

Genotrack

Colony Management & Reporting

Genotrack: Colony Management & Reporting

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Chapter 1. Background Information

It's important to understand how to some extent how Genotrack is structured and how various parts of the system represent real world events or entities. This will help to understand why some parts of the system function the way they do.

A glossary of scientific and other technical terms used will be provided later in the document - this section is more about the general structure of the system and what you need to know to better understand the workflows in Genotrack.

The structure of Genotrack

How do all the parts tie together?

There are many other objects in the system you can use to record information, but it's the relationship between these primary entities which has the biggest impact in terms of your basic understanding of the system.

The following are the primary entities you need to know about to get a feel for how the system works:

Strain	The highest level entity within the Genotrack hierarchy is the strain. The strain should be thought of as an abstract entity with no physical presence - it is the description of a line of animals with a particular set of characteristics.
Allele	<p>Alleles are associated with Strains. The allele entry records information regarding one of two or more alternative forms of a gene at a particular position of the specified chromosome.</p> <p>The allele may be specific to a strain, or a more general variation found commonly in the species. As with the parent strain table, you can record a great deal of information about an allele, but you need only enter the alleles which are of interest for the strain in question. You can add as many alleles to a strain as you like.</p>
Colony	<p>A colony is an instance of a strain - a group of animals of a particular strain at a particular location. You may have more than one colony of the same strain stored in different locations.</p> <p>As a colony is associated with a strain, all animals within a colony have the characteristics detailed by the associated strain record and it's alleles - the information from the strain is inherited by all colonies of that strain.</p>
Matings	<p>Mating records contain information about a specific mating between a male and one or more female animals. Animals can be added or removed from the mating at any time of the duration - you determine when the mating is stopped.</p> <p>A mating is always associated with a colony.</p>
Litters	<p>Litter records contain information regarding the birth of animals. A litter will always be the result of a specific mating, but will only be the result of one male and one female animal. If multiple animals are involved in the mating, you will be asked to specify which female bore the litter.</p> <p>The litter record also allows you to record details of any animals which were stillborn, discarded or culled to enable the production statistics to be calculated.</p>

Weanings

A litter is always associated with a mating.

A weaning records information about the removal of the animal(s) from their mother. This usually involves separating male and female animals into single sex (stock) units. A litter may be weaned all at once, or gradually with some animals removed at each weaning until all animals from the litter have been accounted for.

Each weaning record also allows you to record details of any animals which were found dead, discarded or culled between birth (litter) and weaning to enable the production statistics to be calculated.

A weaning is always associated with a litter.



Tip

The standard operation of genotrack creates the individual animal records at this point.

The exceptions are animals imported into the system, animals accounted for via the Females removed prior to weaning and Males removed prior to weaning fields, and animals born to litters where the Number offspring at birth instead of weaning box is checked. In that instance, the animal records are created for each of the animals born when the litter record is saved for the first time.

By waiting until weaning to create the animal records, animals which are culled, discarded or die prior to weaning are not created in the system, meaning those animal numbers are not "wasted" and storage is not allocated to animal records which will never be looked at again.

Note that these animals are still taken into account when calculating statistics.

Animal

The animal record, as you would expect, contains all the information regarding a particular animal. Each animal is the product of a litter. Each animal is also associated with the colony of which it is currently a member. This allows you to reference information either for the strain related to the animal's current colony, or the strain the animal was originally born to.

Data Security

Access Control within Genotrack

Access to the system is a three level system

Password Control

You must have a person record with a valid username and password to login to the system. The person records must also be have the User is Active checkbox ticked, and either have no expiry date set, or an expiry date which is later than the current date.

Person records can be created by a member of the Administrator group

Group Level Access Control

Membership of a group can add additional access rights to a person's account. See the Groups section for additional information regarding group membership and access rights.

Specified Access Control

At some points in system (eg: Strains, Colonies and Projects) a privileged user can grant access for a particular user to a particular record.

That user can then access the specified record via their user tab.

Dates & Ages

Normal Date Format

A "normal" representation of a date. This is the format used to store dates within the system - other representations are calculated "live" based on the stored date values.

Usually in the form dd/mm/yyyy

Day of the Year (DOY)

(a.k.a. Julian date, Mousedate)

The day of the year is exactly that - the number of days since January 1st (day 1) in the current year.

A Date of the Year field is provided anywhere a date field is used in relation to an animal. You can enter or update either the Normal Date Format or the Day of the Year and the corresponding representation will update automatically. This means you can use whichever format you like to enter dates.

Standard Form: ###/YY

Example 1.1. Day of the Year (DOY) Notation

150/09 represents the 150th day of 2009 (or 30/05/2009 in normal date format)



Leap Years are handled automatically

All Day of the Year calculations automatically check the year entered, and if the year in question is a leap year, the day of the year is adjusted automatically to cater for the inclusion of February 29th in the calendar.

Age/Duration in Weeks

When talking about the age of an animal or litter, it's often useful to know how many weeks old the animal is.

Standard Form: X weeks, Y days

Example 1.2. Age/Duration in Weeks

A litter is **2 weeks, 6 days** old today.

Age/Duration in Days

Similar to the Day of the Year, the age or duration in days is the number of days since a specified event.

Standard Form: # days

Example 1.3. Age/Duration in Days

A litter is **20 days** old today.

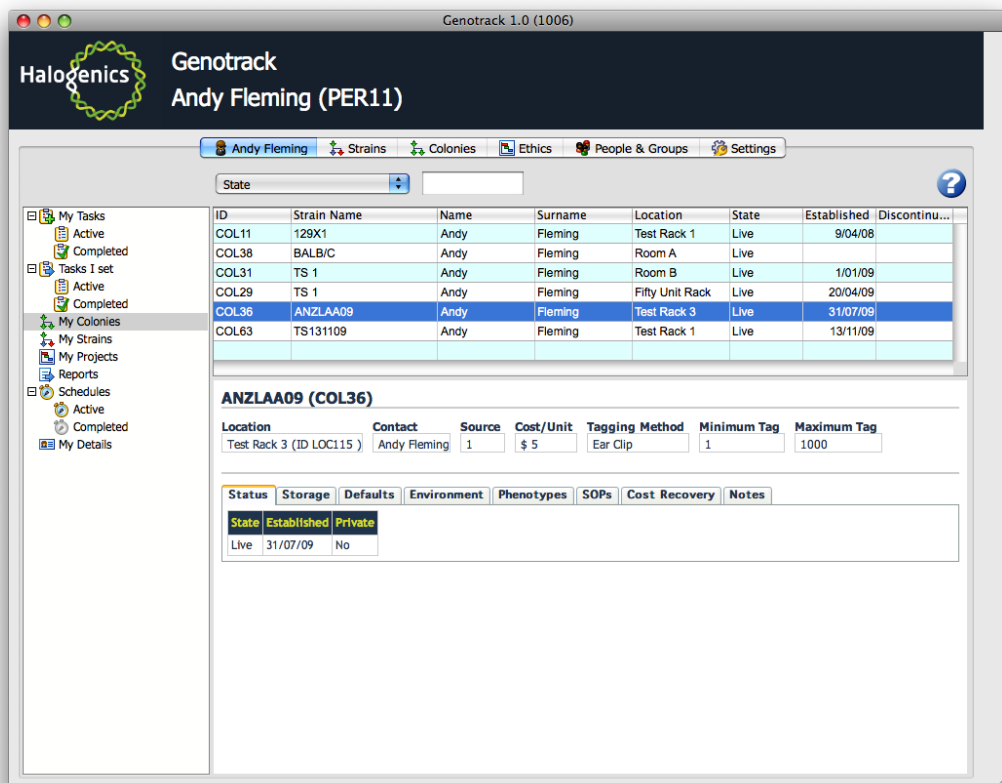
Chapter 2. Layout and Interface elements

Main Navigation Window

The main Genotrack window (shown below) is made up of 3 main areas:

1. Section Tabs
2. Item List
3. Record List & Preview

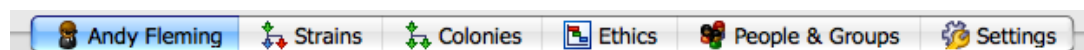
Figure 2.1. The main Genotrack window



Section Tabs

The section tabs are used to select which aspect of the system you're currently working with.

Figure 2.2. Section tabs from the main Genotrack window

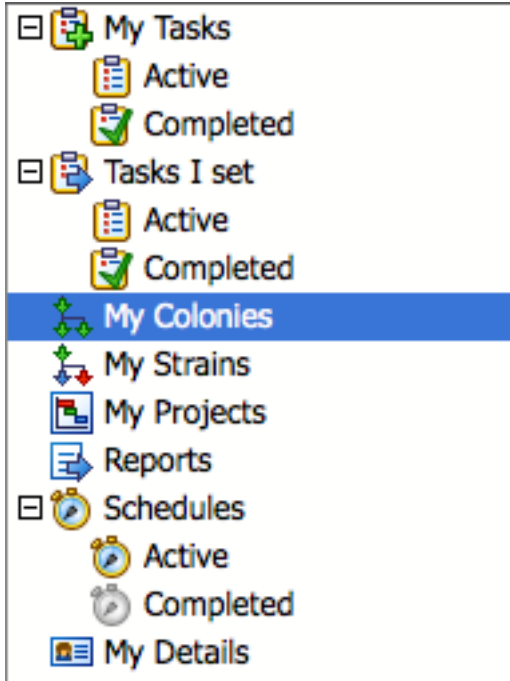


Changing the selected tab changes the item list, allowing you to select and preview records relevant to the selected section.

Item List

The Item list shows what record types or group of record types are available.

Figure 2.3. Item list from the main Genotrack window - User's tab selected



Clicking on a list item updates the records which are displayed in the record list. In some cases, a list item may represent a selection or subselection of records.

Record List & Preview

The record list is exactly that - a list of available records. The records displayed depend on the currently selected item in the item list. Clicking on one of the records in the list at the top updates the preview in the bottom half of the window, as shown below:

Figure 2.4. Record list and a preview of the selected record

ID	Strain Name	Name	Surname	Location	State	Established	Discontinu...
COL11	129X1	Andy	Fleming	Test Rack 1	Live	9/04/08	
COL38	BALB/C	Andy	Fleming	Room A	Live		
COL31	TS 1	Andy	Fleming	Room B	Live	1/01/09	
COL29	TS 1	Andy	Fleming	Fifty Unit Rack	Live	20/04/09	
COL36	ANZLAA09	Andy	Fleming	Test Rack 3	Live	31/07/09	
COL63	TS131109	Andy	Fleming	Test Rack 1	Live	13/11/09	

ANZLAA09 (COL36)

Location	Contact	Source	Cost/Unit	Tagging Method	Minimum Tag	Maximum Tag
Test Rack 3 (ID LOC115)	Andy Fleming	1	\$ 5	Ear Clip	1	1000

Status	Storage	Defaults	Environment	Phenotypes	SOPs	Cost Recovery	Notes
State	Established	Private					
Live	31/07/09	No					

The record list (upper section) and a preview of the selected record in the list (lower section)

Many of the previews include tabs, which you can click on to reveal additional information relating to the selected record.

Buttons and Quickfilters

There are a number of other elements of the interface which you will use on a regular basis. These fall into two main categories, *Buttons* and *Quickfilters*

Figure 2.5. Buttons and Quickfilters



A section of the user interface showing buttons and Quickfilters.

Plus and Trash on the left, and Help on the far right. The State popup menu in the middle and the adjacent text box combine to form a Quickfilter.

Buttons

There are four main buttons which are available throughout the system:

Plus button

Add a new record



If you have permission to add records, or if that function is permitted in the current context of the program, the button will be enabled.

If enabled and clicked, the system will create a new record of the type you have currently selected in the Item list.

Trash button

Delete the selected record(s)



In many places it is not permitted to delete records, due to inheritance and dependencies within the structure of the data. For this reason, this button is often inactive. In some cases, deletion will only be available to members of certain groups, such as Breeding Administrators.

If enabled and clicked, the system will, after confirming with you, delete the currently selected records from the record list.



You can NOT undo this deletion

Make sure you have the correct records selected and are 100% sure you want to permanently delete them from the system.

Task button

Add a new task



Clicking this button will allow you to add a new task into the system. If you're at the main window, the task will be generic (ie: not linked to any particular colony). If you're at the colony level, the task will be specific to the colony you're in.

Help button

Launch the Help system



The Help button is almost always available - you never know when you might need help!

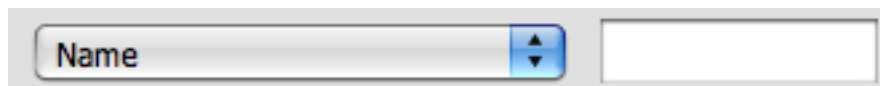
Clicking the Help will launch the Genotrack help system.

Quickfilters

As you work various record lists, it's quite likely you'll be looking for a specific record or records, or wanting to compare records with similar characteristics. To make this easier, the Quickfilter box can be used to reduce the number of records displayed in the list.

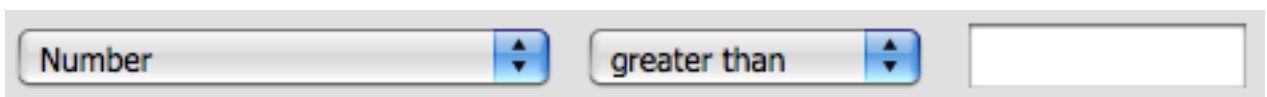
To use a text field Quickfilter, select the field from the popup by which you wish to filter the displayed records, then type the information to match into the box. The number of records displayed will change to include only those which match the text you have entered.

Figure 2.6. Quickfilter on a text field



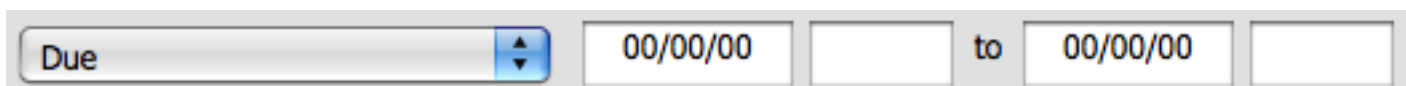
The text Quickfilter uses a "wild card" search not an exact match.
Eg: "male" will return records matching "male" as well as "female".

Figure 2.7. Quickfilter on a number field



To use a number field Quickfilter, select the comparison operator using the second popup menu then enter the numeric value in the number field

Figure 2.8. Quickfilter on a date field



To use a date field Quickfilter, specify both the start and end dates to provide a range. To find a specific date, enter it in both fields.

Contextually aware elements

Many buttons and other elements within the system are context aware - they will be active or inactive (or visible or invisible) depending on a range of factors such as:

- The current user's group membership - if you do not have permission to add records, or if new records must be added from another part of the system, the Plus button will appear inactive, or greyed out.
- The current workflow position:
 - what operation you are currently completing?
 - is what you are trying to do valid given the current circumstance?
- The value of a selected tab or item list item - when adding or deleting a record, the type of record that is added or deleted depends upon the selection in the section tabs and the item list.
- The value of a field or fields - when editing records, the value of a field may prevent you from doing a particular thing?

Figure 2.9. Example of button states depending on context



The Add record button - enabled



The Add record button - disabled

Other aspects of the system are also context aware, but on a broader scale. Depending on the group memberships of the current user, some tabs may not be shown, or may be restricted to read only access.

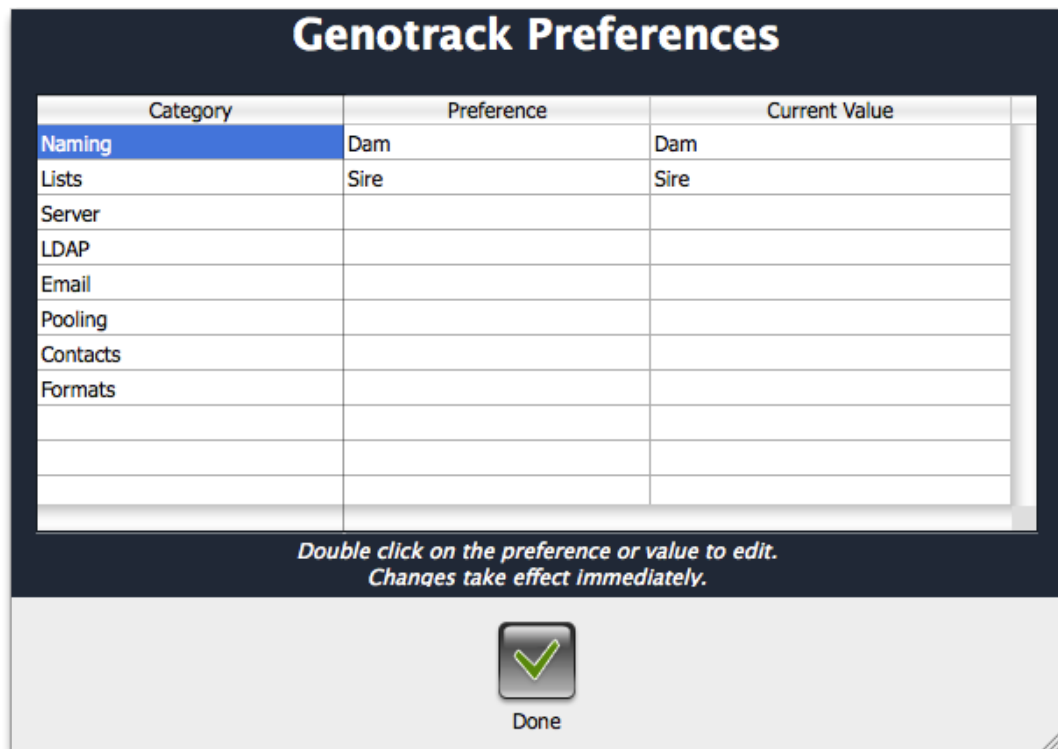
The contextually aware interface controls are intended to ensure that the correct workflows are followed, and that all prerequisite data is present before an operation is completed.

Chapter 3. System Preferences

The Preferences option (found in the Admin menu) allows additional settings and customisations to be made to the system.

Naming

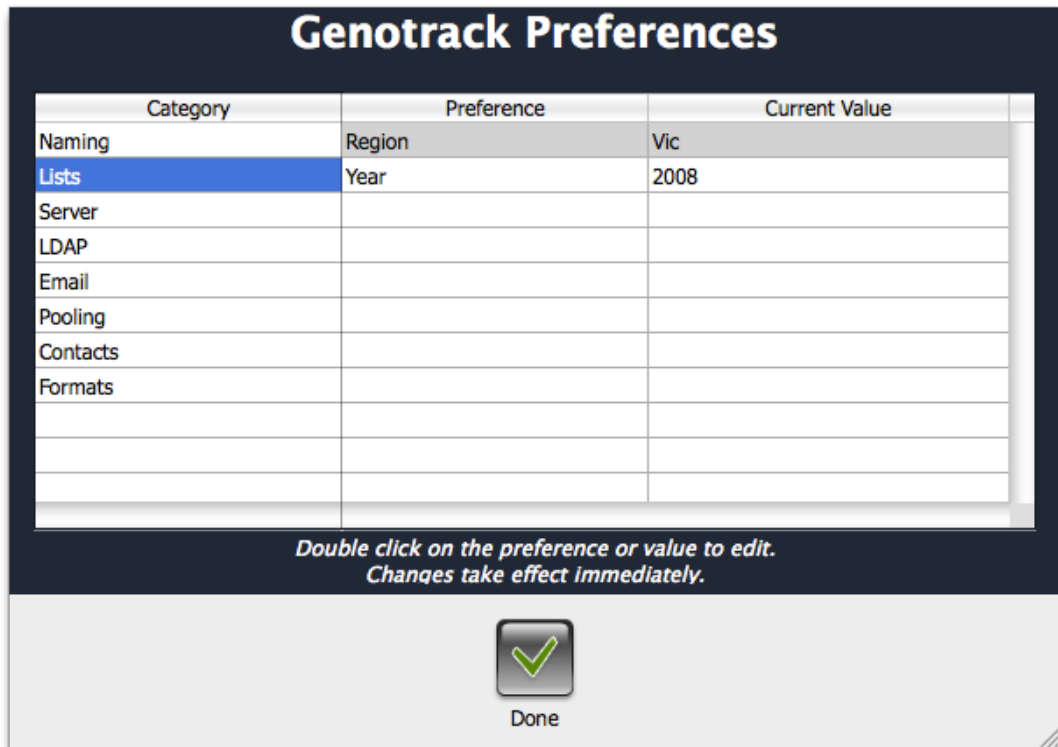
The Naming preferences allow you to change some of the terminology used within the system. This mechanism allows us to allow you to use your preferred naming conventions within the interface of Genotrack itself.



The Naming preferences dialog

Lists

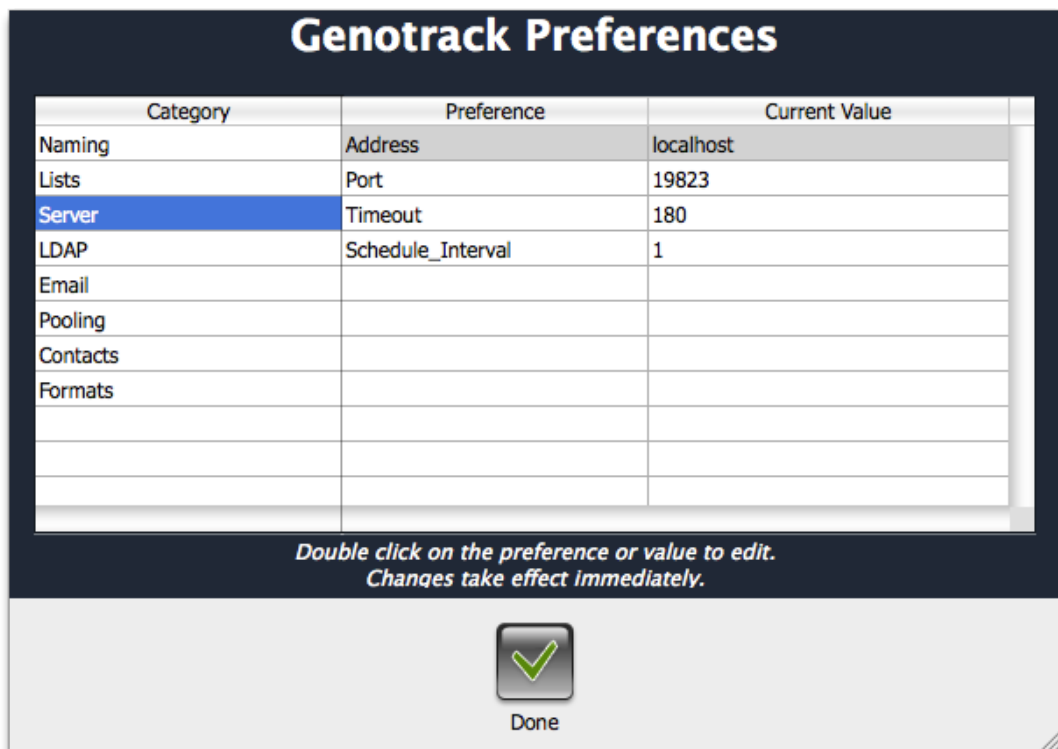
The Lists preferences allow you to specify which lists you wish to use to build the various popup menus relating to the animals within Genotrack.



The Lists preferences dialog

Server

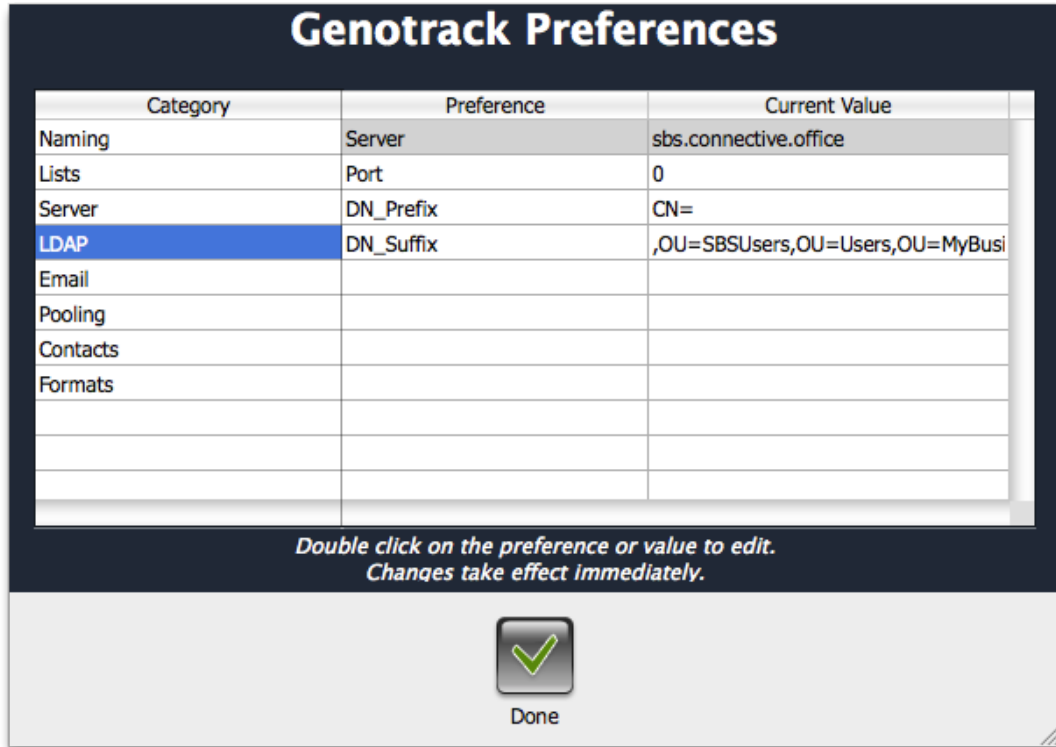
The Server preferences allow you to specify the server IP address, Port and client timeout values. You can also specify the Schedule Interval. This number represents the number of minutes between scheduler checks - ie: how long the system waits before checking if any scheduled tasks need to be performed.



The Server preferences dialog

LDAP

The LDAP preferences allow you to specify the IP address of the LDAP server you use, the Port number, and the DN_Prefix and DN_Suffix which are used to build the UID which can be authenticated against your LDAP server.



The LDAP preferences dialog



Building a UID

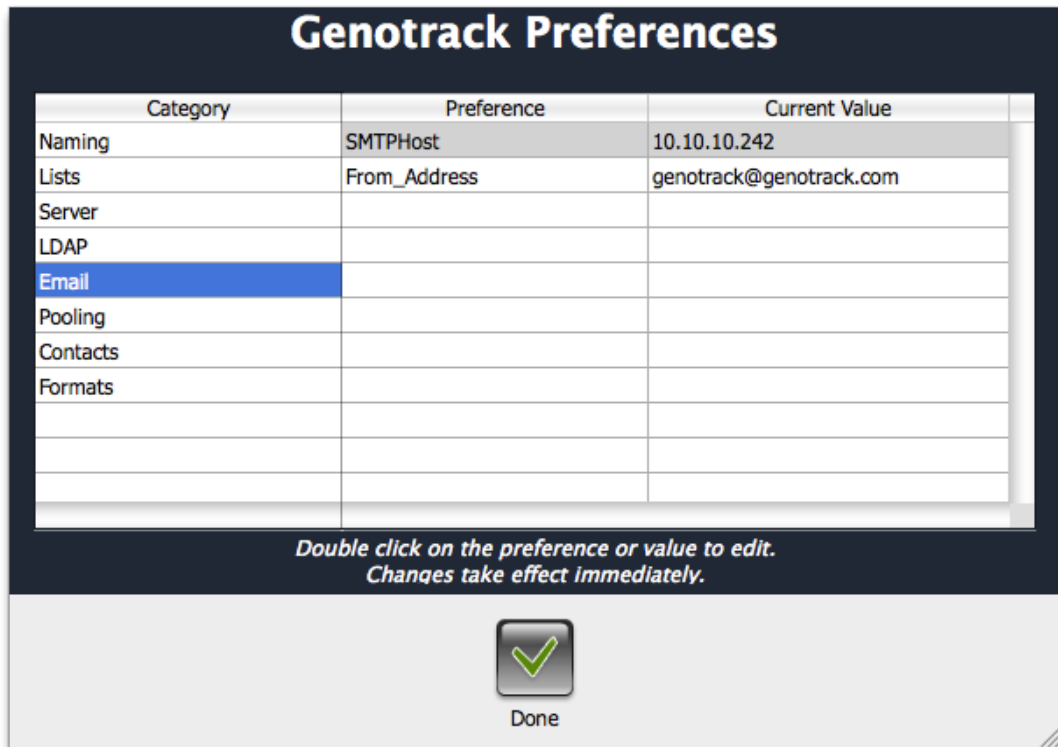
The UID which is authenticated against the server is constructed by simply combining the DN_Prefix, the LDAP_ID from the person record, and the DN_Suffix.

Note that the suffix may begin with a comma - this is not a typo, the comma is necessary to signify the end of the username and the beginning of the remaining information required in the UID.

Email

The Email preferences allow you to set which SMTP Server will be used by Genotrack to send email from within the system. This value needs to be set correctly to allow the system to send emails on task completion, or for the scheduled reporting system.

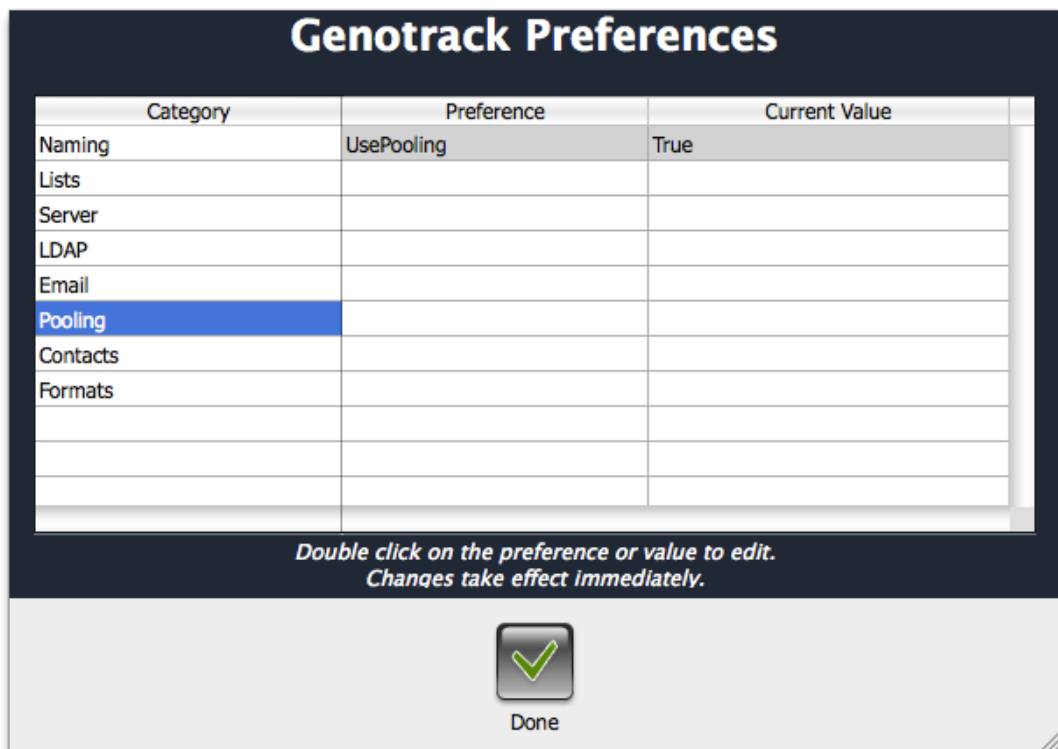
You can also specify which email account the email is sent from. Email is sent from that address, on behalf of the user or person in question.



The Email preferences dialog

Pooling

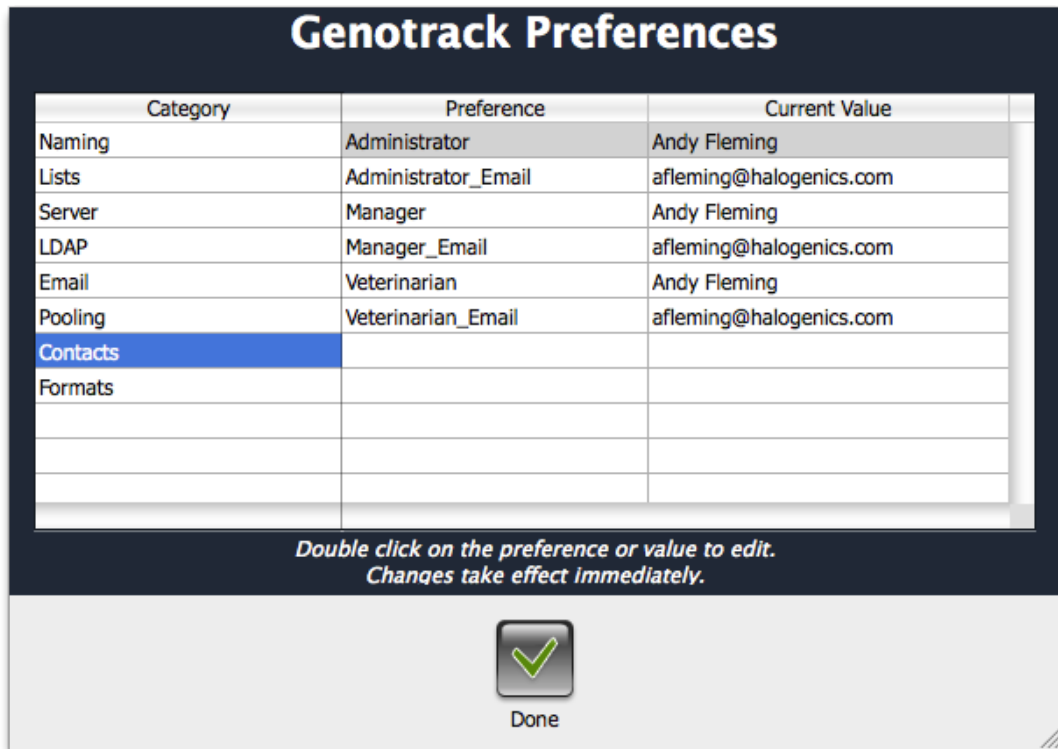
The Pooling preferences allow you enable or disable whether the pooled licencing system is used. If UsePooling is True, the system will be used. If False, the pooling system will be disabled.



The Pooling preferences dialog

Contacts

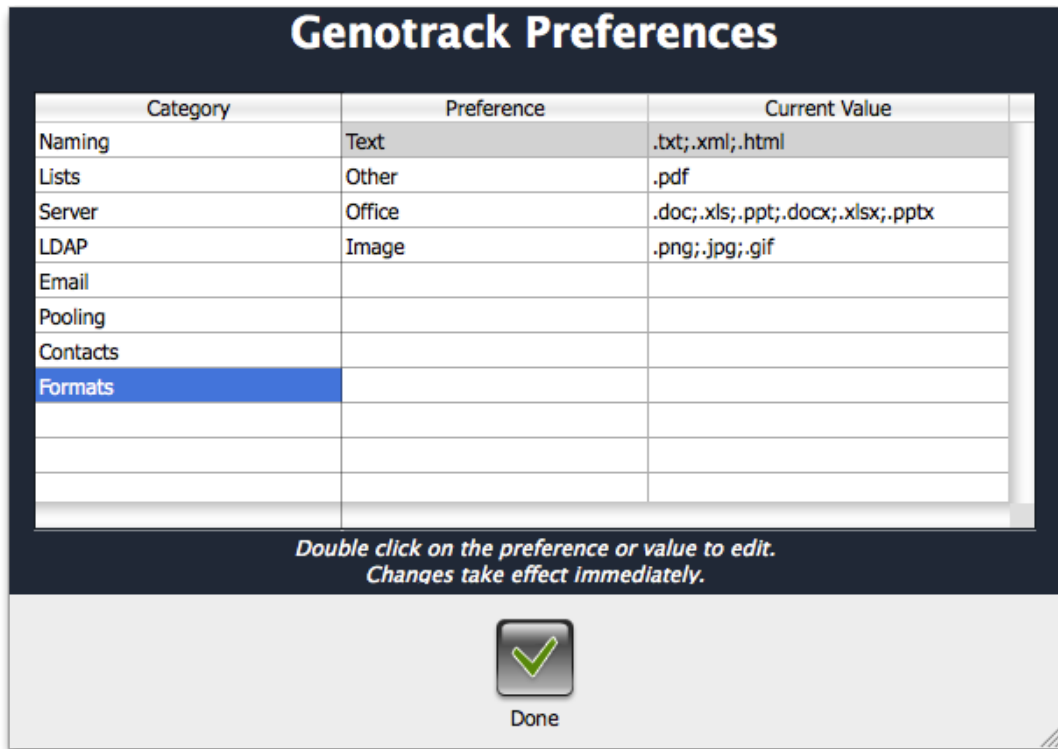
The Contact preferences allow you to specify who is responsible for managing the system, or should be contacted when various events occur.



The Contacts preferences dialog

Formats

The Formats preferences allow you to add additional file formats which will be supported by the system for attached documents. In this way, you are able to use custom file formats that may be created from particular instruments, programs or tools you're using elsewhere in your workflow.



The Formats preferences dialog

Chapter 4. Main Window Operations

The main window is used to set system level information, which can then be utilised by any colony within the system. This system level information includes operational information like users, contact information and access restrictions, housing locations and specification, customisation information such as lists and preferred nomenclature and animal related information such as Strains, Colonies and Projects.

"My" Tab

The first tab of the Main Window is the user's personalised tab. This contains items which the current user has been specifically granted access to, either by group membership or manual access. For most users, this will be the tab used to access the majority of their data, including the available colonies.

My Current Tasks

The My Current Tasks tab lists the tasks assigned to the current user, in order of priority. Overdue tasks are shown first, then current tasks then pending tasks in ascending date order.

Sublists of the My Current Tasks selector can be used to select Completed tasks that were assigned to you, or All My Tasks

Current Tasks I Set

The Current Tasks I set tab lists the tasks the current user requested of other users (or themselves). As with My Tasks they're sorted in priority order.

Sublists of the Current Tasks I set selector can be used to select Completed tasks you set for someone else, or All Tasks I Set

My Animals

My Animals will show you a list of all the animals which have been allocated to you, or allocated to a group of which you have membership. This selector will be modified in future revisions of Genotrack as we work towards a full researcher oriented view of the data.

Sublists of the My Animals selector include:

1. Personal Allocation - a list of all the animals specifically allocated to you (the current user).
2. Group Allocation - a list of all the animals allocated to a group which you're a member of

My Colonies

A list of colonies the current user has access to, either by access being specifically granted to them by the Breeding Administrators, or by Group Membership. If the current user is a Breeding Administrator, all colonies will be displayed.



How do I see my animals?

To view your animal data (and matings, litters, weanings etc) you double click on the colony you're after from the My Colonies tab

My Strains

A list of strains the current user has access to, either by access being specifically granted to them by the Breeding Administrators, or by Group Membership. If the current user is a Breeding Administrator, all strains will be displayed.

My Projects

A list of projects the current user has access to, either by access being specifically granted to them by members of the Ethics group, or by Group Membership. If the current user is a member of the Ethics group, all projects will be displayed.

Reports

A list of reports for the current user. If the current user is a member of the Administrators group, all reports will be displayed.

Schedules

A list of schedules for automated reporting for the current user. If the current user is a member of the Administrators group, all schedules will be displayed.

My Details

Provides access to the person record for the current user, allowing them to update their contact information (or other information, depending on group membership).

Strains

A strain record contains all the information about a particular strain of animals - names, dates, species, type of strain, genetic background and nature of the strain and any allelic variations, associated phenotypes, construction and maintenance methods and much, much more. You must have a strain record in the system to create a colony, and all animals must be associated with a colony - so the Strain information is very important.

Adding a new strain



Access restrictions apply

This feature is only available to members of the Breeding Administrator group

1. Click the Strains tab
2. Click on the Add button - a new strain record will appear. You then need to fill in a minimum of the required information, and once that is done you can save the new Strain.

Required information for a Strain record

There is a large amount of information which can be entered in the strain form. While most of it is not compulsory in terms of strict checking by the database, there is a certain minimum level of information which you must enter, as it is required elsewhere in the system. The Required Information fields that you must complete for a strain are:

- Full Name
- Short Name
- Species
- Strain Type
- Strain Subtype
- Contact Person

The Strain Type and Strain Subtype are used to automatically categorise the strains into the subselectors on the strain list. It is the Generation Type and Generation Method on the Alleles associated with the strain which have a larger impact - these will determine which genotype expression options are available when assigning genotypes to the animals in colonies of the strain.

Colonies

The Colonies tab displays the existing colonies for the strain.



This is the ONLY place in the system you can add a colony

This is to ensure that colonies are always correctly associated with a strain.

Genetics

The Genetics tab has information regarding the background strain and the control strain (if any). You can also add alleles to the strain at this point

Alleles

You can associate any number of alleles with a strain. Each allele entry records genetic and chromosomal information about a particular genetic variation, including its type, how it occurs (generation method), how it is inherited and what (if any) phenotypic information is associated with each version of the allele. You can also add information regarding any typing protocols used to determine which version of the allele is present in an animal.



Setting alleles determines the available genotype expressions

The type and generation method of the allele determines the available genotype expression options for animals in colonies of the strain in question. This association helps ensure that the correct nomenclature is used for animals of a particular type, improving the consistency of data entry.

Required Information for an Allele record

The Required Information that you must complete for an Allele are:

- Allele Symbol
- Allele Name
- Gene Symbol
- Gene Name
- Generation Method (and Generation type for the Targeted and Transgenic generation methods)
- Mode of inheritance

You can also add information regarding the expected phenotype of animals with a particular allele.

Phenotype

The Phenotype tab allows you to enter general phenotypic information for the strain. This should be used to record a more general phenotypic description of the strain in general, rather than the specific details shown by animals with particular allelic variations - which should be recorded in the allele record(s).

Construct

The Construct tab records information regarding the original construction of the strain, and the method used.

Management

The Management tab records information relating to the day-to-day maintenance of the strain, such as particular procedural, husbandry or observational requirements recommended to keep colonies of these strains running.

OGTR

You can also link to the colony any OGTR Dealings which may be relevant.

Screening

The Screening tab allows you to detail any screening protocols which can be used with the strain in question.

Restrictions and References

The Restrictions and References tab is, as its name suggests, for recording any restrictions on the distribution of the strain. This could be:

- Internal restrictions - such as not wanting to share animals of a strain which may involve proprietary intellectual property
- Legal restrictions - such as requiring a contract or materials transfer agreement before distribution
- Technical restrictions - such as the strain containing technology which prevents it being redistributed without additional procedures being followed (eg: Cre-lox technology requiring a written agreement)

Literature references for relevant papers, books or sites can be included here to provide additional information.

Picture

The Picture tab allows you to insert a picture of a typical member of the strain.



You can also attach pictures using the Documents Tab

If you wish to add additional pictures to the strain, you can use the Attach Document... button on documents tab to add pictures or movies.

Access

The Access tab allows you to grant or revoke permission for an individual person to view and edit the strain information.

Notes

The Notes tab allows you to attach general notes to the strain to record additional information which does not fit into any of the other available fields.

Documents

The Documents tab allows you to attach general other files to the current record. Each document is date and time stamped when created and modified, and you are able to save the file back out of the system to another computer from the document window. This means you can store all the relevant information with the record, giving you a central resource for all the relevant information, observations or results.

Colonies

A colony is an instance of a strain. If the strain is the theoretical entity, the colony is the physical instance of the strain. As a colony is associated with a strain, all animals within a colony have the characteristics detailed by the related strain record - the information from the strain is inherited by colonies of that strain.

You may have more than one line of the same strain stored in different locations - these could be considered different colonies of the same strain. Generally speaking, if the locations are geographically separated, or there are significant differences between the environments, you would consider these two (or more) distinct colonies.



Two colonies or not two colonies - that is the question...

You may have C57BL/6 mice in two facilities in your institution, or two distinct areas within a facility. You would consider these separate colonies of the C57BL/6 strain.

On the other hand, C57BL/6 mice of the same line in adjacent rooms of the same facility may be considered the same colony, as the conditions are not distinctly different. It is up to you to make the distinction as to when two groups of animals would be considered separate colonies.

Adding a new colony



You can't add a colony from here!

As discussed in the previous section, adding a colony must be done from the strain form.

You must also be a member of the Breeding Administrator group to add a colony to a strain.

Required information for a Colony record

The colony information deals with a group or colony of animals at a specific location, and the specifics of that location. The Required Information that you must fill in are:

- Current state
- Primary Location
- Primary Contact
- Lead Tech
- Source

Data

The Data tab allows you to enter basic details regarding the current colony, including what state(s) the colony is in. You can nominate a contact person, lead technician, and specifics of when the colony was

considered established (and discontinued for a legacy colony), as well as colony specific information regarding tagging methods and the licence under which the colony is maintained.

You can also specify what the next animal in the colony will be numbered. If you wish to override the numbering sequence for the colony, click the Set Next... button and follow the prompts.



Save yourself some typing!

You can opt to assign default values for project, primary use, impact and procedure.

These values will be automatically set for all animals which are subsequently born to this colony.

For homozygous colonies, you can also set default genotypes for the colony. As with the project, use, impact and procedure all animals born into the colony will be automatically set with the specified genotype(s).

Location

Alternate Locations

The Location tab allows you to specify where the colony is physically located. In addition to this, you can specify any number of additional "overflow" locations, and the order in which they should be used. If when using the "next available" method of housing, there is a problem with availability at the primary location, the system will check the alternate locations in the order specified in an attempt to find available housing for the animal. Only when all alternate locations have been exhausted will the automatic housing fail and report an error to the user.

If using the manual selection method of housing, only the locations specified as Primary or Alternate locations will be available for you to select a housing unit from.

Storage Locations

You can also specify a number of storage locations for a colony. Each storage location indicates a the preservation method used (eg: cryogenic storage of embryos or sperm, ES Cell line that can be used to re-create the colony) and the location of the material referred to in the preservation method.

Management

The Management tab records details of the recommended production method, the number of pairs required as well as strategies for production and management. Information in these fields is supplemental to that inherited from the strain - only include information which is specific to this individual colony of animals. This allows you to take any environmental considerations of a given location into consideration, as well as colony or project specific requirements such as the number of animals which are required.

You can also specify the default mating type for the colony, which if entered will be pre-populated corresponding popup menu on the new mating form for that particular colony.

Criteria

The Criteria tab lets you specify the criteria which are used within this specific colony of animals to determine when certain standard tasks should be performed. These are:

- The age at which animals should be genotyped.
- The characteristics which determine which animals are set aside as reserved breeding animals.
- The criteria used when setting up matings.

- The maximum time an unproductive mating should be allowed to continue before being stopped.
- The selection criteria for animals to be weaned to stock.
- The maximum age at which animals should be weaned.
- The selection criteria for animals to be culled.
- The maximum age at which animals should be reviewed for the above criteria.
- The maximum number of matings permitted for female animals in the colony.
- The maximum number of litters permitted for each female animal in the colony.

There is also a checkbox, used to indicate whether the criteria entered have been approved by the nominated contact for the colony. That nominated contact can check the box at any time, which will set the approval date. Should any of the criteria be modified by someone other than the nominated contact for the colony, an email will be automatically sent to the nominated contact for the colony requesting that the review and approve the new criteria as soon as possible.

This is to ensure that the technicians are always working with the latest approved set of parameters, to ensure the correct management of the animals.

Environment

The Environment tab lets you record any environmental factors specific to the location of the colony which may be relevant. This could be general information such as caging or feed type, or specific information such as temperature or humidity measurements.

Phenotypes

The Phenotypes tab lets you set a range of phenotypic observations which are of interest in the colony. This allows you to easily specify anatomical, behavioural or physiological observations into a discrete numeric (with unit of measurement if relevant), text or boolean data type.

eg: Tumor Growth - what is the volume/tumor size - mm³

This can improve the speed and consistency of observations, and reduce the instance of "bad" data being entered into the system. It can also significantly improve the collation time for the data, as you are processing a series of discrete responses rather than having to categorize and interpret the responses and observations.

When recorded at the animal level, responses relating to these phenotypes are date and time stamped, allowing you to track the observable characteristics over a period of time.

SOPs & OGTR

The SOPs tab lets you associate which of the established Standard Operating Procedures (SOPs) are available for use within a colony. This allows anyone working within the colony to quickly see what procedures have been approved, and what the correct techniques are.



Not all SOPs are available for Colonies

Only breeding and custom SOPs can be specified at the colony level - project SOPs must be assigned to a Project

You can also link to the colony any OGTR Dealings which may be relevant.

Costs

The Costs tab lets add any additional expenses which are applicable to ALL animals within a colony.

For example, if a particular type of housing or feed is used which is not included in the standard agistment fees, you can add an entry here which can be included in the agistment charge for animals from this colony.

Access

The Access tab allows you to grant or revoke permission for an individual person to view and edit the colony information.

Notes

The Notes tab allows you to attach general notes to the colony to record additional information which does not fit into any of the other available fields.

Documents

The Documents tab allows you to attach general other files to the current record. Each document is date and time stamped when created and modified, and you are able to save the file back out of the system to another computer from the document window. This means you can store all the relevant information with the record, giving you a central resource for all the relevant information, observations or results.

Ethics

Projects



Only members of the ethics group can edit projects

Whilst the Ethics tab is visible to all users, you will not be able to modify or add projects unless you're a member of the ethics group.

Adding a new Project

To add a new project, simply use the add record button when the project tab is selected. You should add a project record for any project which will have animals assigned to it. If the project is not entered it will not be available for selection from the animal project popup menu.

Detail

The Detail tab stores basic information about the project, such as the project number, title, when the project was approved, and when it starts and finishes. You can also specify the benefit focus, purpose and licence for reporting purposes.



The project number may not be a number...

The project number is a text field - it can contain numeric or alpha characters, or a combination of both.

Team

The Team tab allows you to link the individuals who are listed on the actual project approval.

These are the scientific and animal house staff who are entitled to perform work on the project. Note that Team membership does not allow the person listed to update the project information in Genotrack - that is controlled by the Access tab.

Approvals

The Approvals tab allows you to specify how many animals of a particular strain are approved for use on the project. If you wish, you can specify the number of female and male animals. A total is calculated for all strains.

SOPs

The SOPs tab lets you associate which of the established project Standard Operating Procedures (SOPs) are available for use with a project. This allows anyone working with animals assigned to a project to quickly see what procedures have been approved, and what the correct techniques are.

Access

The Access tab allows you to specify who is permitted to modify or update the project information. This refers to the specified person's ability to make changes to a project - not who is named on a project (which is recorded on the Team tab).

Notes

The Notes tab allows you to attach general notes to the project to record additional information which does not fit into any of the other available fields.

SOPs - Standard Operating Procedures

Adding a new SOP

SOPs are essentially a link to a predetermined documented procedural description. The SOP record allows you to categorize the SOP into one of three types:

- Scientific - a scientific procedure requiring ethics committee approval
- Breeding - a general husbandry or maintenance procedure which does not require ethics committee approval
- Custom - details of a technique which does not fall into either of the other two categories

In addition to this, SOPs are given a name, a title, and a URL indicating where the detailed procedural information can be obtained from. The two remaining fields are the date on which the SOP was approved (ie: by the ethics committee) and when the SOP was last reviewed and/or updated.

Scoring Sheets

Scoring Sheets are collections of Signs, and are used to allow rapid monitoring and assessment of an animal's state or condition.

Each Scoring Sheet is a collection of Signs, which you put together. At the animal level, you can assign a score to each of the signs in the sheet, and that sheet is recorded with a date and time, allowing you to compile a report showing how the scores have changed across time, and thus track the welfare or treatment of a particular animal based on the criteria which are of interest to you.

Signs

A sign is a general description of an observable characteristic, and then 4 specific examples of that characteristic ranked from 0 (normal) through 3 (severe).

These signs are then combined into Scoring Sheets, which are simply a grouping of signs.

Licences

Licences track the various relevant licences available within the system. These could be licences to breed animals, licences to perform scientific procedures, or a more specific licence permitting a utilisation of a specific technique or technology.

Each licence allows you to record:

- The licence number or code
- The body responsible for issuing the licence
- The date the licence was issued
- The date the licence is valid from (commencement date)
- The date the licence expires

OGTR Dealings

The OGTR dealings allows you to enter all dealings with the OGTR. These dealings can then be associated with a strain, colony or project to ensure that the information is available to anyone dealing with GM animals.

Each dealing allows you to record:

- The identifier provided by the OGTR for the dealing.
- The category of the dealing (eg: DNIR, NLRD, exempt etc.)
- The type of the dealing.
- The title of the dealing.
- The date the OGTR was notified.
- The date the dealing expires.

People & Groups

People

A person record is used to record information about a person. A person's details may be entered so they're available to be listed as the contact for a strain, colony or project.

The person record also has the ability to act as a user record within the system.



Let me in!

To allow a person to login, the "Account is active" box must be checked on their record.

Without checking this button, the person record will only be available as a contact within Genotrack

Adding a new Person

Contact Details tab

The contact details can be emails or phone numbers. This simply allows you to keep a list of ways in which a person may be contacted outside of the system.



Not all contact information is created equal...

The primary email (located in the top part of the form) is the email address that will be used by the system for communication. While you can enter additional email addresses in the Contact Details tab, those additional addresses are for your reference only.

Group Memberships tab

The Group memberships tab allows you to specify which groups the person belongs to. This, in turn, specifies what access the person has and what functions they can perform within Genotrack.

Relationships tab

Relationships are used to represent how people are related to one another. eg: One person may be the supervisor of another, or the designated backup person should the primary person be unavailable. These relationships are for your reference only, and have no direct impact on the working of the system.

Group Roles tab

Similar to relationships, the Group Roles are used to record additional information about group members. Eg: Supervisor of the Breeding Administrator group, or the primary contact for the . Group Roles are for your reference only, and have no direct impact on the working of the system.

Training & Qualifications tab

Training & Qualifications records record information about additional courses or training that a person may have undertaken. These are for information purposes only, and have no direct impact on the working of the system.

Notes tab

The Notes tab allows you to attach general notes to the person to record additional information which does not fit into any of the other available fields.

Groups

There are two main types of Groups:

- System groups - membership of a System group will grant a person access to additional parts of the system, and will usually grant the person access to additional functionality within Genotrack.
- Custom groups - Custom group memberships allow you to create logical groupings of people.



Don't Delete the System Groups!

Membership of System groups gives a person access to specific hard-coded functions within the system.

Deleting these groups could result in the loss of access to certain parts of the system.

System groups

Admin

Members of the Admin group can create and modify person records, and set basic system parameters such as locations and lists.



Admin Membership gives you EVERYTHING

Membership of the Admin group effectively grants the user full rights and privileges and complete access to all aspects of the system, as they can add themselves to any of the other groups within the system.

Breeding Administrator

Generally assumed to be the people overseeing the technicians, Breeding Administrators (BAs) can create and modify strain and colony records and have full edit access to all animal records in all colonies.

If the Breeding Administrator in question has a primary location set, then they will see all colonies at their location.

Technician

Techs are the "hands on" animal staff responsible for doing much of the day to day work involving animals.

Technicians are able to edit mating, litter, weaning and animal records and associated data, but only within the colonies which they have been specifically given access to by their Breeding Administrator(s).

Researcher

Researchers are scientific staff or general staff who are using animals.

By default, Researchers cannot modify mating, litter, weaning or animal records - if your researchers require this access, they should be given membership of the Technician group.

Genotyper

Genotypers are scientific staff or general staff who are using animals, and who need to enter genotyping information..

By default, Researchers cannot modify mating, litter, weaning or animal records - other than the ability to set and confirm genotypes for animals.

Ethics

Ethics members are usually a small number of people acting as a liason to the local ethics committee.

These people are responsible for overseeing the impact of experimental procedures on animals and the compliance of all users with the wishes of the committee. Ethics users can create and modify projects, SOPs, Score sheets and signs.

Custom Groups

You can also add your own custom groups to the system. Other than logically grouping people for your own benefit or amusement, the most obvious practical use of this would be to create a group of technicians who work in a particular location or with a particular colony. If you assign a task to a group, all members of the group would see the new task on their list when they login. This is an excellent way of ensuring that tasks are attended to in the event that staff are on leave or unexpectedly absent.

Cost Codes

The code code section allows you to enter any cost-codes which need to be associated with cost recover items.

The code codes are hierarchical - you can have a code for a division, then codes for the labs within that division. You can then add codes for researchers within those labs - it's up to you.

To create sub-codes, go to the "parent" code record and click the Add Subcode... button.

Settings

Housing Levels

The customisable housing in Genotrack is a powerful and flexible way of mimicking the real world setup of your facility within the system.

The hierarchical structure of the housing lets you build a virtual model of your housing and locations, and to identify where in that structure animals are actually housed. It's worth taking the time to plan your housing setup, as getting this right in the first place will make the system more intuitive and easy to use.

There are two types of housing levels:

- Structure Levels - the structure levels exist to enable the creation of the hierarchy, and are not available as a destination for colonies or animals.
- Housing Levels - levels with the Housing units are at this level box checked are Housing Levels. Checking this box means that you can specify that a colony exists at this location.

At each level, the environment tab lets you record any environmental factors specific to that level which may be relevant, further adding to the comprehensive profile of environmental conditions available for all animals within the system.

Adding Housing

The setup of a housing structure begins with a single level. In most cases this would be a level representing the overall Institution. Beneath this, you might have multiple campuses, buildings, floors and rooms before you drill down to the actual unit of storage. At that last link in the chain, you tick the Housing units are at this level to indicate that that's where the animals are actually located.

A smaller facility may be simply an Institution and Room number.

Example 4.1. Sample structure - Rack of mouse cages

The Institute --> City Campus --> Animal Facility --> First Floor --> Room A --> Rack 1

In the above example, only "Rack 1" would be designated as a housing level - the others are structure levels used to mimic the "real world" location of the animals.

To build this structure, you would perform the following steps:

1. Add a new housing level and name it "The Institute".
2. Click Add Sublevel to this housing level and enter "City Campus" as the name when prompted. Click Save to close "The Institute" record.
3. Edit the newly created "City Campus" location. Note the Full Location shows "City Campus" as a sublocation of "Virtual Institute"
4. Click Add Sublevel to this housing level and enter "Animal Facility" as the name when prompted. Click Save to close "City Campus" record.
5. Edit the newly created "Animal Facility" location.

6. Click Add Sublevel to this housing level and enter "First Floor" as the name when prompted. Click Save to close "Animal Facility" record.
7. Edit the newly created "First Floor" location.
8. Click Add Sublevel to this housing level and enter "Room A" as the name when prompted. Click Save to close "First Floor" record.
9. Edit the newly created "Room A" location.
10. Click Add Sublevel to this housing level and enter "Rack 1" as the name when prompted. Click Save to close "Room A" record.
11. Edit the newly created "Rack 1" location. As this is where the animals will actually be housed, check the "Housing units are at this level" box.

Once you define a level as a housing level, you will see some additional fields appear on the form. These fields allow you record:

- The type of housing - this is intended to be a general description, such as "Box", "Cage", "Paddock" or "Tank".
- The number of units that are at/in the location (in this case the rack)
- The maximum capacity of each unit.

For example: You may have 100 cages in "Rack 1", with a maximum capacity of 6 animals per cage. These values will be used by the automated housing code to place animals into housing units when imported, weaned, mated or when specifically relocated.

You can then add additional sublevels as required. For example, there may be additional floors within the "Animal Facility", additional rooms within "First Floor" or additional racks within "Room A". To add these, go to the parent level and add a sublevel.

For example, to add a second rack to "Room A" edit the "Room A" record, click Add Sublevel to this housing level and enter "Rack 2" as the name. You should now see both "Rack 1" and "Rack 2" listed as sublevels of "Room A".

This flexible structure means that the system can be expanded as your facility expands - addition of racks, rooms, floors or even entire campuses can be handled without needing to modify your existing data.

Attribute Classes

The attributes classes are a set of predefined lists which are used throughout the system. When you install Genotrack, a large number of these classes and the associated attributes are created for you. We understand that different institutions have differing nomenclature and naming conventions for various aspects of their operations. To help Genotrack better fit your operational model, in many cases you can customise the values in these lists so the names and nomenclatures you see within the system match your organisation.

For example, genotype expression symbols can be changed to use your own custom nomenclature, or to support additional shorthanded symbols. Additional animal species, colony states and many more can be added or customised to suit your preferred terminology, workflow or nomenclature.

Unfortunately, not everything is customisable. Some values have special significance within the system, and there are places where actions are automatically triggered when specific values are set. In these instances, the Attribute Classes will be marked as "read only", and you will not be able to modify or delete the class.

In other places, some or all of the attributes within a class may be marked as "read only". Usually, this is because those attributes have special significance within the program, triggering an action or providing the basis for a calculation or report. Mating types are a good example of this - the type of the mating determines the generation numbers of an animals produced from litters of that mating. If the terminology for the mating types changed, errors may be introduced.



If you're not sure, feel free to ask!

If you are not sure which attributes should be customised, please contact Halogenics support via <support@halogenics.com>

Log

The Log selector shows all user log records. These records are created automatically by the system when records are created, modified or deleted.



Create a log report

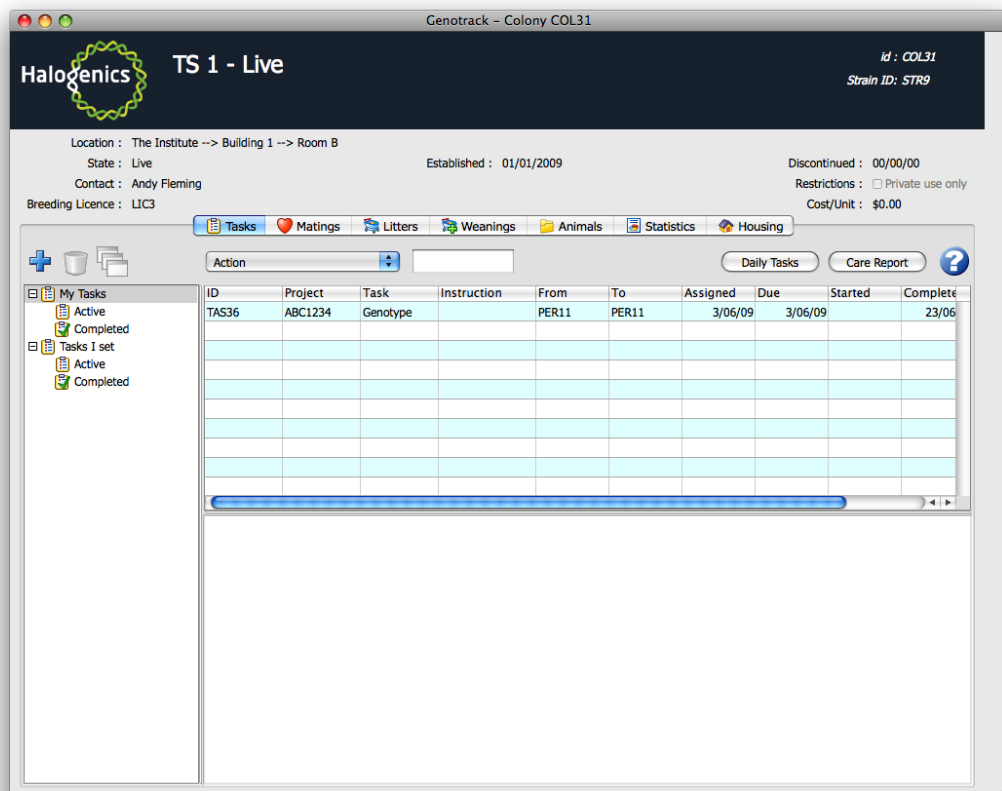
The easiest way to view the log records is to generate a log report.

From the Reports menu select Logging and then either By Record, By Person or By Dates. Answer the prompts and you will get a sorted HTML report showing the log records which match the criteria you've specified - and the report is much easier to read than trying to chase down individual log records!

Chapter 5. Colony Window Operations

While the main window allows you to setup and configure the system overall, it's the Colony window where you will spend most of your time in Genotrack. The colony window is where you deal with Matings, Litters, Weanings and procedures and observations regarding the animals themselves.

Figure 5.1. The Genotrack Colony window



To access the colony window, perform the following steps:

1. Click on the "My" Tab (the leftmost tab with your name on it)
2. Click on My Colonies
3. double click on the colony you're after from the list of your available colonies.

Tasks

Parts of a task

Task Information

The task information records who set the task, the date of the request, the project and possibly the colony the task relates to, and the task type and action. There is room to write a detailed set of instructions, and enter information regarding the date the task must be completed by (due date), when it was started and when it was completed.

Subjects

Subjects are the animals or entities (matings or litters) with whom the task should be performed. Subjects can be one of three entities:

1. Animals - Sample tasks could include requests for genotyping, culling, scientific procedures, creation of or addition to a mating or relocation of the animal to another housing unit or colony. Most tasks relate to animals.
2. Matings - an instruction to stop a specific mating.
3. Litters - an instruction to wean a specified litter.

Actions

Actions can be added progressively as work is completed to provide a history of work done as part of the task. The actions make a note of who does the work and the status of the job once that work is completed.

Notes

The Notes tab allows you to attach general notes to the task to record additional information which does not fit into any of the other available fields.

Adding a new Task

Tasks can be created from a number of places within the system, but usually you will add tasks from within a colony. This makes sense, as it's within a colony where you'll be dealing directly with the animals, and most tasks are animal related. In all cases, the general procedure for adding a task is the same, but depending on the context some information may be pre-populated into the new task for you.

Required Information for a Task

The Required Information for a new task are:

- Who the task is allocated to - This can be an individual or a group.
- Task Requested - you must indicate what the task is that you're setting. In some cases, you will also be required to specify a subtype (eg: for a mating, are you asking for it to be started or stopped?)

Updating a Task

As you progress through the completion of the task, you may wish to update the task to keep the requestor informed. This is done by adding actions.

Adding an action

To add an action, view or edit the task, click the Actions tab then click the Action button. You can enter a description for the action performed, indicate who is performing the action, the date and time and the updated status of the main task.

Cancelling a Task

Under some circumstances, a task that has been requested may no longer be necessary. In this instance, the person who originally requested the task can cancel it. It is NOT possible for anyone else to cancel the task - you can only cancel tasks that you have requested.

Adding an action

To add an action, view or edit the task, click the Actions tab then click the Action button. You can enter a description for the action performed, indicate who is performing the action, the date and time and the updated status of the main task.

Matings

A mating record represents a grouping of animals. Animals can be added or removed from a mating, and this will be automatically tracked.

Any females who have participated in the mating can be listed as the parent of a litter produced by that mating. The mating will only be stopped by setting the stop date of the mating.

Parts of a Mating

Mating Information

The mating information records where the mating is taking place, the type of the mating, the setup of the mating, who setup the mating and the start and stop dates.

You can also enter a mating Label which will be used as the base of the litter labels.

Example 5.1. How a mating label forms the basis of the litter label

If the mating label is ABC then the first litter produced from the mating will be ABC.1. The next will be ABC.2 and so on.

Litters tab

The Litters tab shows any litters which resulted from the mating you're viewing, and a brief summary of the animals that resulted (if they've been weaned or numbered at birth).



This is the ONLY place in the system you can add a litter

As a litter must be associated with a mating.



Fast access to litter information

You can double click on a litter entry to jump directly to the record for that litter.

Events tab

The Events tab lists animal movement events relating to this mating. When participants are added or removed from the mating, an event record is create to note the change. In effect, this shows you the history of the groupings which make up this particular mating,

Past Participants tab

The Past Participants tab shows a list of the animals which were participants of the mating at some point. Current participants will be listed here if they have been removed and re-added to the mating previously.



Fast access to participant details

You can double click on an animal in the list to jump directly to the animal record

Notes tab

The Notes tab allows you to attach general notes to the mating to record additional information which does not fit into any of the other available fields.

Mating Types

The type of the mating is very important. The type of the mating, in conjunction with the generation numbers of the parent animals, will determine the generation numbers of any offspring born to litters resulting from the mating. The mating types are as follows:

Outcross

A mating between two animals or strains considered unrelated. This could be two inbred strains or a member of an inbred strain and a non-inbred animal which has a genetic variation of interest.

An outcross is the initial step in the production of a new strain, or of the outcross-backcross or outcross-intercross systems used for linkage analysis. Offspring produced by an outcross mating are the first filial generation "F1 hybrid" animals. These are then often inbred with each other by Backcross or Intercross (to complete the systems mentioned above).

If both parents/strains are inbred, then the F1 animals will be identical with the heterozygous genotype A/a. If either or both parents/strains are not inbred, then the F1 siblings will not be identical.

Outcross Generation Numbering

As any offspring resulting from this mating type are considered members of a new strain, and are given the generation numbers F1 N0.

Backcross

A mating between a heterozygous F1 animal and one that is homozygous for one of the parental alleles. The backcross is accomplished by mating F1 animals with other members of a parental strain (or back to an actual parent, which is where the term originated).

A backcross is often used for linkage analysis or the production of Congenic strains.

Offspring from a backcross will, according to Mendel's first law, be distributed in roughly equal proportions between two genotypes at any single locus - approximately 50% heterozygous and 50% homozygous.

Backcross Generation Numbering

If both parent animals are F1 hybrids (F1 N0), offspring will be F1 N2 otherwise:

- F# = The same as HIGHEST parental F#.
- N# = The HIGHEST N# of the parents will be incremented.

Intercross

A mating between siblings of the F1 generation, or between two animals that are identically HETEROZYGOUS at a particular locus.

An intercross mating is primarily used for linkage analysis.

Offspring Characteristics Offspring from an intercross will, according to Mendel's first law, be distributed amongst three genotypes at any single locus - 50% heterozygous, 25% homozygous A/A and 25% homozygous a/a.

Intercross Generation Numbering

- F# = The LOWEST F# of the parents will be incremented.
- N# = The same as the LOWEST parental N# (Usually, only animals with the same N number will be mated in an inbred mating).

Incross

A mating between two animals which are identically HOMOZYGOUS at the designated loci, but which are not siblings.

Incross matings are primarily for maintenance of strains of animals which are inbred or carry particular alleles of interest.

All offspring from an incross mating will have the same homozygous genotype identical to present in both parents.

Incross Generation Numbering

- F# = The LOWEST F# of the parents will be incremented.
- N# = The same as the LOWEST parental N# (Usually, only animals with the same N number will be mated in an inbred mating).

Inbred

A mating between two sibling animals of the same inbred strain.

Inbred matings are primarily used for the maintenance of strains of animals which are inbred or carry particular alleles of interest.

At F20, any subsequent offspring are considered "inbred", meaning they are genetically homogenous and homozygous at all loci. At F20, statistically, 98.7% of the loci in the genome of each animal will be homozygous. This is the operational definition of inbred. From F20 the level of heterozygosity will fall off by 19.1% with each subsequent generation, until at F60 and beyond, offspring are considered 100% homozygous and genetically indistinguishable from all siblings and close relatives.

Inbred Generation Numbering:

- F# = The LOWEST F# of the parents will be incremented.
- N# = The same as parental N# (which are the same, as they're siblings).

Microinjection

The microinjection mating type is used to indicate which animals are involved in the DNA or ES Cell microinjection to produce genetically modified animals, even though this is not a "traditional" mating.

Microinjections are primarily used for the construction of a new genetically modified strain.

Microinjection Generation Numbering

Animals produced from microinjections are set to F0 N0.

Mating Setups

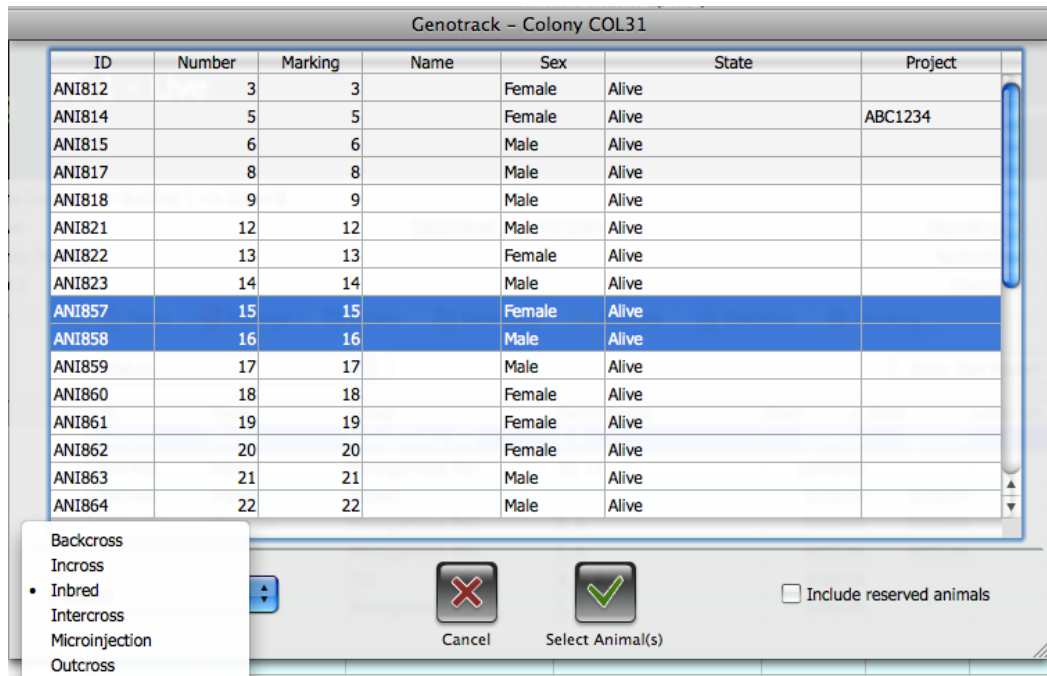
The system recognizes three mating setups by default:

- Monogamous Pair - one female, one male
- Trio - two females, one male
- Harem - multiple (more than two) females, one male

Adding a new Mating

Matings must be created by selecting the Matings tab then clicking the Plus button and following these steps:

1. You will then be presented with an animal selection dialog displaying the available animals in the current colony.



If the animals you wish to mate are already reserved (eg: a task was set marking the animals as reserved, or you are using Reserved Breeders) then you can check the Include reserved animals button to show both available and reserved animals

2. Highlight the animals you wish to mate.
3. Check/Select the mating type from the popup in the lower left hand corner.
4. Enter a label for the mating (optional).
5. Click Select Animal(s).

Once you've clicked Select Animal(s), the animals will be automatically moved from their current housing to the next available housing unit for the current colony and will have their state and status set to Reserved - Mating

Required information for a Mating

The mating information must include certain information to enable other related functions to work correctly. The Required Information that you must fill in are:

- Mating Type
- Mating Setup (this will be filled in automatically in most cases based on the number of animals involved)
- Start date

Stopping or Updating a Mating

The mating system is designed to allow you maximum flexibility. You can add and remove participants and the mating will continue until you specifically end the mating by setting the Stop Date

In the event of adding a participant, or removing or killing a participant the Past Participants tab will be updated to show when the animals were added or removed.

Removal of a participant

Removing a participant can be done in one of two ways:

- To remove a participant from a mating, open the mating record, select the animal you wish to remove and click the Remove Participant(s) button. You will be prompted to select the destination housing unit for the animal you're removing.
- Relocating the animal using any of the methods available from the Animal detail form. The system will recognise that the animal being moved is part of a current mating, and will update the mating accordingly.

Marking one (or more) of the participants as dead

If an animal has died or is killed, the mating will be updated to reflect the new grouping, and show the deceased animals as past participants.

Adding a participant

The only way to add a participant to a mating is by opening the mating record and clicking the Add Participant(s) button.

Clicking this button will present the animal selection dialog. Once you've selected an animal (or animals), the existing mating will be updated to include the new animal, and an even record created to show when the animal was introduced to the mating.

Stopping a mating

The only way to stop a mating is by entering a Stop date for the mating. Please note that while this will mark the mating as complete on the date you entered, the animals will not be automatically separated. You must remember to relocate the animals to ensure no accidental pregnancies occur.

Litters

The litter record records information relating to the offspring produced by a mating.

The litter specifies the Dam (mother) and Sire (father) of the offspring, and provides details of the genetic background of those animals. If there are multiple female participants in the mating, you will need to indicate which female carried the litter. Once the parents are specified, the Filial and Backcross generation numbers of the litter offspring will be displayed.

By default, the litter will be labelled as [MATING LABEL].## where ## is the sequential number based on how many litters have been produced by the mating. You can change the default label if you wish.



You can't add a litter from here!

As discussed in the previous section, adding a litter must be done from the Mating form.

Required information for a Litter

The litter information must include a minimum of the following information:

- Birthdate - the date the litter was born.
- Dam

- Sire (this will be filled in automatically, as there's only one male in a mating)
- Total born - how many animals were born in the litter.

Parts of a Litter

Litter Information

The Litter information records the date the litter was born, litter label (based on the mating label), the parent information (Dam and Sire), who recorded the litter, the generation numbers of the offspring, and information regarding the animals born to the litter. This includes:

- Total Born - how many animals were born in the litter.
- # Stillborn - how many animals were stillborn
- # Culled - how many animals were culled due to medical reasons (such as illness or deformity) or behavioural issues such as fighting.

You can also indicated the reason for the culling via the corresponding popup menu.



Add your own reasons

Like most popup menus in Genotrack, you are able to customise the available options for the cull reasons. Your system administrator can add, remove or modify the available selections from the Attribute Classes section of the Settings tab.

- # Discards - how many HEALTHY animals were discarded as they were unsuitable under the criteria specified for the colony. It is assumed that this animals would otherwise have survived to weaning. They were not culled for medical reasons, but were discarded simply because they were unsuitable (eg: wrong genotype).

You can also indicated the reason the animals were discarded via the corresponding popup menu.

- - how many female animals were removed prior to the litter being weaned.
- - how many male animals were removed prior to the litter being weaned.
- - how many of the animals have been identified as female when the litter was recorded.
- - how many of the animals have been identified as male when the litter was recorded.
- - how many of the animals have been identified as being homozygous when the litter was recorded.
- - how many of the animals have been identified as being heterozygous when the litter was recorded.

Many of these values are used to calculate the colony production statistics.

There is also a radio button which indicates whether the system should Create animal records at birth or Create animal records at weaning. See the next section for an explanation of this function.

Animals born in litter tab

The Animals born in litter tab shows a list of the animals which were born in the litter. This information will not be available until the animals have been weaned.



This is the ONLY place in the system you elect to wean animals from a litter

This is to ensure that the weaning is associated with the correct litter.

Notes tab

The Notes tab allows you to attach general notes to the litter to record additional information which does not fit into any of the other available fields.

Create animal records at birth

Generally speaking, the individual animal records are created when the animals are weaned. This is to prevent the creation and allocation of numbers to unnecessary records - such as animals which were stillborn or discarded as they were of no use (according to the criteria set for the colony). It is possible, however, that under some circumstances you would want records created for every single animal born. If this is the case, selecting the Create animal records at birth radio button (instead of the default Create animal records at weaning) will cause records to be created for each of the animals listed as live. In this case, the # Females remaining and #Males remaining fields will be used to determine the sex of the animals, with any other animals being sexed as "Unknown".

Weanings

A weaning represents the process of removing animals from the litter and separating them into stock units. A litter can be weaned a number of times, until all live animals available for weaning have been accounted for.

Example 5.2. Weaning Example

If 10 animals were born alive to the litter, you may wean 4 on one occasion, then wean the remaining 6 on another occasion.



You can't add a weaning from here!

As discussed in the previous section, weaning animals must be done from the Litter form.



You can only enter the weaning information once

As the process of weaning creates the animal records, it's not possible to retrospectively update or "unwean" a weaning. Once you complete the weaning record, those animals have been accounted for from the litter and are no longer available for weaning.

If you do make a mistake, contact your system administrator.

Weaning Information

The weaning form is a single page, displaying summary information regarding the litter (eg: date of birth, how many animals were born) and providing space to enter the following information:

- The number of animals which died pre-weaning - this figure should include any animals which were found dead between birth and the date of the weaning being entered.
- The number of animals culled - this figure should include any animals which were culled due to medical reasons (such as illness or deformity) or behavioural issues such as fighting.
- The number of animals discarded - this figure should include any HEALTHY animals which were discarded as they were unsuitable under the criteria specified for the colony. It is assumed that this animals would otherwise have survived to weaning. They were not culled for medical reasons, but were discarded simply because they were unsuitable (eg: wrong genotype).
- The number of animals weaned - this figure indicates how many animals were taken from the litter and reallocated into stock units.

For each of these criteria, you have the ability to specify the number of female and male animals that make up each total, and the cause or rationale for the action.



Specifying the sex breakdown is optional

The female and males entered should add up to the total figure provided. It should be noted that the colony statistics, when calculated, will use the total figure as the primary value. For this reason, if you fail to specify the sex breakdown, the totals for female and male animals shown in the colony statistics may not add up to the total shown.

Weaning information for litters numbered at birth

If the litter is numbered at birth, animal records have already been created for all animals recorded as being alive when the litter was recorded. While you can still wean the litter (separating any female, male and "unknown" animals remaining with the original litter into same sex housing units) you are only able to enter a reduced amount of information for the weaning.

As the records have already been created within the system, the Died pre-weaning, Culled, Discarded and Weaned fields (and the corresponding sex totals) are not shown.

This is to prevent any mis-match between the data recorded and the corresponding animal records.

To record deaths, culls or discards, you would go to the animal record itself, as it was created at litter. Similarly, you are able to sex the unsexed animal records at any time after the litter is initially recorded.

Notes

The Notes area allows you to attach general notes to the weaning to record additional information which does not fit into any of the other available fields.

Animals

The animal record holds information relating to an individual animal. This ranges from basic information such as number and sex, through to genotypes, phenotypes, observations, experimental results, environmental factors, cost recovery items and more. By looking at the litter the animal was born to, you can trace back through the mating to the colony and then the strain that the animal came from. This allows you to build quite a detailed picture of the animal, its characteristics and history.

Parts of an Animal Record

Animal Information

A number of identifying features are saved for each animal. These include:

- Generation Numbers - these are obtained by looking at the litter the animal was born in and are displayed as F# N#, representing the filial and backcross generation numbers respectively.
- Litter Label - this is looked up from the litter record the animal came from
- Update Status - have any new notes or events been attached to the animal in the last 5 days.
- Animal Number
- Reference - this is an alternate number, used to allow the animal to be cross-referenced with another system.
- Marked - this records the number the animal is marked with, such as an ear clip number or RFID identifier. This will usually be the same as the animal number, but the additional field is provided to cater for any animals which require remarking due to error, injury or because the animal has been relocated and requires an additional mark to prevent the duplication of a number in the new colony.

- Name - another alternate identifier you can use
- Sex - this will be female, male or unknown. Unknown is used primarily when animals are numbered at birth instead of weaning and the sex may not be able to be determined.
- Description - another reference field you can make use of.
- Animal has been previously used for breeding - this box is automatically ticked when an animal is added to a mating.
- Project - what (if any) project is the animal currently assigned to.
- Primary use - animals are categorised as either Experimental or Breeding animals for reporting purposes. Any animal undergoing a scientific procedure requiring approval by the ethics committee (other than standard approved breeding and husbandry procedures) should be set to Experimental
- AEC Date - when was the project assignment last updated?
- State - is the animal alive, dead, reserved, missing etc.
- Status - the status provides additional information about the state of the animal, and the options available will depend on the assigned state of the animal.
- Animal is allocated checkbox - use to indicate that the animal has been allocated to a researcher or group.
- Date of birth - what date was the animal born, and the current age of the animal.
- Animal is currently checked out checkbox and checkout information - used to indicate that the animal has been taken by someone - usually for a specific procedure - before being returned.
- Death date - when was the animal killed - if this date is not set, the animal is considered to be alive.
- Fate - the fate is a customisable list containing common causes of animal death, and can be used to quickly set an animal that has died or been euthanased with the appropriate values.
- Housing - where is the animal located. This is a complete path showing the housing structure and the housing unit number, type (stock or production) and ID
- Genotype - the current genotype label for the animal.

History

The history tab shows a report outlining all significant events in the animals life in chronological order. The list begins with the animal's birth and litter, then lists all events such as matings, litters, events and procedures impacting the animal.

Genetics tab

The Genetics tab displays information regarding the genetic background of the parents of the animal, and allows you to specify the genotypes of the animal.

Setting a Genotype

To set the genotype expression for an animal, simply follow these steps:

1. Click one of the alleles shown in the box at the bottom of the screen.



Which alleles are shown here?

The alleles shown in the animal record are the ones that have been specified for the parent strain of the colony that the animal is currently in a member of.

If you have an additional genotype of interest which is not shown, contact your Breeding Administrator to get an additional allele added to the strain.

2. Click on the genotype popup above the allele list - you will be able to choose from the approved genotype expressions for the allele generation method and type for the allele you have selected.

eg: For a Knockout allele you'll get knockout nomenclature. For a transgenic allele you'll get transgenic nomenclature and so on.

3. Click Set - you should see the selected value appear in the expression column of the allele list.
4. You can then optionally confirm the genotype by clicking Confirm. This is intended to allow the entry of provisional genotypes, which are then later confirmed either through breeding (such as a test cross) or genotyping.

The advantage of this system is that the genotype expression you're presented with corresponds to the preferred nomenclature for the allelic variation at the locus you've selected. This can be set and customised by the breeding administrators on a strain by strain basis. The technicians and researchers are saved the hassle of selecting the appropriate nomenclature - it's predetermined by the strain and presented in a simple popup.

Deleting a Genotype

To delete a genotype, simply double click on the expression you wish to delete - you will be asked to confirm the deletion. If you confirm the deletion, that entry will be removed from the animal.

AEC Data

The AEC Data tab records information which is utilised in the generation of animal use reports. These include:

- Source - where the animal was obtained from.
- Particular Procedure - which procedure category applies for this animal.
- Impact - what was the impact of the procedure.

Observations & Results

The Observations & Results tab allows you to store observations relating to any phenotypes specified for the colony, and also generic observations. This allows the technicians to quickly respond to the key criteria for the animals, which are available from a convenience popup menu (if set for the colony).

All observations are date and time stamped automatically.

Scoring

This tab allows you to record a scoresheet for the animal. A scoresheet, as explained earlier, is a date and time stamped set of observations, designed to allow rapid tracking of welfare or treatment.

Adding a Scoresheet

1. Click the Add Score Sheet... button.

id : SCA22
sheet_id : SHE2
animal_id : ANI2374

Cancel Save Record All Signs

Scored by : Andy Fleming Change Operator... Created : 04/10/2010 2:52 PM Modified : 00/00/00 12:00 AM

Sign	Score	0	1	2	3
On Handling - Alert	0	normal	dull or depressed	little response to handling	unconscious
On Handling - Body conditic	0	normal	thin	loss of body fat, failure to g	loss of muscle mass
On Handling - Bodyweight	0	normal weight and growth	reduced growth rate	chronic weight loss >15% C	acute weight loss >10% chr
On Handling - Breathing	0	normal	rapid, shallow	rapid, abdominal breathing	laboured, irregular, skin blue
On Handling - Dehydration	2	none	skin less elastic	skin tenting	skin tenting & eyes sunken
On Handling - Eyes	0	normal	wetness or dullness	discharge	eyelids matted
On Handling - Faeces	0	normal	faeces moist	loose, soiled perenium OR e	running out on handling OR
On Handling - Nose	0	normal	wetness	discharge	coagulated
On Handling - Urine	0	normal	?	abnormal colour/volume	no urine in 24 hours OR incc
On Handling - Vocalisation	2	normal	squeaks when palpated	struggles and squeaks loud	abnormal vocalisation
Undisturbed - Activity	0	normal	isolated, abnormal posture	huddled/inactive OR overac	moribund OR fitting
Undisturbed - Alertness/Sle	0	normal	dull or depressed	little response to handling	unconscious
Undisturbed - Breathing	0	normal	rapid, shallow	rapid, abdominal breathing	laboured, irregular, skin blue
Undisturbed - Coat	0	normal	coat rough	unkempt, wounds, hair thin	bleeding or infected wounds
Undisturbed - Drinking	0	normal	increased OR decreased int	increased OR decreased ovi	constantly drinking OR not c
Undisturbed - Eating	0	normal	increased OR decreased int	increased OR decreased ovi	obese OR inappetence over
Undisturbed - Movement/G	0	normal	slight incoordination OR abr	incoordinated OR walking o	staggering OR limb dragging

Actions :

Comments :

4. Enter any actions or comments required, then save the record.

Care Report

The Care Report tab holds any care reports associated with the animal.

Adding a Care Report

A care report is used to track the treatment of an animal which requires medical attention or special care.

Care Report Information

The main section of the care report records the date and time the report was created, where the animal is located, which project (if any) the animal is assigned to, who is making the report, and which researcher is responsible for the animal. The consequence of the condition for other animals at the location and the probability of that consequence are entered, which allows the automatic calculation of a risk factor.

The risk is calculated according to the following matrix:

Table 5.1. Matrix for Risk Assessment

Consequence	Frequent	Probable	Occasional	Remote
Fatal	High	High	High	Medium
Critical	High	High	Medium	Low
Marginal	High	Medium	Low	Low
Negligible	Medium	Low	Low	Low



High Risk assessment results in automatic notification

If a care report is assessed as High risk, the nominated Head Veterinarian (as specified in the Contacts preferences) will automatically be emailed a copy of the care report.

You can also check the Notify regardless of Assessed Risk checkbox to send the report to the nominated vet regardless of the assessed risk.

Additional fields allow for the entry of:

- Symptoms & Condition
 - Symptoms - what are the observable characteristics of the condition.
 - Condition(s) - a detailed explanation of the condition and/or a diagnosis.
 - Consequences - what impact the animal's condition will have.
 - Notify regardless of Assessed Risk - override the default "send for high risk only" default behaviour.
- Contact History - a list of any consultations made in relation to the care of the animal. These include:
 - Who was contacted
 - The date and time of the contact
 - The response of the person
 - Additional detail(s) resulting from the contact.
- Actions & Treatment - a list of treatments and observations with the animal in question. These include:
 - Date & Time of the observation/treatment.
 - The weight of the animal
 - The condition of the animal - is it improving, stable, deteriorating etc.
 - What action or treatment was performed.
 - Who performed the action or treatment.

Environmental Factors

The Environmental Factors tab allows you specify one or more of a set of standard environmental conditions which may be relevant to the animal or colony. This, in conjunction with the environmental data from the colony allows you to keep a record of any environmental factors which may impact on the animal, colony or project.

Animal Specific Charges

The Animal Specific Charges tab allows you to record any additional costs applicable to the animal (eg: a particular test or procedure may have an associated cost which needs to be charged back or accounted for).

The animal specific charges, in conjunction with the colony specific cost recovery items can be added to the standard agistment costs to get a price for the individual animal.

Events

Current Partner(s) listbox - if the animal is currently part of a mating, this will display other participants in the mating.

Events are used to detail other significant events in the animal's life. This could include medical procedures, relocations or other operations which may be of interest to either the researchers or the animal staff. Each event includes the start and end date and time of the event, along with a description and the identify of the person making the entry or responsible for the event.

Notes

The Notes tab, like everywhere else in the system, allows you record any additional information about the animal which does not fit into any of the other available fields.

Documents

The documents tab allows you to import a file into the animal record. The document is kept electronically within the system, and can be saved back out to an external file when required.

The documents tab is an excellent way of storing results, images or other relevant data or information in the format of your choice.

Statistics

The Statistics tab shows a breakdown of the production information for all matings/litters involving the current animal. See the Statistics section for further details

Statistics

The colony statistics provide a breakdown of the animals in the colony.

The following statistics are shown:

Litters	The number of individual litter records in the colony (or in the colony during the dates specified).
Total born	The sum of the Total born field from the litter records for the colony.
Stillborn	The sum of the Stillborn field from the litter records for the colony.
Culled pre-weaning	The sum of the Culled field from the litter records for the colony.
Discarded pre-weaning	The sum of the Discarded field from the litter records for the colony.
Removed pre-weaning	The sum of the Females removed prior to weaning and Males removed prior to weaning field from the litter records for the colony.
Died prior to weaning	The sum of the Died pre-weaning field from the weaning records for the colony. Breakdown into females and males is shown if entered.
Total live for weaning	The number of animals which were/are available for weaning within the colony.

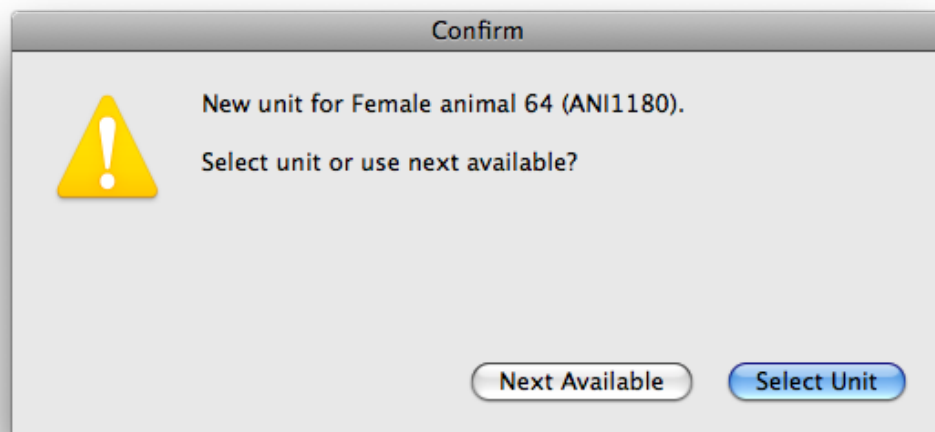
	This is calculated by subtracting the number of animals stillborn, culled, discarded, that died prior to weaning or that were removed prior to weaning from the total number of animals born.
Total weaned	The sum of the Weaned field from the weaning records for the colony. Breakdown into females and males is shown if entered.
Weanings with no live animals	How many of the weanings completed had no animals actually removed into stock cages (ie: all animals processed died prior to weaning, were culled, or discarded).
Discarded at weaning	The sum of the Discarded field from the weaning records for the colony. Breakdown into females and males is shown if entered.
Culled at weaning	The sum of the Culled field from the weaning records for the colony. Breakdown into females and males is shown if entered.
Total viable	Viable females from litter + Viable males from litter + # Healthy Animals discarded (litter and weaning) Healthy discards are included in the viable total, as it's assumed they would otherwise have survived to weaning. ie: They were not culled for medical reasons, but were discarded simply because they were unsuitable for some reason (eg: wrong sex or genotype).
Total Discards	The sum of the totals of the animals discarded at litter and at weaning.
Total Culls	The sum of the totals of the animals culled at litter and at weaning.
Mortality	The total number of animals that died or were stillborn. This number does NOT include culls, it's the death rate without human interaction.
Total Discards	The sum of the Discarded field from the litter and weaning records for the colony.

Housing

The housing tab is a list of the stock and production housing units which are assigned to the colony. Selecting a unit will show the type and current occupants of the unit. This may be useful in cross checking animal locations.

How to House an Animal

The housing system within Genotrack has two mode of operation, both of which are available at any time when housing or relocating animals



Modes of Housing Allocation

Next Available

Selecting Next Available causes the system to select the next available unit from the specified locations for the colony the animal is currently associated with, or is being moved to.



What is an available housing unit?

An available housing unit is one which does not currently have any animals in it.

During normal operations, when the last animal is relocated or removed from a housing unit, that unit is marked as being available for re-use.

This happens in the following way:

1. The next available housing unit from the primary location for the colony will be selected.
2. If no units are available at the primary location, the first nominated alternate location is checked for available units.
3. This process is repeated for each of the nominated alternate locations in the specified order until an available unit is found.

You will be presented with a confirmation dialog detailing the relocation. If no available unit can be found, the operation is cancelled.

Select Unit

Select Unit will present you with the specified locations for the colony the animal is currently associated with, or is being moved to.

ID	Location
LOC113	Test Rack 1
LOC114	Test Rack 2

ID	Label	Occupied?	Production	Label Text	Max. Occupants
HOU774	34	<input type="checkbox"/>	<input type="checkbox"/>		
HOU775	35	<input type="checkbox"/>	<input type="checkbox"/>		
HOU776	36	<input type="checkbox"/>	<input type="checkbox"/>		
HOU777	37	<input type="checkbox"/>	<input type="checkbox"/>		
HOU778	38	<input type="checkbox"/>	<input type="checkbox"/>		
HOU779	39	<input type="checkbox"/>	<input type="checkbox"/>		
HOU780	40	<input type="checkbox"/>	<input type="checkbox"/>		
HOU781	41	<input type="checkbox"/>	<input type="checkbox"/>		
HOU782	42	<input type="checkbox"/>	<input type="checkbox"/>		
HOU783	43	<input type="checkbox"/>	<input type="checkbox"/>		
HOU784	44	<input type="checkbox"/>	<input type="checkbox"/>		

Include Occupied Units

Cancel Select Housing

Method of Housing Operation

1. Select the desired location in the upper part of the dialog
2. You will be presented with the available (empty) units in the lower part of the dialog. Click to highlight the desired housing unit
3. Click the Select Housing button to house the animal.

You will be presented with a confirmation dialog detailing the relocation.

Chapter 6. Help & Support

Built in Help

The built in Genotrack Help system is a web portal with a collection of predefined useful links, starting with a link to the support section of the Halogenics web site.

Halogenics Support Portal

The Halogenics Support Portal is an online resource for bug reporting and feature requests. You can browse current and past bugs and feature requests, or get an RSS feed of the latest issues. You also have the option of registering in the portal. Once registered, you are able to submit bug reports and feature requests and track their progress. You can elect to receive automatic emails as the job progresses.

Reporting a Bug

If you believe you've found a bug or problem in Genotrack please let us know! We're constantly working to improve the product and are more than happy to investigate any issues you may have.

To report a bug please go to <http://support.halogenics.com> and submit a feature request.

Feature Requests

Genotrack is a work in progress. We're continually working to develop and improve the system and new features are being added all the time. If there's a feature or capability you'd like to see added to the product, please go to <http://support.halogenics.com> and submit a feature request.

Online Support

Halogenics utilises the ConnectNow technology from Adobe to remotely assist you with your Genotrack installation. If you have a problem that cannot be solved locally or are having difficulty explaining what is happening over the phone, contact Halogenics and arrange a remote assistance session.

Our tech support team member will direct you to <http://connectnow.acrobat.com/halogenics>, where you will be able to login as a guest (there is no need to register - though it's free so you can if you like). Once logged in, you'll be directed to a virtual meeting room. You can then chat to the support team member, and have the option of sharing your screen so the support staff can see exactly what you're seeing.



ConnectNow System Requirements

ConnectNow requires a web browser and the Flash Plugin.

The plugin is free and can be downloaded from Adobe at <http://get.adobe.com/flashplayer/>

To share your screen, a free additional plugin is required - installation of this plugin will begin automatically if you attempt to share your screen.

Chapter 7. Reports

New reports are continually being added to Genotrack. If you have a report or a set of information you're regularly producing, please contact Halogenics or lodge a feature request through the support portal at <http://support.halogenics.com>.

The Reports Menu

Colony Access Report

This report lists all colonies within the system and lists who has access to them.

Location Reports

Census by Unit

This report shows all housing units in the specified location, with a list of the current occupants of each unit.

This report would be ideal for cross-checking what you have on the rack with what Genotrack says you should have on the rack.

Census by Colony

Similar to the Census by unit report, this report shows all occupants of all housing units associated with the specified colony, at all locations.

Status

This report examines all designated storage locations within the system and calculates their current capacity. Locations approaching capacity are colour coded to highlight which locations may require attention.

Tasks

This report shows all tasks which are due or pending for the specified location.

Stocktake Reports

All Strains/Lines

The stocktake report shows the current status of all storage locations within the system. The number of stock and production units is shown, along with the number of units currently occupied by matings and litters. The number of units in use is shown along with the maximum for each location, with color coding used to quickly identify those locations which are at or approaching capacity.

GM Lines

A subset of the All Strains/Lines report, showing only GM Strains and Lines.

Non-GM Lines

A subset of the All Strains/Lines report, showing only Non-GM Strains and Lines.

For Location

Similar to the All Strains/Lines report, but restricted to those Strains/Lines located at the specified location.

For Project

Similar to the All Strains/Lines report, but restricted to those Strains/Lines listed on the specified project.

Tasks

Today's Tasks

The daily task report shows all tasks due today, and any tasks which are new but are not yet marked as being underway.

Completed

This report prompts you to enter the number of days to report on, then produces a report listing all the tasks completed during the specified period.

Animal Use

Animal Use vs Approval (All Projects)

This report shows the approved totals for all projects in the system, and a current usage total and percentage for each strain/line listed on the project.

Victorian

Animal Use Return (All)

The Victoria Bureau of Animal Welfare (BAW) requires that animal use for scientific purposes be reported. This report produces the return in the format specified by the BAW for all projects.

Animal Use Return (Project)

The Victoria Bureau of Animal Welfare (BAW) requires that animal use for scientific purposes be reported. This report produces the return in the format specified by the BAW for a specified project.

Logging

By Record

View all history/log entries relating to the specified record ID.

By Person

View all history/log entries relating to the specified person.

By Dates

View all history/log entries between the specified dates.

Colony Based Reports

Daily Tasks

The daily task report shows all the tasks due for completion today (including those past due but still incomplete), and for each of the next 5 days to aid with job assignment and prioritization.

Care Report

The Colony Care Report shows all care reports lodged for the current colony in chronological order.

Animal Specific Reports

Animal History

The animal history report is identical to the information shown on the History tab of the animal record, and outlines all significant events in the animals life in chronological order. The list begins with the animals birth and litter, then lists all events such as matings, litters, events and procedures impacting the animal.

Care Report

You can display an individual care report and all associated consultations and treatments from the care report form.

Appendix A. System Requirements

Mac OS X

- **CPU:** Power PC G5 or better (Intel only for server)
- **OS Version:**
 - Mac OS X 10.4.11+
 - Mac OS X 10.5.8+
 - Mac OS X 10.6.4+
- **RAM:** 512 MB (1 GB recommended)
- **Screen Resolution:** 1280x1024 or better

Windows

- **CPU:** Pentium III or better
- **OS Version:**
 - Windows 7
 - Windows Vista SP2
 - Windows XP SP3
 - Windows Server 2003 SP2/R2
 - Windows Server 2008 SP2/R2*
*excluding "Server Core" options
- **RAM:** 512 MB (1 GB recommended)
- **Screen Resolution:** 1280x1024 or better

Flash Player

Genotrack and online support from Halogenics requires Adobe Flash Player version 10.1 or later.

<http://get.adobe.com/flashplayer/>

References:

Online Books

Mouse Genetics - Concepts and Applications. Silver, Lee M. <http://www.informatics.jax.org/silverbook/> .

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