can create new subject IDs by typing them in the ***Subject ID*** text box above the site list and clicking ***Create Subject***.

©2023 Data Sciences International

If you do not have any specific subject designation but want to make sure each subject ID is new and unique, you can type a subject ID root name into the ***Subject ID*** text box and click ***Bulk Add***. This will use the text you specify in the ***Subject ID*** text box and append a number onto it for each subject it creates.

You do not need to assign a subject ID to each site. Only sites with assigned subject IDs are acquired, so you can use this as a way of running with fewer sites if you choose.

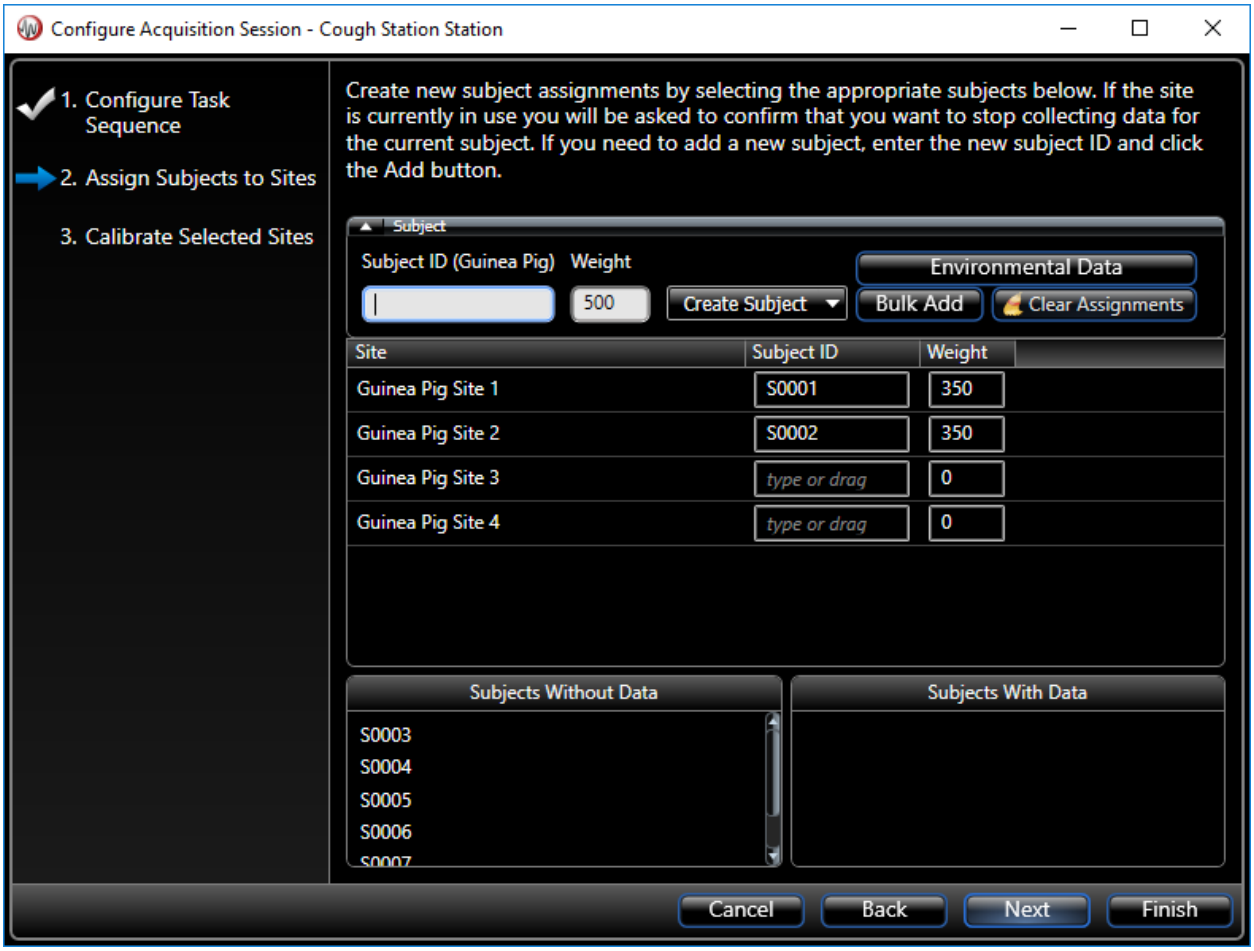


Figure 37. This shows the Assign Subjects to Sites form with only subject IDs assigned to Site 1 and Site 2. So, if you click Finish, only Site 1 and Site 2 will be acquired. Site 3 and Site 4 will not.

After you have assigned subject IDs to the sites you will run, click the ***Finish*** button. FinePointe™ Station will begin acquiring live data.

Configuring Views for the First Time

If you are running for the first time, you may need to arrange the view settings. While you should feel free to pick an arrangement that suites your needs best, the following is a recommended arrangement for cough applications.

Select ***Charts->Signals*** on the main menu on the summary display.

©2023 Data Sciences International

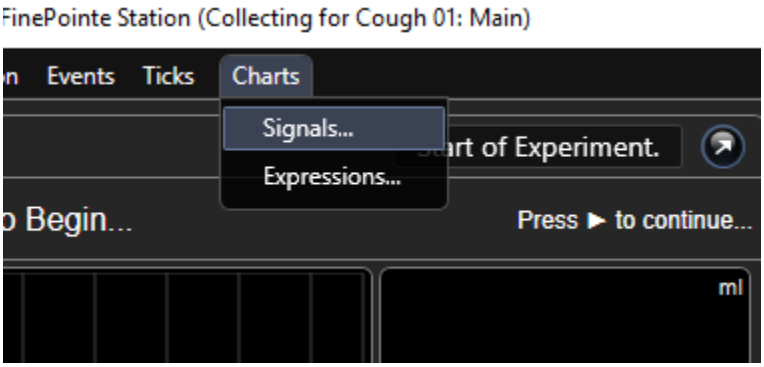


Figure 38. This picture shows you where to find the Chart->Signals menu.

The Signals Options form is presented. Figure 39 shows recommendations for guinea pig:

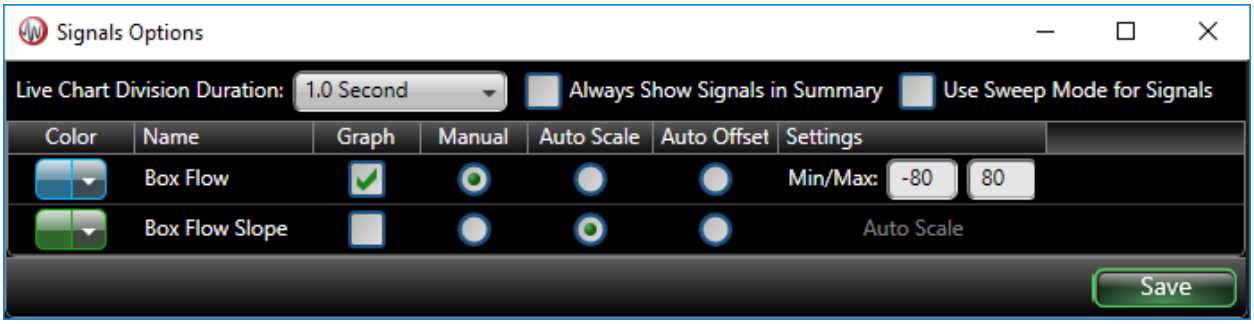


Figure 39. Recommended Signal View options for guinea pig acquisitions.

Figure 40 shows recommendations for mouse:

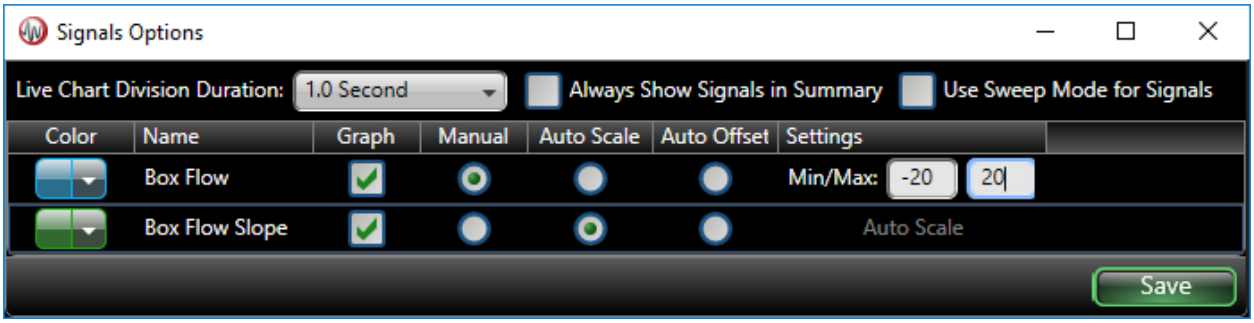


Figure 40. Recommended Signal View options for mouse acquisitions.

Next select ***Chart->Expressions*** from the main menu. This allows you to configure which parameters are shown on the dashboard and plotted on the trend chart. See Figure 41 and Figure 42 for recommended settings. You can change these settings at any time.

©2023 Data Sciences International



Figure 41. This shows a recommended Expressions view setup for guinea pig.

©2023 Data Sciences International



Figure 42. This shows a recommended Expressions view setup for mouse.

FinePointe™ Station provides 2 kinds of views: summary view (only 1), and detail view. The summary view shows you a summary of all your sites on a single page. The detail view shows full detail and content for a single site. With a 2-site station configuration, you have a possibility of arranging 3 windows on your computer: 1 summary

©2023 Data Sciences International

window, and 2 detail windows. They can be present all at once or you can choose to have only some displayed at a time.

The View menu located on the summary view allows you to select from many predefined arrangements. You can even design and save your own if you choose.

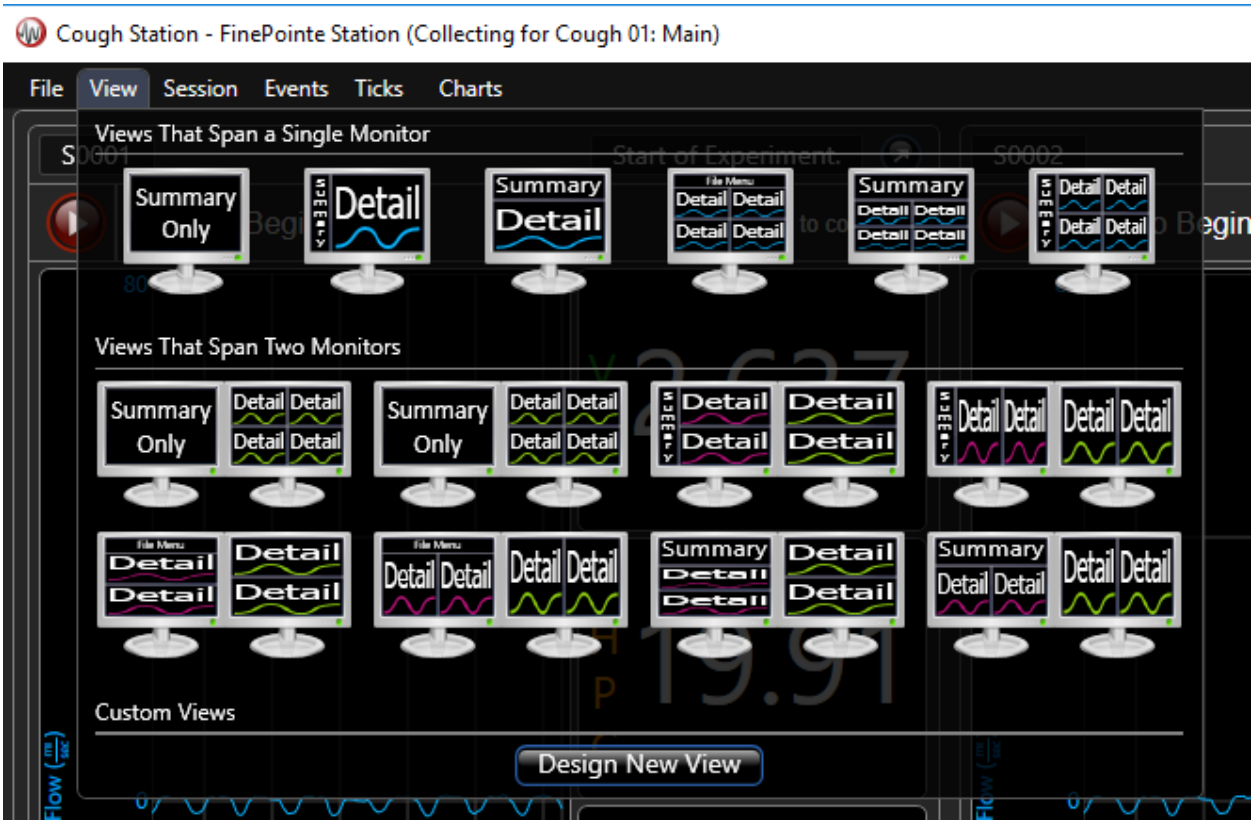


Figure 43. This shows the view menu for a computer with 2 monitors.

FinePointe™ Station populates the View menu content by looking at how many monitors you have installed on your computer. It is easiest to choose one of the layouts provided, or you can click the ***Design New View*** button to explore creating a layout of your own.

Walking Through the Task Sequence

FinePointe™ Station provides a task sequence that allows FinePointe™ to walk through your data collection tasks with you. FinePointe™ allows each site to be acquired independently. So each site can be at a different point in the data collection task sequence at any given time. However, if the sites are not actually independent (e.g. they all share a nebulizer), then you will have to run all the sites together, synchronized.

On the summary view and on each detail view, FinePointe™ provides a task sequence control console. This console shows you:

- where it is in the current task sequence (current task).
- what, if anything, you can do, and a button (***Play*** button) to say you've done it.

©2023 Data Sciences International

- if it is in the process of executing something, what is the progress.

If you are using FinePointe™ WBP controllers, the first two items are presented on the associated site console on the FinePointe™ WBP console bar.

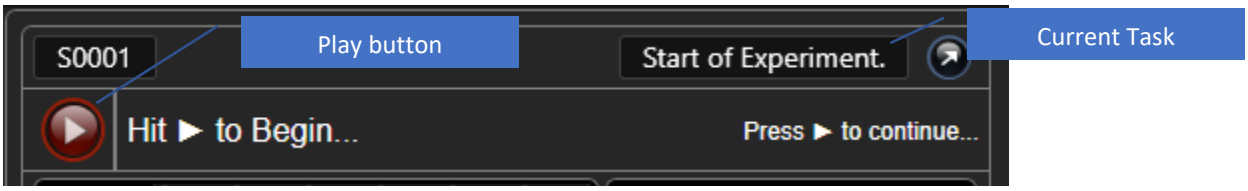


Figure 44. An example FinePointe™ Station console.

In the example shown in Figure 44 the console says "Hit ▶ to Begin…" This message tells you what you can do now. The Current Task is indicated as "Start of Experiment". If you click on that text, a dialog box opens showing you the complete task sequence. You can click ***Cancel*** to close the window.

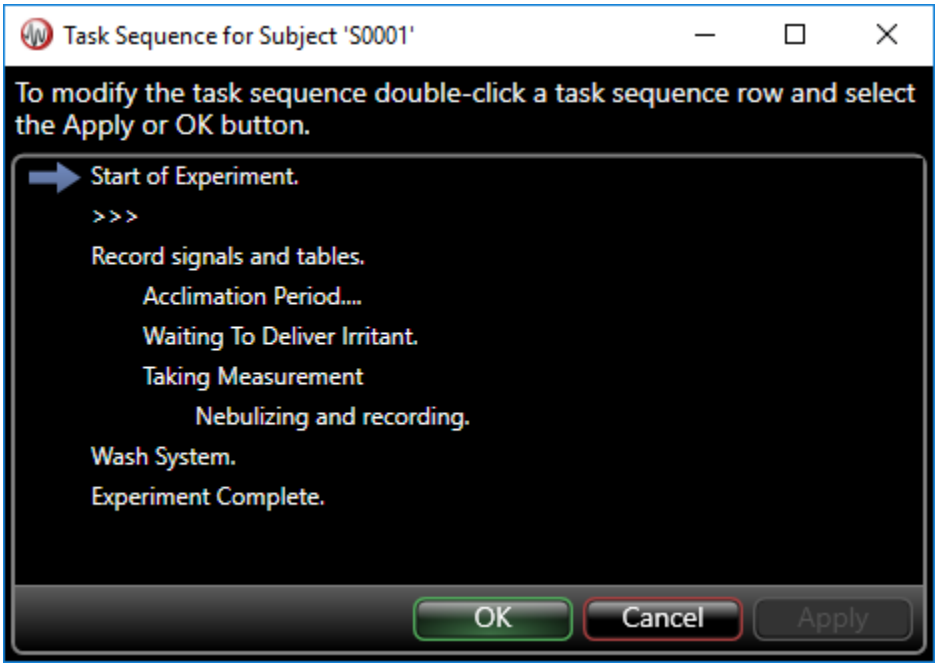


Figure 45. The complete task sequence for a cough study.

FinePointe™ executes the task sequence from the first step to the last step. By reading this, you can see what is needed to acquire data for this study. In this example, FinePointe™ waits for you to begin. At this point, you should make sure the apparatus is properly setup, and the data being acquired from the animals looks good.

When you are ready, click the ▶ (play) button. FinePointe™ starts the recording and begins timing the acclimation period. You can interrupt the acclimation period by pressing the ▶ button again. Next FinePointe™ waits again for you to deliver the first challenge (PBS).

©2023 Data Sciences International

Once you do, press the ▶ button again, and FinePointe™ delivers the aerosol and times the measurement interval. When done, it waits for you to load the nebulizer again with the next challenge concentration.

The arrow indicates the current task. You can select a task and click ***Apply*** if you want to skip to that task, but that should only be necessary in unusual circumstances.

If you need to run all the sites together (i.e. due to a shared nebulizer), you can use the F12 button to hit ▶ on all the Sites at once. Make sure the summary window is selected, otherwise the F12 button press may end up going to another window (and FinePointe™ will not be aware of it).

End the session

Once you have completed the data collection task sequence, select the ***File->End Session*** menu on the summary window. The End Session wizard is presented.

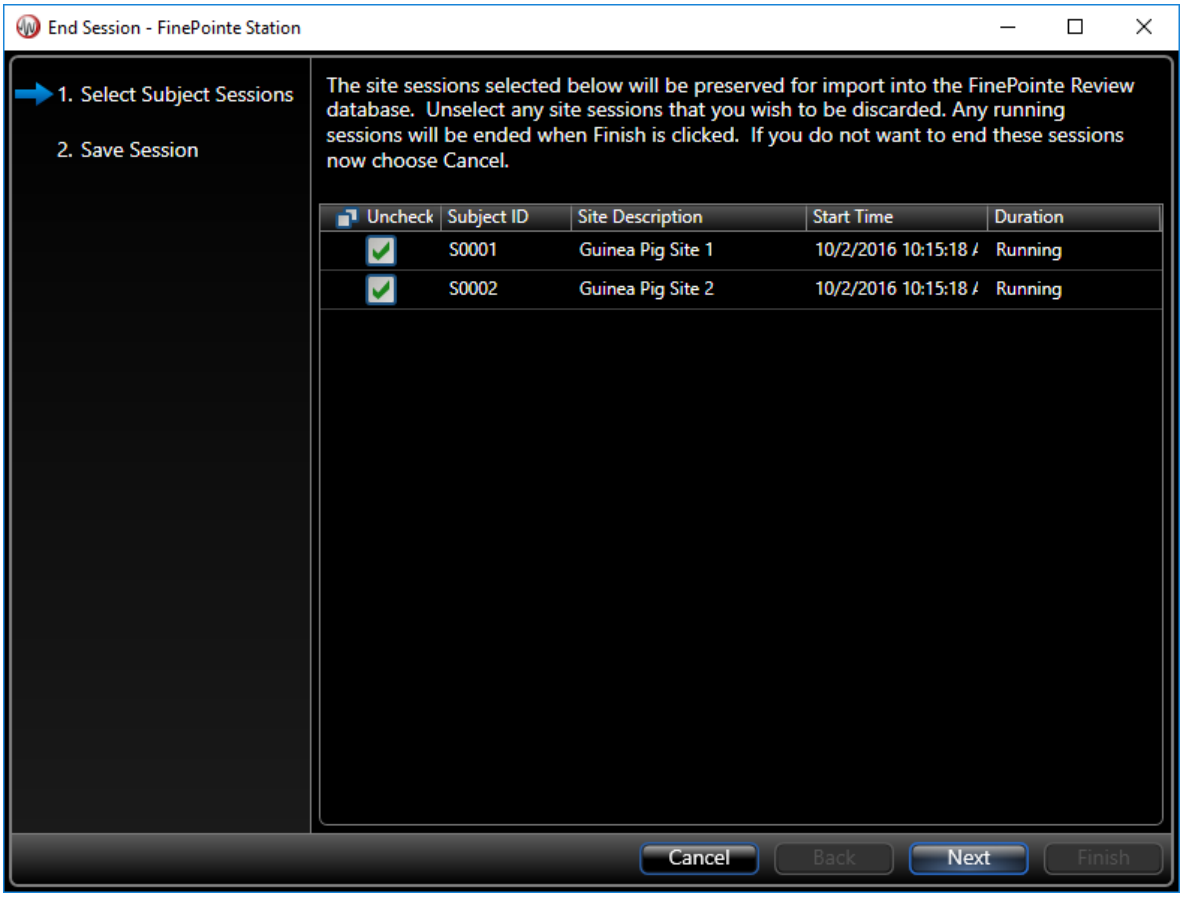


Figure 46. The first page of the End Session wizard. Select the subjects you want to save to the database. By default, they are all selected.

©2023 Data Sciences International

Usually, you will not do anything here since the default is the save all the data. The first page of the wizard does give you a chance to reject data here. If you do, it will not up upload into the study database.

Click ***Next***.

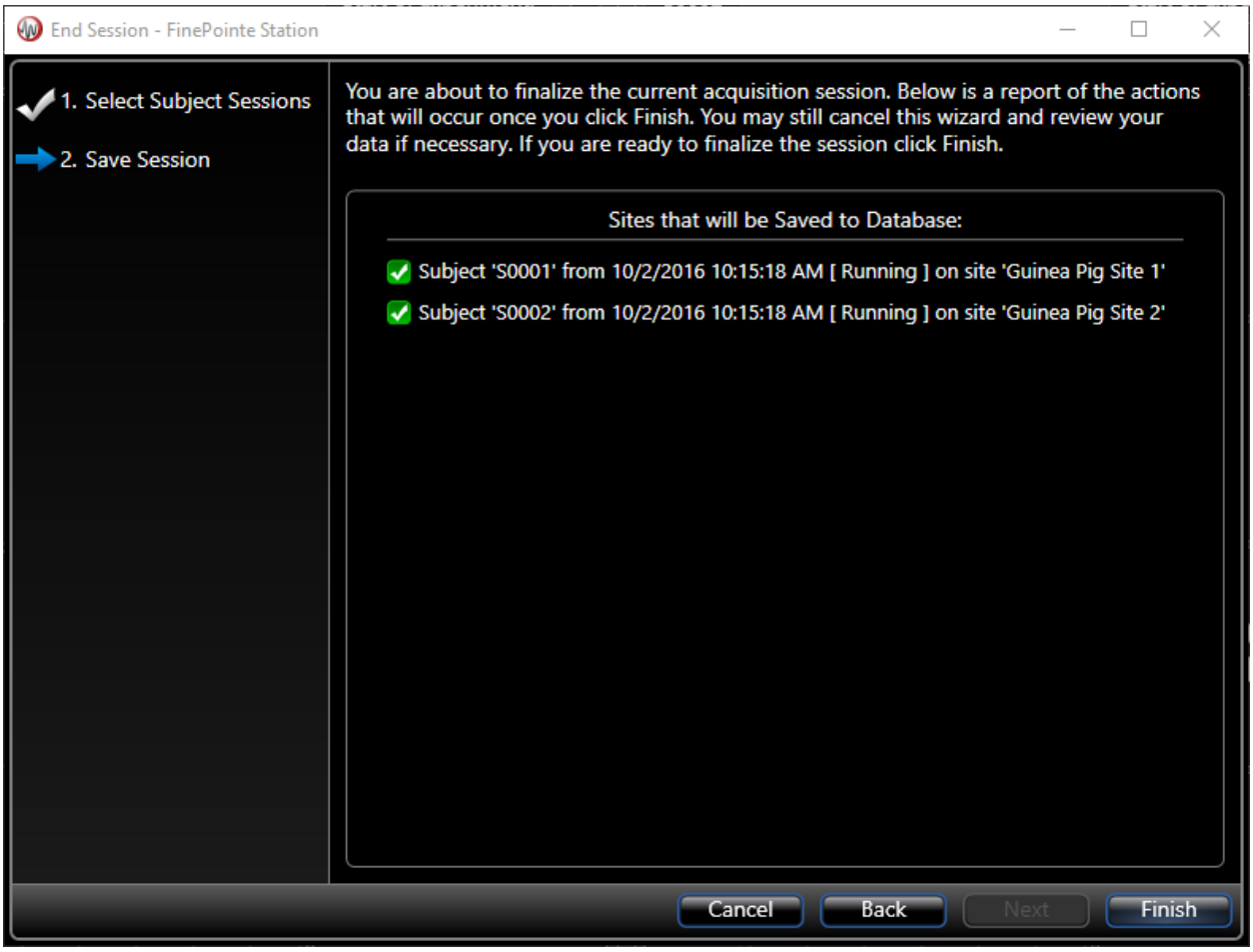


Figure 47. The final page of the End Session wizard. This page simply confirms what you selected on the first page.

The final page of the wizard confirms what you selected on the first page. If satisfied, click ***Finish***. Otherwise, click ***Cancel*** or ***Back***.

If you click ***Finish***, FinePointe™ will begin the process of importing the data into the study. This can take a few minutes, but you can launch FinePointe™ Station again (even before the data is fully imported) and begin data collection of the next subject.

©2023 Data Sciences International

Cough Detection

The cough detection algorithm is different depending on the species. Broadly speaking, both algorithms first detect an event and then apply criteria to decide if the event is a cough. If it is, the IsCough parameter is set to a non-zero value. For guinea pig, it is set to a 1 for a cough, and 0 for a non-cough event. Patented fuzzy logic criteria that are applied to a detected event to determine if the event is a cough. For mouse, the IsCough parameter is coded to a value which indicates the type of cough event that occurred. The mouse algorithm uses a set of fixed properties to decide.

Multi-cough Event

A multi-cough event occurs when the animal coughs in rapid succession. You may want all the coughs within such an event combined and reported as a single cough, or you may want to count each one individually. An example of what a multi-cough event might look like on the box flow signal is shown in in Figure 48.

In addition, when such an event occurs, the coughs that occur after the first may not be fully formed, and so if the cough criteria is applied to each, it is possible the second event may not get counted as a cough.

To deal with these issues associated with multi-cough events, you need to select how FinePointe™ handles these events. FinePointe™ provides 3 possible modes for handing this:

Multi-cough Mode	Multi-Cough Treatment
Each	Each multi-cough event is treated as a single cough.
Multiple	Each cough in a multi-cough event is treated as its own cough. But, the full cough criteria are only applied to the first cough. Subsequent coughs only need to meet threshold conditions.
Single	Each cough in a multi-cough event is treated and counted independently. The full cough criteria are applied to each cough within the event.

©2023 Data Sciences International

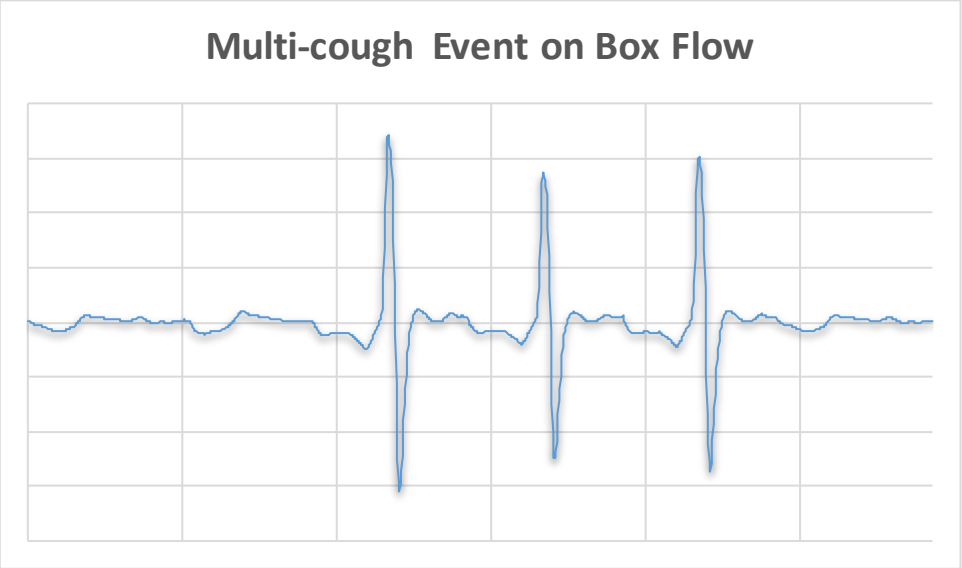


Figure 48. An example of a multi-cough event.

Guinea Pig and Rat Analysis

Analysis of the box flow signal begins with filters applied to the box flow signal to remove any DC drift. A high pass filter with a very low cutoff is used. The filtered box flow signal is then passed into a state machine which looks for the box flow to exceed a positive threshold, and then fall below a separate negative threshold within a certain time. If that is found, then an event is identified, and it waits until the box flow returns to zero to find the end of the event. The main parameter collected during this processing is the DHCP parameter. This parameter is based on the last positive threshold crossing and the last negative threshold crossing (since it is possible that each threshold can have multiple crossings in a single event).

The following is the logic used to determine if an event is a cough:

To Compute IsCough, first we calculate $IsCough_{fuzzy}$ using the following formula:

$$IsCough_{fuzzy} = \frac{\left(1 - \frac{1}{1 + e^{\left[\frac{C_{V2}}{T_{V2}} \cdot \left(\frac{V2 \cdot 1000}{Weight} - T_{V2}\right)\right]}}\right) \cdot I_{V_2} + \left(1 - \frac{1}{1 + e^{\left[\frac{C_{DHPC}}{T_{DHPC}} \cdot (DHPC - T_{DHPC})\right]}}\right) \cdot I_{DHPC}}{I_{V_2} + I_{DHPC}}$$

Where:

V2	is the value of V2.
Weight	is the weight of the animal (as entered in the algorithm settings).
C_{v2}	is a value which defines the “crispness” of the V2 contribution.
T_{v2}	is a value which defines the “threshold” of the V2 contribution.
I_{v2}	is a value which defines the “importance” of the V2 contribution.
C_{DHPC}	is a value which defines the “crispness” of the DHPC contribution.
T_{DHPC}	is a value which defines the “threshold” of the DHPC contribution.

©2023 Data Sciences International

I_{DHPC} is a value which defines the “importance” of the DHPC contribution.

Then additional values are used along with conditions to determine the value of IsCough:

Pessimism is a number (from 0 to 1) which is used overall to decide if it is a cough
Multi-event-rule is an enumerator used to decide how to handle events which occur close together.
previousIsCough is 1 if the last reported event is a cough.

The following logic is applied:

If (Multi-event-rule = 0) or ($IsCough_{fuzzy}$ < Pessimism) then
    IsCough = 0
else
    IsCough = 1

If (Multi-event-rule = 1) and (previousIsCough = 1) then
    IsCough = 1

©2023 Data Sciences International

Parameters Reported for Guinea Pig

Name	Description	Units
Vinsp	Not defined for guinea pig or rat	n/a
V2	The volume due to compression	mL
F2	Not defined for guinea pig or rat	n/a
dFdt	Not defined for guinea pig or rat	n/a
DHPC	Delta Half Peak Crossing. A time index which reflects the time it takes to transition from the compression phase to the expulsive phase.	Samples (5ms interval)
IsCough	A value of 1 or 0. When value is 1, then the event is judged to be a cough. Otherwise it is not.	
CCnt	The number of coughs since the last analyzer reset.	

Mouse Analysis

Analysis of the box flow signal begins with filters applied the box flow signal to remove any DC offset. The DC-corrected box flow signal is then differentiated, and the resulting slope and corrected box flow signals are passed into a state machine to identify cough events.

The state machine looks for events where the box flow first exceeds a threshold on the expiratory side (a likely compressive phase) followed by the box flow slope falling below a negative threshold (a likely transition to expulsive phase). If these events are detected, and the box flow returns to zero within a certain period of time, then it is an event considered for the cough criteria.

Parameters Reported for Mouse

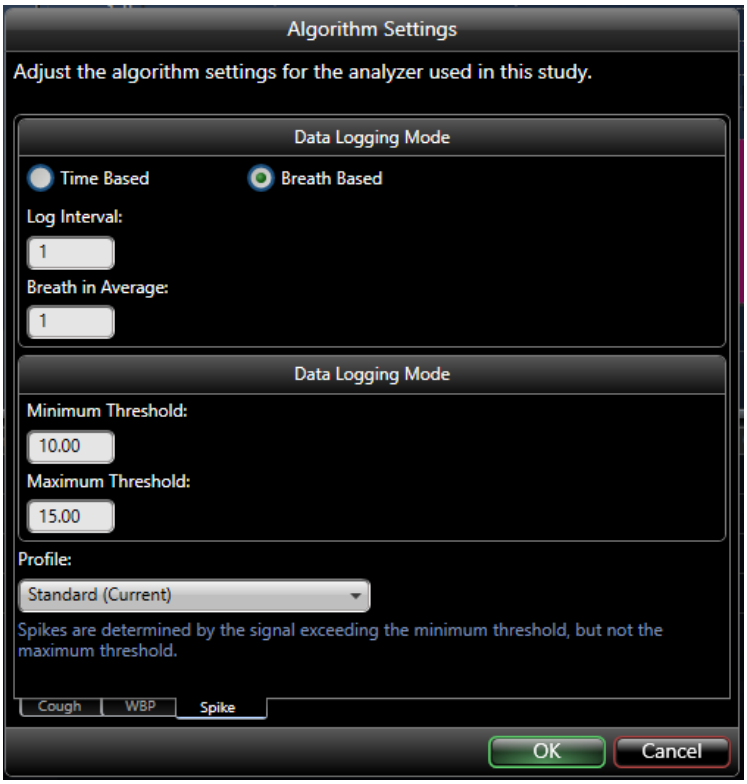
Name	Description	Units
Vinsp	The volume inspired immediately before the event	mL
V2	The volume due to compression	mL
F2	The box flow as the compression phase begins to transition to expulsive phase	mL/sec
dFdt	The maximum rate of change (falling) of box flow when transitioning from the compressive phase to the expulsive phase.	mL/sec^2
DHPC	Not defined for mouse	n/a
IsCough	A coded value which scores the cough event. If zero, it is not a cough, otherwise it is a cough.	
CCnt	The number of coughs since the last analyzer reset.	

©2023 Data Sciences International

Spike Detection

FinePointe™ version 2.9 introduced an additional feature to the Cough analyzer. There is a new tab available in the Algorithm Settings and Data Table labeled “Spike”. This Spike Detection feature is for researchers who want an alternative to the FinePointe™ cough algorithm, so that they can count simple spikes in the signal rather than requiring the compressive/expulsive phases of a true Cough. In this instance a spike is simply an elevated period of flow determined by thresholds, which may or may not correlate to a physiological “cough”.

FinePointe™ will detect any positive spikes in the flow signal and mark them as such. This is run in parallel with the existing cough algorithm.



There are only two thresholds that need be set to detect a spike in the flow signal: a **Minimum Threshold** and **Maximum Threshold**. These thresholds are evaluated as an additional flow above the bias flow setpoint.

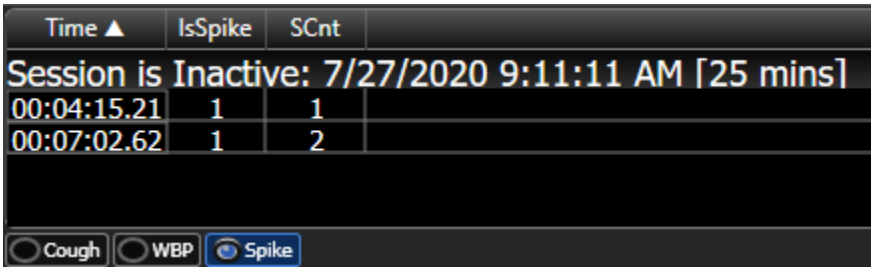
The **Minimum Threshold** is the minimum flow above the bias flow for a spike to be considered.

The **Maximum Threshold** is the maximum peak above the bias flow for a spike; if the spike goes above this threshold it is considered noise and will not be counted as a spike.

These thresholds should be determined by the end user after an assessment of their data, the flow patterns, and what values would make the most sense.

The Spike tab in the data table gives two new parameters: **IsSpike** and **SCnt** (Spike Count)**.** These are functionally identical to the IsCough and CCnt parameters in the Cough analyzer discussed on the previous page.

©2023 Data Sciences International



Some Spikes will also be counted as Coughs and some Coughs as Spikes; the two analyzers are run completely separately from each other so their results may naturally overlap.

©2023 Data Sciences International

References

US Patent # 7,104,962, “Cough/sneeze analyzer and method”

Chen L, Lai K, Lomask JM, Jiang B, Zhong N (2013) ***Detection of Mouse Cough Based on Sound Monitoring and Respiratory Airflow Waveforms***. PLoS ONE 8(3): e59263. doi: 10.1371/journal.pone.0059263

©2023 Data Sciences International

Contact Information

We are available to help you with your questions and concerns. Should you hit a roadblock or need some additional training, please feel free to visit DSI Support Center at https://support.datasci.com to find articles and helpful information in our knowledge base, Chat with an agent, or setup time to receive one-on-one consultation. We are happy to help!

Data Sciences International (DSI)

119 14th Street NW
New Brighton, MN 55112

DSI Technical Support—North America

Email: Support@datasci.com

DSI Technical Support—Europe

Email: Europe-support@datasci.com