

TierBase Handbook

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Getting Started

Welcome to TierBase, a relational database designed to manage many aspects of work with experimental animals in the environment of a research institute or breeding facility. We are confident that this software will rapidly establish itself as an important tool to help you cope with the ever-increasing demands of animal breeding and experimentation. We also would like to take this opportunity to thank you for choosing TierBase.

Package contents - Software components

The TierBase CD contains the following files:

- the TierBase structure file. On Macintosh, it is a single file with a name consisting of the database abbreviation and the version number (eg. TM388). On Windows, the structure file consists of 2 files named as above but with the extension 4DB and RSR (eg. TB388.4DB and TB388.RSR).
- the TierBase data file. On Macintosh, it is a single file with the name as above but with the extension "data" (without quotes). On Windows, the data file consists of 2 files named as above but with the extensions 4DD and 4DR.

- a readme file (in the doc folder) describing the installation procedure. This is for the busy database administrators that don't want to read the installation procedure described in this handbook.
- a database handbook (in the doc folder) describing in detail how to use TierBase. In case you didn't know, that is what you are reading now.

System requirements

Hardware:

The server and client computers can be either Windows or MacOS. It is recommended that a relatively fast computer is used as the server. Also, the amount of RAM strongly affects the speed of the system. The more the better. In order to achieve a good stability of the system, it is important that other, potentially problem-causing, software is not installed on the server. The best solution is a dedicated server running only the database software. The server and clients should be configured as follows:

Windows

CPU: PC with a Pentium III or higher.

Operating System: Windows 98, 2000 or XP.

RAM: 128 MB minimum (256 MB or more is recommended)

Monitor: 17" SVGA, 256 Colors minimum

MacOS

CPU: Power Macintosh with a Power PC 601 Processor minimum

Operating System: MacOS 8.6 or higher

Ram: 128 MB minimum (256 MB or more is recommended)

Monitor: 17", 256 Colors minimum

Software:

If you plan to use TierBase as a single user installation, you will need the 4D runtime software. If you will be using TierBase in a server / client configuration, you will need to install 4D Server software on the server and 4D Client software on each computer that will access the database. In both cases, the software you install must be compatible with the operating system of the computer.

Licences:

If you have purchased a single user TierBase license, you also have a license to use the runtime software. If you have a TierBase server license, you automatically have 2 client licences. This means that 2 client computers can simultaneously connect to the server. If you anticipate that more users will need to simultaneously connect to the server, you must purchase more TierBase client licences. Clients can be added at any time.

Network Requirements:

If you plan to use the server/client configuration for TierBase, you will need to connect your client and server computers. There are a variety of possibilities to do this but you should have at least 1Mb/sec transfer speeds (10Mb/sec is recommended and 100Mb/sec is even better). ISDN (usually 64Kb/sec) is too slow for most users.

Database Backup Requirements:

It is absolutely necessary that precautions are taken to avoid permanent data loss. This includes software to backup the database. A 4D Backup Module is supplied as part of the Server software. Alternative backup software or strategies is recommended.

Estimated risk of data loss

At the moment, we are not able to exactly quantitate the risk of data loss while using TierBase. However, after intensive use of TierBase at the Max-Planck-Institute for Immunobiology in Freiburg since 1999, we have never

needed to recover data from a backup and we have no evidence that data has been lost due to software or hardware malfunction.

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Installing the database

Installing the database is as easy as copying the files from the CD to your hard-drive. If you are using Windows, don't forget to check that the read-only status of the files is removed.

Installation of the 4D Software is done according to the instructions on the 4D Installation CD. If you are using server/clients, you will need to copy the client software to each client computer.

Entering initial data (customising) in the datafile

If the TierBase data file has just been installed, the Database Administrator (DbA) and the Breeding Administrator (BA) will have to enter several pieces of information specific for the institute where TierBase is installed. This should be done before anyone else begins using the database. If you are not the DbA or BA, no one will get angry if you read this section but you can also skip it.

To customize the datafile, follow the steps listed below in the order given. This is just a brief check-list of what needs to be done. For more details, consult the DbA and BA chapters in the handbook.

- login as the database administrator (DbA)
- if the TierBase license number has not been entered, do it now
- create user accounts so that other users can login (user -> new user account)
- if desired, specify the SMTP server address so that TierBase can send e-mails

- create various lists needed throughout the database. These lists include; departments at the institute, species of animals used, etc. Note: the BA can also create or modify these lists so if you cannot fill out the lists, ask the BA to help you.
- enter the database preferences for the institute address, animal ethics officer (AEO), and BA.
- logout
- login as the breeding administrator (BA)
- create or complete the lists started by the DbA. The lists include, animal source, immunization method, strain characteristics, cause of death, etc.
- create at least one breeding environment
- create preferences for breeding, job and projects
- create animal line records
- create colony records
- check the job type records supplied with the data file for possible changes. The job type records store the prices which can be used for creating invoices
- logout
- login as the animal ethics officer (AEO)
- create at least one animal ethics project and specify who has access to the project
- logout

That's it! You should now be able to start using TierBase. Enjoy !

Overview of TierBase

Introduction

TierBase is divided into two major functional areas called the Job area and the Analysis area.

Job area

The Job area provides access to the lines and colonies stored in the database. It also is the place where jobs are created. These jobs serve as a means of communication between the animal technicians in the breeding facilities and the “end users” of the animals. This includes animal ordering, setting up or stopping matings and many other types of jobs that are created by the “end user” and sent to the animal techs. The breeding and use of animals for experiments is also registered in animal ethics projects in the Job area. Several other functions are also integrated such as invoicing and messaging. (see below for a more detailed description of the functions available).

Analysis area

The Analysis area stores detailed information about the animal breedings. It is here that matings with resulting litters and offspring are stored. Thus, it is possible to analyze the results of the breedings and to keep track of important information such as animal genealogy, breeding productivity, phenotypic and genotypic characteristics, experimental results for individualized animals etc. The matings can be analyzed in the following ways:

- an overview of the current matings can be created showing how many litters have been produced, the number of male and female offspring, litter size, etc.
- a frequency analysis of genotypes for a given set of matings. For example, with a couple of simple steps, it is possible to calculate the frequency of homozygotes resulting from matings with heterozygote parents.
- a genealogy analysis to create a family tree is also possible.

For each colony, it is possible to use only the job area of TierBase without the analysis area. This is usually done for colonies where it is not necessary to register individual offspring from the breedings. A more detailed description of the analysis area can be found in the **Generic user** chapter.

Some of the information stored in TierBase includes:

- A list of animal lines including their names, phenotype, breeding information, etc.
- A list of colonies maintained at the institute including owner, persons responsible, location of the colony, etc.
- A list of animal ethics projects (abbreviated in this Guide as projects) approved by the authorities for work with experimental animals. Information stored with each project includes the types of experimental procedures, the number of animals allowed, as well as the names of users registered with the project.
- An ordering system which allows users to submit a variety of jobs to the breeding facility. This permits users to electronically communicate with animal technicians who may not be so accessible because they work within a restricted area of the breeding facility.
- The kinds of jobs include:

ordering animals for experimentation
ordering animals for shipment outside of the institute
ordering of staged pregnant females for embryos
ordering of tissues from specified animals
start or stop a mating
eliminate animals
eliminate a line
cryopreservation
embryo transfer
primary and secondary immunizations
isolator breeding
transgene or ES cell injection
microbiological tests
extra jobs

- Invoices can be created for services rendered by the breeding facilities.
- Animal ethics officers can easily analyze the use of animals for a given project or a given line. This can be done for a given time span for individual users or for the entire institute.
- A list of information relating to the use of TierBase and to animal work at the institute is available "online".

TierBase Groups and responsibilities

TierBase provides functions to its users appropriate for which group they belong to. A user cannot belong to more than one group at the same time. The groups are:

Database Administrator (DbA)

- is responsible for creating new user accounts with a password
- is responsible for putting users into appropriate user groups
- creates and maintains data lists which are used throughout the database. These include lists such as: departments, species, cause of death, etc. These lists are usually configured when TierBase is first installed but can be modified at any time.
- is usually responsible for creating backups of the data.
- is responsible for collecting reports of database bugs and user suggestions.

Animal Technician Group

Animal technicians are responsible for processing jobs submitted to the breeding facilities. They have access to all active colonies at the institute and can create jobs in the name of any user in the database.

Breeding Administrator Group (BA)

- is responsible for adding new lines and colonies to the database and for keeping the lists up to date.
- is able to inactivate a line or colony so that no ordering can take place if problems with the line arise.
- can create cage and animal inventory records.
- can create invoices for completed jobs.
- can create new job type records
- can specify the cost of each job type.
- can analyze the use of lines for a given time period or according to department.
- processes certain types of jobs that require special attention before being redirected to the breeding facilities. This includes jobs for sending or receiving animals, immunizations, cryoconservation and others.

Animal Ethics Officer Group (AEO)

- is responsible for maintaining the animal experimentation project list, including who is registered for each project to work with animals.
- can deactivate or activate projects.
- can create summaries of animal use for a project or for the institute.
- can activate or deactivate a user for animal ordering.
- can add, modify or remove users, treatments and animal sums from projects.
- can modify the list of treatments and associated severity (see Project description).

Generic User Group

This group consists mainly of the people like scientists and laboratory technicians who use TierBase to:

- place job orders, for example to order animals for an experiment
- enter and analyze breeding results for a colony they are responsible for
- provide other users with access to animal colonies for which they are responsible
- project leaders can keep track of the use of animals within their projects

Online Information

Within TierBase, it is possible to store a variety of information which might be helpful for users of TierBase. By selecting the File -> Info menu item, you might see a list of topics pertaining to the use the database. Details about each topic can be viewed by double clicking on the record in the list. Topics available might be things like institute-specific requirements for ordering or sending mice, or perhaps the ear marking system used in the breeding facilities. The topics can be created either by the breeding administrator (BA) or by any other user. With time, this info list can store a wealth of tips and guidelines for working with the database or with experimental animals.

Conclusion

This ends the overview chapter. To get a more detailed description of various functions, consult the appropriate chapters in this handbook. Don't forget to have a look at the chapters describing tips, occasionally asked questions (OAQ), and the glossary.

Generic User Group

Introduction

The generic user group (hereafter called users) are typically scientists and laboratory technicians. They use TierBase to order animals for experimentation, to view animal lines available at the institute and possibly to store and evaluate a detailed list of the breedings and resulting animals from their colonies. They also can use TierBase to keep totals of experimental animals used so that periodic reports for governmental or other authorities can easily be generated. This chapter describes the functions available to the generic user group. At the end of the chapter, a list and description of the menu commands available to this group is provided.

Responsibilities / Access

Generic users are responsible for maintaining the line information for their lines. This information includes various aspects of the phenotype such as anatomical, behavioral changes, breeding requirements, method of construction, genetic screening, etc. The access of users to colonies is restricted in TierBase. If a user is listed as being responsible for the colony, or if they are owner of the colony they automatically have access to it. In

addition, the owner or responsible scientist can give access for their colonies to other users in the database. Users cannot order animals from a colony unless they have access to the colony. If a colony should be accessed by all users, the breeding administrator (BA) will designate the colony as being a “common” colony.

Navigator

When logging in, users are presented with the navigator window.

Navigator

scientist
nielsen

Welcome to TierBase+

privB environme grp

Create New Job

- order: order Animals
- tissue: order tissue sample (blood, tail biopsy, etc)
- eliminate: eliminate animals from an existing mutant strain
- Start Stop: start or stop a mating from an existing mutant strain
- other: other Jobs

Line

- Mutant WT: show mutant or wild type lines present in the institute
- surplus: display surplus animals for selected lines

Message

- S-E S-TB: Send E-Mail (S-E) Send in TierBase (S-TB)

Analysis

- analysis: analyze breeding results
- Q_find: quick animal find using its ID

Exit TierBase

This window contains several buttons that activate the most frequently used functions. This includes things like creating a new job, viewing colonies at the institute, or examining the breeding results for a given colony. Additional functions can be accessed using the menus at the top of the screen. Before describing some of these functions, it is important to be aware of the concept of the breeding environment. If you look carefully in the upper right hand corner of the navigator, you will see a small boxed area entitled environment

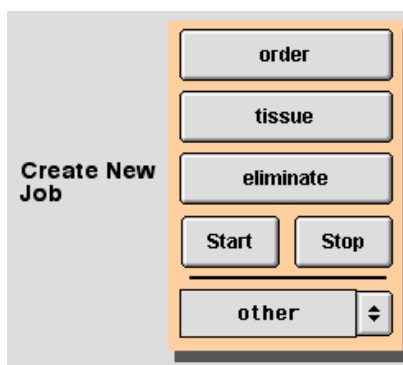


This area displays the currently selected breeding environment. This means that if an environment is selected (SPF/OG in the example above, A), only the jobs or colonies for that environment will be displayed. You can change the environment by using the popup button on the right (B). By clicking on the word “environment” (C), you can clear the current breeding environment. The result is that jobs from all environments will be displayed. The small box labelled “priv” (D) is the private colony toggle. If this is clicked, only the private colonies and jobs will be listed. Private colonies are useful in the following situation. If scientists are breeding their own animals in an area of the institute, the animal techs do not need to get jobs for these animals since the scientists have direct access to the animals. However, the governmental authorities require that all breeding and experimentation is registered and reported. The problem, then, is to find an easy way to also keep track of the use of these animals. That is where private colonies come in. You can take advantage of the job-logging capabilities of TierBase to keep track of animal use. The BA will setup the colony and mark it as private breeding stock. The scientist can create order, elimination, mating start etc. jobs for this colony and immediately mark the job as completed. In this way, the animals are registered in TierBase but the animal techs. don't even see the jobs since they are for private colonies.

Jobs

Submitting a job

Animal use is registered in TierBase through the creation of jobs. Creating a job is fairly straight forward. The navigator has a group of buttons with an orange background that contains the common jobs.



Simply click the corresponding job button and you will get an input form where you can enter the information needed.

There are several conditions, which must be met before a user can submit a job to the breeding facilities of the institute:

- The user must have first entered an institute-internal account number in his/her user record. This is required for invoicing (see “Costs” on page 33).
- To order animals, the user must have access to the colony (see “Responsibilities / Access” on page 16). If the colony has been specified as a common stock, all users have access to the colony.
- To order animals, the user must have access to an approved project (see “Animal Ethics Projects” on page 32).

Once the job is submitted to the corresponding breeding unit where the animals are being breed, the animal technicians working there check whether the animals can be delivered on the specified day and if so, they change the

job status to running. If the scientist checks the job status and sees that it is running, he or she can assume that the animals will be delivered on the specified day. The animal techs can reject the job if it cannot be executed. They also can specify a reason for the rejection. If the email function in Tier-Base has been activated by the database administrator, the scientist automatically gets an email saying that a job has been rejected and can react accordingly. Jobs are processed on a first-come-first-served basis. When a job is completed, it is marked as such.

You can only modify (or delete) your own jobs if they are not completed. You cannot change the status except if you modify a rejected job and resubmit it, in which case it is marked as submitted again. Only animal techs can change the status of a job, but not if it is already completed.

When an order is placed for staged, pregnant females, it is quite often the case that the number of actual plug-positive females does not match the number ordered. Thus, if you have submitted such an order for embryos, one day before the delivery date for your order, the animal tech will note the number of pregnant females and you will be asked to confirm the order. You confirm the order by:

- select the order in the order output form.
- click the modify button at the bottom of the form.
- click the confirmation button on the second page of the order form (only visible when a confirmation is asked for).
- click the save button.

If you do not confirm the order, the animal tech will not deliver the ordered animals.

Keep in mind that the animal tech checks the orders early in the morning for the delivery day. Thus, you should confirm an order on the day before the delivery

Job types

TierBase has a variety of job types built in. Each job has an associated abbreviation which is used throughout the database. With time, you should become familiar with these abbreviations. They include:

TABLE 1.

	Job Type Description	abbreviation
1	animal maintenance for holding costs	am
2	animal orders, mice, rats, rabbits, fish	ao
3	tissue orders (blood, tail biopsies, etc)	tio
4	start a mating for a particular strain	mst
5	stop a mating for a particular strain	mSP
6	eliminate animals from a given strain	elm
7	cryopreservation of a strain	cc
8	cryopreservation with strain elimination	cce
9	embryo transfer of a strain into the SPF	et
10	send animals within EU	send
11	send animals outside EU	send
12	primary immunization of rabbits, mice	imnz
13	secondary boost of rabbits	imnz
14	order of staged pregnant females	pf
15	isolator breeding	cage
16	cage maintenance of mice outside of the SPF	cage
17	cage maintenance of rabbits	cage
18	cage maintenance in SPF	cage
19	transgene or ES cell injection	tgES
20	eliminate a strain	elmStr
21	receive animals from other EU institutes	recpt
22	receive animals from other non-EU institutes	recpt
23	microbiological test	mictst
24	extra jobs	xtra

Most jobs require input for the user account number, colony desired and job processing date. Additional information is also required depending on the job type. For example, a scientist is planning an experiment which requires 5 BALB/C mice. The scientist would login to TierBase and create an animal order job using the form displayed below.

Animal order job (ao) and (pf)

21.11.2003 21:49:01		Animal order form		Order ID 28769 page 1 ao
User Name *	<input type="text"/>	UserID 0	Lab	
Project Name *	<input type="text"/>	ProjectID 0	Tel:	
Account # *	<input type="text"/>	<input type="radio"/> Mouse <input type="radio"/> Rat <input type="radio"/> Rabbit		
Line name *	<input type="text"/>	<input type="text"/>		
#	<input type="text"/>	<input type="text"/>		
colony	<input type="text"/>	animal source	<input type="text"/>	
room	<input type="text"/>	<input type="text"/>		
Animal numbers (, or -)		<input type="text"/>		
		<input type="button" value="check"/> <input type="button" value="disp"/>		
Quantity *	<input type="text"/> Females	<input type="text"/> Males	<input type="text"/> unimportant	<input type="text"/> total
Age <input type="radio"/> d <input checked="" type="radio"/> w *	<input type="text"/> min.	<input type="text"/> max.		
Order Type	standard <input checked="" type="radio"/>	embryos <input type="radio"/> no Superov. <input type="radio"/> + Superov. <input type="text"/> 0.5 days (from vag. plug)		
Use:				
Organ :	<input type="checkbox"/> Bone Marrow	<input type="checkbox"/> Spleen	<input type="checkbox"/> Blood	<input type="button" value="clear use"/>
	other: <input type="text"/>			
Treatment : *	category <input type="text"/>			
	duration (days)	<input type="radio"/> <1	<input type="radio"/> 1-7	<input type="radio"/> 8-30 <input type="radio"/> >30
Notes to caretaker	<input type="text"/>			
<input type="button" value="next page"/>		<input type="button" value="print"/>		<input type="button" value="cancel"/>

The order contains information about who is ordering the animals, which project the animals belong to, how many animals are needed and when and

where they should be delivered. After being created by a scientist, jobs are processed by the animal technicians in the breeding facilities. The status of the job changes with each stage in the processing, going from submitted to received, to running, to completed. By checking the status, all users know at any time what the state of their jobs is. If a job is rejected, the user is notified and the reason for the rejection is given.

Job cloning

If you would like to submit a job which is very similar to one previously submitted, you can avoid having to fill out much of the same job form again by cloning a previous job. This is done by first displaying all your jobs (or animal orders), then selecting the previously submitted job and pressing the "New Order" button at the bottom of the list of jobs. This will take you immediately to the new order form with most of the information already filled in. Please check each entry field to make sure that it is actually what you would like to order.

Standing orders

A standing order can be created for any combination of the 5 working days and for any frequency of weeks from every week to every fourth week. For example, you can specify, that you would like to have 5 Balb/C males every Tuesday. At the appropriate time, TierBase automatically generates daughter jobs based on the entry in the parental standing order job.

Tissue order jobs (tio)

Tissue jobs (tio) are probably the most complicated job in TierBase.

Job 16494

Orderer: _____
Account number: _____

Line # _____
name _____

colony _____ ID# -1

Tissue Samples

date 05.05.2002
time 18:33:44

UserID: _____
Lab: _____
Tel: _____

Mod. by: _____
page print 1 2 Page 1
Status confirm

breeding source _____
room _____

complete job

increment generation

deliv. date 00.00.00 dd.mm.yy
comp. date 00.00.00

sex birth date mating display test results use tissue

female (F) Cw: 17 m=mating # +(N)=wild type retain/behalten (r) (t) tail
male (M) > < C=cage T=transgene eliminate (e) (h) heparin blood
(?) d=defective mate/verpaar (m) (b) blood
0 p=loxP mFemale1_Female2_X_Male:: (e) ear
(o)

number	sex	B-date	charact	parents	genotype	use	comments
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16							
17							
18							
19							
20							
21							
22							
23							
24							
25							

comment >

print

auto print

cancel

save

The typical procedure for creating and processing the job is :

- the animal tech creates the tio job when tail DNA samples are taken from new offspring at weaning. The offspring numbers, sex and birthdate and parents can be entered now, or later by the scientist. A printout is automatically generated. If the birthdate and parents have been entered for the new offspring and the analysis environment is active for the selected colony, the litter and offspring records will automatically be created by TierBase.
- the job gets the status “confirm” and the scientist gets an e-mail saying that a tio job must be confirmed and that tissue sample may need to be picked up.

- the scientist analyzes the tail-DNA samples
- the scientist modifies the tio job by entering the results and specifies the use of the offspring (eliminate, retain or mate). Before saving the job, the “confirm” check box is clicked. This changes the status of the tio job to “running” and sends it back to the animal tech. They process the job according to the “use” column and mark the job as completed.

When the tio job is completed, TierBase automatically creates the necessary elimination and mating jobs as specified by the scientist during the confirmation process.

Elimination jobs (elm)

Elimination jobs are either created by the animal technician group when surplus animals are eliminated from a colony or when a scientist decides that certain animals are no longer needed. You create the job by clicking the “eliminate” button. The elm job input form is displayed and the data is entered. This includes the colony, the account number and the number of animals to be eliminated. If the analysis area is active for the selected colony, the names of the animals must be entered in the area called “animal numbers” (A).

The image shows a screenshot of a web form for creating an elimination job. The form is divided into several sections. Callout A points to the 'name' field containing 'Bob1'. Callout B points to the 'check' button next to the 'animal numbers' field. Callout C points to the 'notes to caretaker' text area. Callout D points to the 'Status' dropdown menu, which is currently set to 'completed'. Callout E points to the 'elimination date' field, which is set to '00.00.00' and includes a 'dd.mm.yy' label.

Line	name	Bob1
	#	0363/1
colony		SPF/06
room		R 6
animal numbers	check	
total animals		0
notes to caretaker		<input checked="" type="checkbox"/> mark offspring
elimination date		00.00.00 dd.mm.yy
Status		completed

The “check” button can be clicked to check if the entered animals are present in the database. If the animals are reserved or dead, they cannot be put in the elimination job. The status of elm jobs created by the animal technicians are automatically set to “completed” (D). For colonies with an active analysis area, the offspring are marked as dead when elimination jobs are completed.

Mating start (mst)

Mating start jobs are usually created by scientists to tell the animal techs to setup the mating but animal techs can also create mst jobs. Filling out the mst input form is fairly straight forward. For colonies with active analysis areas, a mating cage record is created and the offspring are marked as being in a mating when a mst job is completed (not when it is submitted).

Mating stop (msp)

Mating stop jobs are usually created by scientists to tell the animal technicians to stop an existing mating. Filling out the msp input form is fairly straight forward. After selecting the colony, two popups are filled with information which makes it easy to fill in the parental information.

* parents F1,(F2)xM	name (geno)	female 1 []	female 2 []	X	male []	mating # []
mating selection	** parents	mate#	date			
start mat. jobs						
cage recs.						

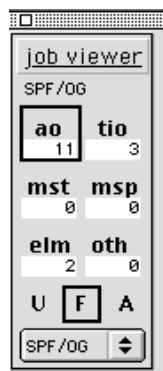
The first popup is a list of recent start mating jobs (A). If the scientist submitted a mst job and the mating was setup, you can select the mst job and the parents will automatically be filled into the msp input form. For colonies with active analysis areas, the second popup is filled with the current mating cage records for the selected colony (B). Selecting one of them automatically fills in the information for the parents. The corresponding mating cage record is marked as discontinued and the offspring records are marked as no longer being in a mating when a msp job is completed (not when it is submitted).

Special jobs

There are several jobs which probably are less frequently used. They are called special jobs and have been placed in a popup menu labelled "other" on the navigator (in the job creation area with an orange background). These jobs include, sending or receiving animals from another institute, cryoconservation, line elimination, immunization and transgenic / knock-out line creation. When the scientist creates one of these special jobs, it usually goes to the breeding administrator first so that it can be checked. This is often necessary, for example, when animals are being sent and airway bills,

custom forms etc. must be filled out. The BA then redirects the job to the animal techs in the breeding facility when all formalities have been taken care of.

Job Monitor



The Job Monitor is a small window which allows the user to display their jobs and easily navigate between different job types. Calling the menu item jobs -> job monitor displays two windows, the Job Monitor window and the job output window.

Clicking on the abbreviations for the job types in the Job Monitor selects and displays that job type in the job window. The lower buttons in the Job Monitor labelled “U”, “F” and “A” specify whether the unfinished, finished or all jobs are to be displayed.

Lines and Colonies

Line and colony creation

A variety of situations can lead to the necessity of adding a new line or colony to the database. Some examples are: whenever a new line is created by ES cell or transgene injection, or when a mutant line is obtained from another institute. A new line and colony must also be created when two single mutant lines are intercrossed to generate a double mutant. A new colony must also be created, for example, when a second breeding unit is opened and breeding of a line is carried out in both the old and the new units. New lines and colonies can only be added to TierBase by the breeding administrator (BA). He/she usually enters only the initial information about the line on page 1 and 2 of the input form. This includes the line name, number, species and the gene-model (see below). As is the case for most input forms in TierBase, the mandatory fields are marked with an asterisk. Then the BA creates a colony for this line. At this point the colony is not

available for use. If e-mail capability is active, the responsible scientist is automatically informed by e-mail when the colony is created. The scientist should then fill in the rest of the information about the line. Keep in mind that if information about the phenotype (eg, mortality, behavior, breeding requirements etc) is entered, you must specify the genotype associated with the information being entered. The genotype (usually heterozygote or homozygote) can be entered in the upper right hand corner of the input form on pages 4-7. When the line information has been added, the BA will activate the colony and it can then be used.

User access to colonies

To order animals from a given colony, you must be given access to the colony . You automatically have access to all colonies where the owner is specified as “common” (or whatever alternative word your BA has designated). For modified-gene lines, you have access if you are either the owner of the colony, the responsible scientist or the alternate responsible scientist. You also have access to a colony if one of these three individuals has given you this access. You can only give or remove colony access to others if you are one of these three people.

To give a user access to one of your colonies, select the “user -> add line access to user” menu item. Then select the user who will be getting the colony access. Finally, select which colony the user will get access to.

You can only order animals from colonies that are marked as "available" by the BA. Colonies lacking the information necessary for maintaining and/or breeding the strain will not be available for ordering. The owner and the responsible scientists can modify all line information for their lines (except the availability and cost factor, see Costs section).

Line gene-models

Most lines used in scientific research institutes are being studied because they carry genetic modifications in genes relevant for the studies. These changes can be of “natural” origin or created by scientists (knock-out, knock-in, transgenic lines, etc.). The type of modification (gene-model) must be specified in TierBase. This is done by the BA during the creation of the line or later by the scientist. Please keep in mind that if the gene-model for the line is specified and then, after working with the line for some time,

the gene-model is changed, your data may be inconsistent with the new characteristic. The resulting analysis of the breedings will be, at best, wrong. Please specify the information for the line gene-model carefully so that you will not have to change it. This means that when you ask the BA to create the line, you must decide whether the line will be listed as a knock-out, a transgenic, etc. The available gene-models are listed in table 2.

TABLE 2. Gene-models

type	genotypes
knock outs and other mutations (point mutations, deletions, etc)	+/, +/d, d/d ??
transgenics	+/, +/T, T/T, T/?, ??
double knockouts or double mutants	+/+ +/+, +/+ +/d , etc.
double transgenics	+/T +/T, etc
knockout + transgene	+/d +/T, etc
loxP-flanked gene with a cre transgene	+/p = the “floxed allele” +/d = the deleted allele +/mix = partially deleted allele ??

View colonies

Users can list all colonies in the database simply by clicking on the navigator button mutant and WT. A list of all active colonies in the database is displayed. Keep in mind that if a breeding environment is selected or the private box is clicked, only the colonies matching these criteria will be displayed. The ability to view colonies can be useful if users are planning an experiment and need animals from a particular line. They can check whether the line exists in the breeding facilities and who is responsible for it. There is one exception to this. It is possible for the BA to specify a colony is being non-public. This means that only those people who have specific

access to the colony will be able to see it. This may be useful in the rare case where a group of users does not want other users to see their lines.

Animal Ethics Projects

In most countries, it is not possible to perform experiments on animals at a research facility without first obtaining permission for the experiments from the governmental authorities. In Germany, there are two common types of animal ethics projects (abbreviated “projects” in this Guide) which require either notification or approval of the impending experiments. Projects must specify, in detail, not only the types of experiments approved, but also the names of the people performing the experiments and their qualifications, the number of animals approved, and the length of time over which the experiments will be performed. All of this information is stored in TierBase. TierBase also keeps a running total of the number of animals used in each project so that project leaders and animal ethics officers (AEO) can follow animal use and apply for new projects in a timely fashion.

Creation and modification of projects

Entry of new projects into the database can only be done by members of the animal ethics group. Likewise, activation, inactivation or modification of projects can also be done only by this group.

Information about a project

Each project leader and user can also view the current project information for which they have access. This includes the running totals and maximum number of ordered animals permitted for the project, when the project expires, etc. At any time, project leaders can also view a summary of animal orders associated with each of their projects for a specified time-span.

Ordering animals with a project

To order animals, you must also have access to an approved animal ethics project. You have access if you are the project leader, an alternate project leader, or have been included in the project application. At anytime, project leaders can view the users with access to their projects. Only the animal safety group can add or remove users associated with a project.

Costs

The Breeding Administrator can create a billing invoice for each account number with a listing of the associated jobs. This invoice bill can be given to each account owner and a copy (without a listing of the individual jobs) can be given to the bookkeeping department of the institute.

The cost of each job is determined by the product of the Job Type cost and the cost factor for the strain ordered. Job Type costs can be viewed by choosing the Job Type Menu. The cost factor for each strain can be found by viewing the details of the line record. For animal orders, the BA or animal techs can also add an additional cost factor to the individual job if needed.

The analysis area

The analysis area stores the information about breedings, litters and offspring for a given colony. Thus, it is possible to analyse the results of the breedings and to keep track of important information such as animal genealogy, breeding productivity, phenotypic and genotypic characteristics, experimental results for individualized animals etc. The matings can be analyzed in the following ways:

- an overview of the current matings can be created showing how many litters have been produced, the number of male and female offspring, litter size, etc.
- a frequency analysis of genotypes for a given set of matings. For example, with a couple of simple steps, it is possible to calculate the frequency of homozygotes resulting from matings with heterozygote parents.
- a geneology analysis to create a family tree is also possible.

TierBase manages the breedings for each colony separately. In this way, it is possible to decide for each colony, whether only the job area of TierBase or both the job and the analysis area will be used. For colonies where it is not necessary to follow the breeding results down to the individual animal, the analysis area can be left inactive. This is usually the case for common lines where the offspring are not numbered.

This section will describe how to use several aspects of the analysis area so that you can begin using these functions. When you feel comfortable with this, you can begin to explore other capabilities available. You should have a look at the menu Table (see Figure 5, “Analysis Area Menu items,” on page 47) which briefly describes all menu commands available in the analysis area. In many cases, there is more than one way to do the same thing. You can try each and decide which is more comfortable for you.

This chapter will describe the following functions:

- communication between the job area and the analysis area
- move to the analysis area
- displaying mating, litter and offspring records
- add a mating
- add a litter
- stop a mating
- switch to another colony

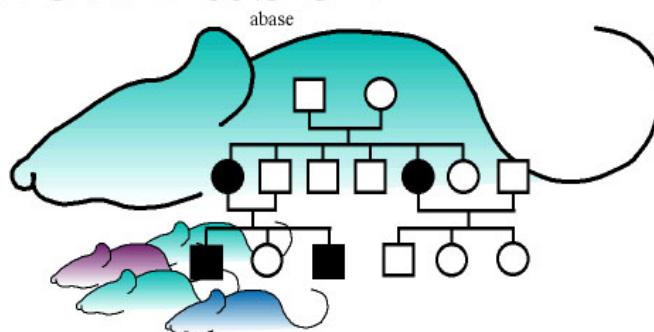
Communication between the job area and the analysis area in TierBase

When the analysis area is active for a colony, there are several instances where information is automatically exchanged between the job area and the analysis area of TierBase. The kinds of communication are listed in the Table below. In all cases, the communication requires that the analysis is activated for the colony in question.

TABLE 3. Communication between job and analysis areas

job	abb	communication
animal order	ao	When the job is submitted, the animals are marked as reserved. This prevents double ordering of the same animal. When the job is completed, the animals are marked as dead.
start mating	mst	The entered parents are checked that they are available and that the sex is correct. If all is OK, the animals are reserved and the jobID is saved with the animal record. When the job is completed, a mating cage record is automatically created and marked as a current mating.
stop mating	msh	The corresponding mating cage record is checked that it exists. When the job is completed, the mating cage record is marked as not current and the parents are marked as available.
tissue order	tio	When a tio job is saved for the first time, the names of the new offspring are checked that they are unique for the strain. Litter and offspring records are automatically created for the listed offspring. If you delete a tio job after it is running, the litter and offspring records are not deleted. You have to do this in the analysis module yourself. All data entry in the tio job such as genotypes or comments, is stored with the individual animals.
send animals	send	Upon submission, the availability of the animals is checked. If all is OK, they are reserved. When completed, the animals are marked as dead.

TierBase+



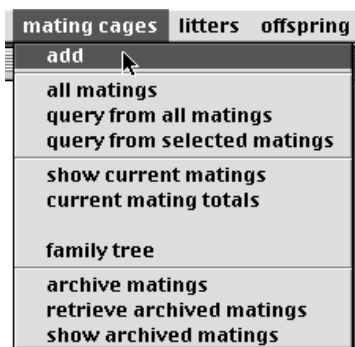
Display mating, litter and offspring records

To display existing records for each of the four record types stored in the analysis area (holding cage, mating cage, litters and offspring) simply click the corresponding menu “all” (eg. mating cage -> all, or offspring -> all). An output form containing the corresponding records will be listed. This list of records can be alphabetically sorted by clicking on the column title in the form (this is true for all titles that are underlined). You can sort in reverse order by pressing the alt key while clicking on the column title. In most cases, if you would like to get more information about a particular record in the list, you can access this information by double clicking on the record. When you are finished with the display, click the done button.

Add a mating

There are two ways to create a new mating in the analysis area. The first way uses the mating input form. The second way uses the Cage Maker (CM).

To create a mating cage directly, call the mating cage -> add menu.



The mating input form will be displayed and you can enter the information for the mating.

mating

bob1
 mat#

start date	<input type="text" value="15/12/01"/>	<input type="checkbox"/> current mating	<input type="text" value="building"/>
stop date	<input type="text" value="00/00/00"/> <small>dd/mm/</small>	<input checked="" type="radio"/> yes <input type="radio"/> no <input type="radio"/>	<input type="text" value="room"/> <input type="text" value="cage"/> 29

♀ female	* name <input type="text"/>	genotype <input type="text"/>			
	born <input type="text" value="00/00/00"/>	<small>dd/mm/</small>	<input type="checkbox"/>		
	name <input type="text"/>				
	genotype <input type="text"/>		<input type="checkbox"/>		
	born <input type="text" value="00/00/00"/>	<small>dd/mm/</small>			

♂ male	* name <input type="text"/>	genotype <input type="text"/>			
	born <input type="text" value="00/00/00"/>	<small>dd/mm/</small>	<input type="checkbox"/>		

comment

first	prev	next	last	cancel	save
-------	------	------	------	--------	------

The parent names are mandatory (marked with an asterisk) If you enter the name of a parent and the animal is already stored in the colony because it is the offspring of a previous mating, the genotype and birthdate are automatically entered in the form. A mating can have either one or two females and only one male. When you are finished, click the save button.

Note: The first time you start entering data in the analysis area for a colony, you will have to start a founder mating with parents that are not in the database. It is allowed to enter "orphan" parents but they will not be displayed in the offspring list. All offspring records must be linked to a litter and mating cage record already stored in the database.

To create a mating using the cage maker, display the living offspring records (offspring -> living offspring). Select the parental animals by single clicking the offspring so that they are high-lighted. If the parents are not listed next to each other, you can select them individually by pressing the command (MacOS) or strn (Windows) button while clicking on the record.

Next, open the Cage Maker window by clicking the "CM" button at the bottom of the offspring output form.



selected	offspring	0
*	cage #	29
	room	
	building	

Mating Holding

If desired, the cage number, room and building where the mating cage is can be entered in the Cage Maker window. If the room and the building has been specified for the colony, they will automatically be entered. You can change the entry if you like. A cage number is automatically provided but you can also change it. Consecutive cage numbers are offered starting with the smallest number. Cage numbers are reused for the line when a cage is deleted.

Click the “Mating” button. You will be asked if you want to create a mating start (mst) job. If you say yes, you will be presented with a mst input form and most of the information will already be filled out. When you save the mst job, the selected offspring will be marked as reserved for the mst job. The mating cage record will not be created until the mst job is completed. If you say no when asked if you want to create a mst job, the mating cage will immediately be created and the offspring will be marked as being in the mating.

Add a litter

TierBase will not let you add a new litter unless it knows which mating it came from. If you add a new litter by calling “litter -> new” menu item, the mating selection dialog will be displayed (see figure below). You can select the mating by entering one or several selection criteria such as the name of the parent, the start date, whether the mating is current, etc. You submit the query by clicking the “select” button. If more than one mating matches the selection criteria, they will be displayed and you can select the mating you want by single clicking on it and pressing the “select” button. If only one

bob1			♀			♂			cur	room	cage
mating			female	geno	born	male	geno	born			
#	start date										
1	19	01/01/99	a4	+/d	01/06/00 00/00/00	a5	+/d	01/06/00	<input checked="" type="radio"/>		0
2	18	01/01/99	a2	+/d	01/06/98 00/00/00	a1	+/d	01/06/990	<input checked="" type="radio"/>		0
3	42	03/06/01	58	+/d	01/01/01 00/00/00	62	d/d	01/01/01	<input checked="" type="radio"/>	R23	19
4	37	03/06/01	51		01/03/01 00/00/00	53		01/03/01	<input checked="" type="radio"/>	R2	13
5	38	03/06/01	33	d/d	01/09/00 00/00/00	34	+/+	01/10/00	<input checked="" type="radio"/>	R2	14
6	14	03/07/00	32	+/d	01/09/00 00/00/00	31	+/d	01/09/00	<input checked="" type="radio"/>	R10	9
7	36	03/06/01	8	d/d	01/03/00 00/00/00	3	+/+	01/03/00	<input checked="" type="radio"/>	Bt3	12
8	66	15/12/01	298	+/d	01/10/01 00/00/00	296	+/d	04/10/01	<input checked="" type="radio"/>		29
9	13	03/07/00	28	+/d	01/09/00 00/00/00	27	+/d	01/09/00	<input checked="" type="radio"/>	R10	8
10	10	03/07/00	25	+/d	01/08/00 00/00/00	22	+/d	01/08/00	<input checked="" type="radio"/>	R10	5

delete mod seq add litter litters overview sort all subS print done sur
H mod siml ofs pg

mating matches the search criteria, the litter input form will immediately be displayed.

An alternative way to add a litter is simply to display the matings, for example by calling “mating cage->current matings”. Then you single-click the mating you want and click the “add litter” button at the bottom of the form.

Independently of how you selected the mating, the litter input form will be displayed and you can enter the data for the litter.

Bob1
SPF/OG

litter/offspring entry

mating: 971 2521 g# 0 2535 g# 0 X 2559 g# 0

31.07.02 +/d +/d d/d

mother

litter: 5199 # born 0 # survived 0

birthdate 05.09.02 females 0 males 0

offspring names

comments

prefix

father

increment generation

create holding cages

max/cage 4

room R 6

building

print cage cards

name	sex	ear	geno	character	analysis	†	comments
1			0	<input type="checkbox"/>			<input type="checkbox"/>
2			0	<input type="checkbox"/>			<input type="checkbox"/>
3			0	<input type="checkbox"/>			<input type="checkbox"/>
4			0	<input type="checkbox"/>			<input type="checkbox"/>
5			0	<input type="checkbox"/>			<input type="checkbox"/>
6			0	<input type="checkbox"/>			<input type="checkbox"/>
7			0	<input type="checkbox"/>			<input type="checkbox"/>
8			0	<input type="checkbox"/>			<input type="checkbox"/>
9			0	<input type="checkbox"/>			<input type="checkbox"/>
10			0	<input type="checkbox"/>			<input type="checkbox"/>
11			0	<input type="checkbox"/>			<input type="checkbox"/>
12			0	<input type="checkbox"/>			<input type="checkbox"/>
13			0	<input type="checkbox"/>			<input type="checkbox"/>
14			0	<input type="checkbox"/>			<input type="checkbox"/>
15			0	<input type="checkbox"/>			<input type="checkbox"/>
16			0	<input type="checkbox"/>			<input type="checkbox"/>
17			0	<input type="checkbox"/>			<input type="checkbox"/>
18			0	<input type="checkbox"/>			<input type="checkbox"/>
19			0	<input type="checkbox"/>			<input type="checkbox"/>
20			0	<input type="checkbox"/>			<input type="checkbox"/>
21			0	<input type="checkbox"/>			<input type="checkbox"/>
22			0	<input type="checkbox"/>			<input type="checkbox"/>
23			0	<input type="checkbox"/>			<input type="checkbox"/>
24			0	<input type="checkbox"/>			<input type="checkbox"/>
25			0	<input type="checkbox"/>			<input type="checkbox"/>

The data you will enter includes the birth date, number of animals born and survived and the number of females and males in the litter. Notice that when

you have entered the number of animals survived and the number of females, the number of males is automatically filled in when you move out of the females field. Also note that when you tab out of the males field, the animal names and sex are automatically filled in. You can continue to fill in information about individual animals in the lower part of the form. You can fill in a column using the value in the selected row (the row number highlighted) simply by clicking on the column heading. This works for all columns whose heading is underlined. When you are finished, click the “accept” button to save the litter. The offspring records will automatically be created.

Stop a current mating

All mating cage records are marked as being current or not. The current matings are of course those matings which currently exist. When animals are no longer mated, you DO NOT delete the mating record, but rather mark it as not current. **DELETING A MATING WILL DELETE ALL LITTERS AND OFFSPRING DERIVED FROM THE MATING.** Be sure you know what you are doing when you delete matings.

To mark a mating as no longer current, call “mating cages -> current matings”. From the list of current matings, select the mating records you want to “stop” by single-clicking them. Call the “modify -> stop mating” menu item. You will be asked whether you want to create a stop mating (msp) job. If you say yes, the stop mating input form will be displayed with most of the information filled in. When you save the msp job, the job is created. The mating cage will be marked as not current when the job is completed. If you say you do not want to create a msp job, the mating is immediately marked as no longer current. If the parents were in a mating that had a cage number stored with it, a window will open asking whether you would like to put the parents in holding cages.

You must specify which of the parent should be put in holding cages and what the cage number should be. If you don't use holding cage records in the database, just click the "accept" button when the window first appears. No holding cage records will be created.

Printing cage cards

Both holding and mating cage cards can be printed, either during cage record creation or later. To print cage cards during cage creation, click the corresponding check box labelled "cg", either in the CM window or on the litter input form. To print cage cards after cage or offspring records have been created, simply display and select the mating cage, holding cage or offspring records and then call the "print cage card" menu item.

Switch to another colony

If you are finished working with a colony and want to move to another colony, you can do this without going back to the navigator. You can do this by calling the menu item `analArea_util -> analyze breeding`. This will again display the list of colonies you have access to and you can select another colony.

Menus and menu items for the Generic User

TABLE 4. Menus and Menu items for the Generic User

Menu	Menu Item	Description
File	about TierBase	displays info about the TierBase creator
	TierBase info	online information about TierBase and the ordering of animals at the institute
	send e-mail	if e-mail function has been activated, an e-mail message can be created
	switch user	allows user to switch to another user without logging out of the database
	change password	allows the user to change his/her password. Passwords are case sensitive
	Quit	quit TierBase
Line_Colony	mutant colonies available	
	wild type colonies available	
	lines removed from stock	these are discontinued lines and colonies
	colonies available	
	colonies responsible	this lists the colonies you are responsible for
	colonies private breeding	this lists colonies you may have in private breedings (these are colonies you manage by yourself)
	colonies inventory	this allows you to get a quick overview of how many animals you have for the colonies you have access to
	search colony	displays the query editor

TABLE 4. Menus and Menu items for the Generic User

Menu	Menu Item	Description
	inventory_cages	displays cage inventory records for your colonies
	inventory_animals	displays animal inventory records for your colonies
	breeding_analysis	displays a summary of the breeding results for your colonies
	unproductive matings	displays matings which have not produce a litter within a given time (which you can specify on the third page of your user record)
Animal Orders	new order	allows entry of a new order job
	show all animal orders	shows all animal orders you have made, independent of their status
	show unfinished orders	lists all unfinished animal orders
	select animal orders	calls the 4D Query editor to allow a selection among all your animal orders
	modify animal orders	allows modification of uncompleted animal orders
Tissue Orders	new order	places a new order for tissues like tail, blood, etc.
	show all tissue orders	shows all tissue orders you have made, independent of their status
	select tissue orders	calls the 4D Query editor to allow a selection among all your tissue orders
	modify tissue orders	allows modification of uncompleted tissue orders
Jobs	JOB MONITOR	displays a job display floating window which can be used to navigate between job types
	all jobs	

TABLE 4. Menus and Menu items for the Generic User

Menu	Menu Item	Description
	animal orders	displays all animal orders
	tissue jobs	displays all tissue jobs
	elimination jobs	displays all elimination jobs
	mating jobs	displays all start and stop mating jobs
	uncompleted	displays all jobs not yet completed
	show proxy jobs	displays jobs for other users who have designated you as an alternate job user
	modify jobs	displays uncompleted jobs so you can modify them
	show standing orders	displays any standing order jobs you might have
	eliminate standing orders	allows you to delete your standing orders
	start new mating	create a mating start job
	stop mating	create a mating stop job
	new eliminate job	create an elimination job
	show job categories	shows a list of the kinds of jobs that can be submitted
Projects	list your projects	displays the project for which your are project leader or alternate project leader
	list your active projects	shows only your active projects
	list accessible projects	shows projects to which you have access
	show users in your project	lists the users in your projects
	analyze user of your projects	allows project leaders to see jobs that have been charged to their projects
User	active users	displays all active users in the database
	inactive users	displays all users which have been inactivated

TABLE 4. Menus and Menu items for the Generic User

Menu	Menu Item	Description
	modify your user record	allows users to modify information specific for them, eg. telephone number, preferred language, e-mail address, etc.
	update user vars	updates various information specific for the user such as colony access, working line lists, etc. This is only necessary when the user has modified such information. This menu item initializes user variables as if the user were logging into the database again
	add line access to user	this allows colony owners to give access to other TierBase users
jobArea_util	to Navigator	displays the navigator window (the one which is first displayed at login)

Menu items - Analysis Area

TABLE 5. Analysis Area Menu items

Menu	Menu Item	Description
File	about TierBase	
	info	information about using TierBase or about the animal facilities at the institute
	change password	allows the user to change his/her password. Passwords are case sensitive
	Quit	quit TierBase

TABLE 5. Anlaysia Area Menu items

Menu	Menu Item	Description
Holding cages	add new holding cage	creates a new holding cage by displaying the offspring
	add orphan holding cage	allows the creation of holding cages with animals not in the offspring list (orphans)
	show all holding cages	lists all holding cages
	query holding cages	search in holding cage list
	clear empty cages	clears holding cages that contain no offspring. Usually, animals are automatically removed from a holding cage when they are marked as dead or are put in another cage. If the cage is empty, it should be deleted automatically.
	verify cage numbers	checks that the cage numbers match with the offspring in the cage
	reset cage numbers	
	diagnose cage_dist	diagnostic function for the developer
	reset cage_ID	resets the automatic generation of unique cage ID numbers. This function is normally not necessary but may help if you cannot store a new cage because of an error message that the ID is not unique.
	Mating cages	add
all matings		display all matings
query from all matings		calls 4D Query editor to select matings from all matings
query from selected matings		calls 4D Query editor to select matings from the matings presently selected
show current matings		
current mating totals		displays the breeding results for the current matings
family tree		allows ancestor analysis up to 5 generations

TABLE 5. Analysis Area Menu items

Menu	Menu Item	Description
	archive matings	creates an archive for a selected set of matings. Records (with associated litters and offspring) are copied to a specified medium and then deleted from the database
	retrieve archived matings	creates records for matings, litters and offspring from an archive
	show archived matings	displays a summary of mating archives created
Litters	add new litter	
	show all litters	display all litters
	query from all litters	calls 4D Query editor to select litters from all litters
	query from selected litters	calls 4D Query editor to select litters from the litters presently selected
	litter overview	displays litters with associated offspring for viewing
	reset litter_ID	resets the automatic assignment of the litter ID. This is only necessary when the data become corrupted
Offspring	all	displays all offspring for the current colony
	living offspring	
	reserved offspring	
	available offspring	
	query from all offspring	calls 4D Query editor to select offspring from all offspring
	query from selected offspring	calls 4D Query editor to select offspring from the offspring presently selected

TABLE 5. Analysis Area Menu items

Menu	Menu Item	Description
	query with ID	allows a search for an animal with it's unique ID number (not the same as the animal name)
	erase generation number	deletes the generation number for all selected offspring
	reset offspring_ID	resets the automatic assignment of the unique offspring ID This is only necessary when the data become corrupted
analyArea_util	analyze breeding	allows the user to select another colony for analysis
	trans all offspg to new colony	this allows the breeding administrator to transfer all offspring from the current colony to another colony of the same line
	to Navigator	moves user to the navigator window (the one which first appears at login

Messages

In order to support the communication between the animal technician group and the rest of the database users, TierBase has two integrated message systems. The first is used when the animal techs would like to send a message to a scientist. Provided the SMTP server has been set by the database administrator (DbA), the techs can send an e-mail which is then read by whatever e-mail program the scientist uses (Eudora®, Outlook Express®, etc.). The second message system contained within TierBase does not involve sending an e-mail. This system is primarily used by the scientists when communicating with the animal techs. The message is sent to a breeding unit so that anyone there can read it. This can be useful when animal techs are absent because of illness or are rotated through different breeding units.

Sending an e-mail

To send an e-mail to one or more scientists, click the “S-E” button in the message area of the navigator or chose the *File->send_e-mail* menu item. The message input form is displayed.

The screenshot shows a dialog box titled "E-mail Message". It has two tabs: "general" (which is selected) and "available animals". The "general" tab contains the following elements:

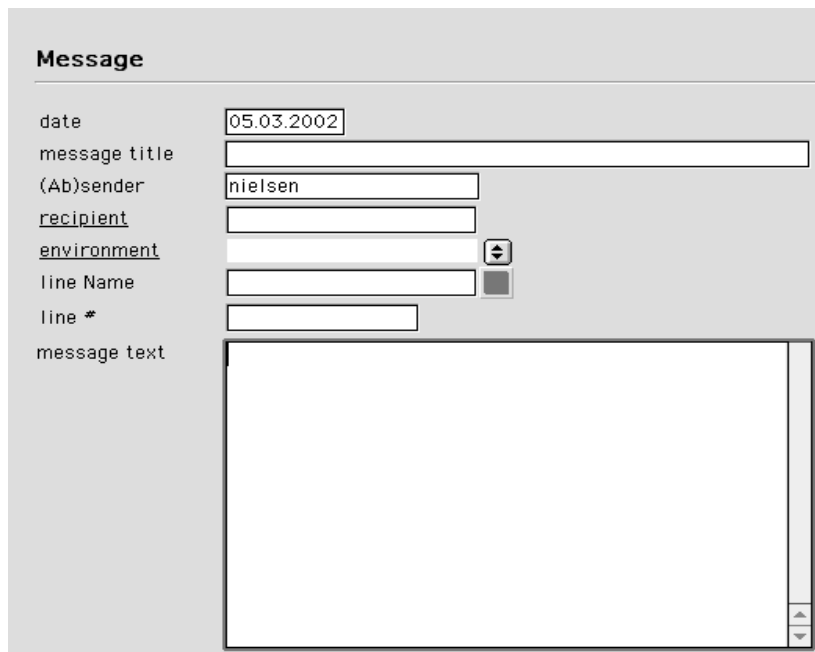
- A "Recipient*" field with a "select" button and a "0" counter.
- A "Subject*" field.
- A large "Message" text area.
- An "attachment" field with a "file" button.
- Another "attachment" field with a dropdown arrow.
- A note: "* mandatory".
- "Cancel" and "send" buttons at the bottom right.

First select the recipients, either by typing the name in the field or by clicking the “select” button. If you would like to send the same e-mail to several users, use the “select” button and commant-click the user records dis-

played. The number of selected recipients will be displayed to the right of the select button. Next, enter the subject and the message text. You can also include an attachment document by clicking the “file” button. If you are sending the mail from a Mac to Mac, you do not need to encode the document. If you are sending from Win to Win or Win to Mac, use base64 encoding. When you are finished, click the send button.

Sending a message to the animal techs

To send a message to the animal tech group, click the “S-TB” button in the message area of the navigator.



The screenshot shows a web form titled "Message". The form contains the following fields and controls:

- date**: A text input field containing "05.03.2002".
- message title**: A wide text input field.
- (Ab)sender**: A text input field containing "nielsen".
- recipient**: A text input field.
- environment**: A dropdown menu with a small square icon to its right.
- line Name**: A text input field with a small square icon to its right.
- line #**: A text input field.
- message text**: A large text area for entering the message content.

The input form will allow you to enter a message title, the recipient, the breeding unit, the name of the animal line if applicable, and the message text.

The Breeding Administrator

Introduction

The Breeding Administrator (BA) is responsible for organizing most aspects of the breeding facilities at an institute. This includes being responsible for the animal technicians, the animal colony breeding logistics (hygienic status, colony distribution, etc), deciding which lines will be maintained and how, coordinating special jobs such as sending and receiving animals from other facilities, eliminating lines, etc. Likewise, the BA plays a key role in organizing and maintaining information in TierBase. This chapter is intended to inform the TierBase BA about the special functions available to them in TierBase. Many functions available to the BA are also available to all other users of TierBase. A description of these functions can be found in the TierBase main Guide.

This chapter is not intended as an alternative to the other chapters in the handbook. They should also be carefully studied by the Breeding Administrator.

TierBase Breeding Administrator Responsibilities

The Breeding Administrator Group is one of the most powerful users of Tier-Base. This group has access to and control of all lines, colonies and jobs stored in the database. They also can view all animal ethics projects in the database. The following list gives an overview of these functions with cross-references to the detailed descriptions.

The Breeding Administrators (BA) :

- are responsible for entering all new animal lines and colonies and for keeping the line list up to date.(see “Creating new lines and colonies” on page 55).
- are able to inactivate a colony so that it cannot be ordered. This can be useful, for example, if breeding problems with the colony arise and the animal stock must first be expanded.
- can create invoices for completed jobs when users are to be charged for services performed (see “Invoices” on page 71).
- can archive jobs, invoices and mating records.
- can specify the cost of each job (see “Job Types” on page 69).
- are responsible for processing several types of jobs which do not go directly to the animal technicians in the breeding facilities. This includes jobs like, cryoconservation, immunization, line elimination, and animal shipments.
- are the only users that can modify standing order jobs (see the maintenance menu). Normal users can create, view and delete their standing orders but cannot modify them.
- can create an inventory of the number of cages and or animals for any and all colonies in the database.
- can specify cage and animal quotas for each colony. These quotas can be used during an inventory to flag colonies exceeding the allowed quotas.
- can specify user quotas (either animal or cage). These quotas can be used during an inventory to flag users that have exceeded the number of animals or cages they are allowed.
- can inactivate a user so that they cannot create new jobs.

- can create online Info text, that can be read but not modified by all users in the database. This feature is often used to store institute-specific details about procedures and guidelines.
- can access the animal technician environment and has access to all the functions of the animal techs.
- can transfer offspring from one colony to another colony.

Online Information

TierBase provides the ability to store general information that can be accessed at any time by all users of the database. This can be particularly useful to store institute-specific information. For example, when a scientist wants to send animals to another institute, it may be that he/she must first obtain the confirmation from the recipient and fill out an animal transfer form. The BA can create a TierBase Info record that stores this information so that any scientist can read the check list before submitting a send job to the BA. Any user can create an info record but only the BA can create infos that are read-only. Infos are displayed by selecting the *File -> TierBase Info* menu item. Each topic can be viewed by double clicking on the record.

Creating new lines and colonies

Before being able to order animals or to enter a mating, the line record and the colony for that line must exist in the database. New lines or colonies are created by the Breeding Administrator (BA) from the *line_colony* menu. First, the line record must be created. The reason for differentiating between lines and colonies is that in this way, it is possible to create several colonies for the same line. This is often the case when the database manages breeding in several breeding units which can be semi-independent of each other. For example, two separate breeding buildings or two floors of an SPF-unit. The line information is only stored once in the database. Tier-

Base treats each colony separately and responsible scientists or owners are designated at the colony level. In most cases, each line will probably have only one colony. To create a line and colony, you first create the line record and then the colony record.

create a line record

1. call `line_colony` -> create new line
2. the line input form is presented

line name ID **Animal Line Entry Form** page 1

ownership | gene | construct | breeding 1 | breeding 2 | phenotype 1 | phenotype 2

line number cost factor

full name

working name*

species

current breeding colony

breed unit	owner	dept.	scientist1	scientist2	tech 1	tech 2

comments

literature reference

date entered dd.mm.yy date modified

*mandatory

3. fill in the information for the line. As a minimum, you must enter 4 things

- the line name (working name), up to 40 characters are allowed but it is best to keep the name in the range of 5-15 characters to make it easier to remember. There is also a field for the full name if necessary.
- the line number. This number is designed to be used as an alternative for the name since it is sometimes easier to remember the number than the name. The line number is actually stored as a text in the database so you can include letters, slashes, dashes etc in the number. Since the number is really a text, sorting on the number will always go from left to right. This means that if you have the line numbers 1, 6, 24 and 107 and you sort on the number from smallest to largest, you will get the order 107, 2, 24, 6. To avoid this somewhat un-intuitive sorting order, it is best to pad the number with zeros. Thus you should use numbers 0002, 0006, 0024 and 0107. Then the sorting will work as expected. This may seem trivial when you have 10 lines but when you have 500, it is very useful to be able to sort on the number and get the expected results.
- the species of the line. If no species appear when you click the popup button, the species list probably has not been created. You should do this now (see “creating lists” in the database administrator chapter). You can access the lists by the “BA_utilities -> edit lists” menu.
- the gene model specifies whether the line is a knockout, transgene, double transgene, etc. This is done on the second page of the line input form (labelled “gene”). (You move between pages on the input form by clicking the tabs at the top of the form). All mutant lines, either natural mutants, knockouts, etc use the genotype designation “d” for defective allele and “+” for the wildtype allele. All transgenic line use “T” for the transgenic allele.

There is a substantial amount of additional information that can be entered for the line but it can be done later, either by the BA or by a scientist who either owns or is responsible for a colony of this line. The additional information includes things like who created the line, references, phenotype, special breeding requirements, etc. The BA can also set the **cost factor** for the line (page 1 of the input form). The cost factor is used as a multiplication factor in the calculation of invoices. The cost for each job will be multiplied by the cost factor corresponding to the line ordered. The default cost factor is 1.

Create a colony record

call *line_colony* ->create new colony

the colony input form is presented

line_colony ID: 10 page 1

ownership | **breeding** | comments

* line name: Adp ID#: 10
line #: 0806

* department: solter tel. _____

* scientist1: wei 570
scientist2: solter 565
animal tech1: Iddouche 634
animal tech2: friedrich 633

* owner: Wei 570

* analysis environment inactive active

* mandatory

Previous Record Next Record Cancel OK

The following information for the colony must be filled in.

- the **line** in the colony. Select the line by clicking on the underlined title word “line name”. A list of all lines in the database is presented. Select the appropriate record by clicking on it with the mouse and then press the select button. (Now you know why you must first create the line record before creating the colony record.) The line name and number will appear in the colony input form.
- enter the **department** to which the colony will belong. If no departments appear when you click the popup button, the department list probably

has not been created. Ask the database administrator to create it or do this yourself now. (To create the department list, see the topic, “creating lists” in the database administrator chapter). You can access the lists by the “BA_utilities -> edit lists” menu.

- enter the **responsible scientists** (at least one must be entered) and the **colony owner**. This is most easily done by clicking on the underlined “scientist1” title word. A list of all users in the database will be presented and you can select one. The name and telephone number should automatically appear in the appropriate area of the colony input form..
- similarly, you can enter the **animal technicians** responsible for the colony.
- at the bottom of the page, you will see buttons near the title “analysis environment labelled “**active and inactive**”. These buttons determine whether the analysis area will be active for the colony or not. If you are not sure what this means, you should refer to the section of the chapter called “The analysis area”. It is extremely important that you understand what the analysis area is. If you are creating a new colony and are not sure what to do, you should stop what you are doing and first read this section!
- on the second page of the colony input form, you must specify the **breeding environment** for the colony by using the popup button to the right of the breeding unit area. If no breeding environments popup, the list probably has not been created. You can access the lists by the “BA_utilities -> edit lists” menu. (see the topic “creating lists” in the database administrator chapter).
- you can specify whether the colony is a **private breeding**. This means that users manage the breeding of this colony themselves. All jobs created for such a colony will not be directly visible by the animal technicians. In this way, the database can store the use of animals for a colony, the animal techs. are not bothered with these data and the animal ethics officer can create totals for experimental and breed animals which include the privately bred animals. This is often necessary for annual reports to the authorities.
- you can specify whether the colony is a **no public access** colony. This means that the colony is only visible to the owner, responsible scientists, the BA and the animal techs. This can be useful for strains which contain sensitive information that should not be available to other users in the database.

- quotas can be entered for the number of cages and/or animals allowed for the colony. This is not mandatory.

When you are finished, click the save button. The newly created colony record can be viewed by clicking the mutant or wild type button in the navigator window, or by selecting the *line_colony ->mutant colonies* or *line_colony ->wild type colonies* menu items.

Line_Colony Menu Items

Additional line_colony menu items only available to the BA include:

line_colony -> private colonies

This item displays all privately bred colonies in the database. When the privB checkbox in the upper right hand corner of the Navigator window is clicked, only colonies and jobs that are private will be listed when the appropriate buttons are clicked.

line_colony -> discontinued colonies

This item displays all colony records that are marked as discontinued. These are usually old colonies which have been eliminated from the institute.

line_colony -> lines without a colony

This item displays all lines that have no colony record (either active, inactive or discontinued) associated with it.

line_colony -> colony report

This item allows the BA to display the number of animals and cages currently present for a selection of colonies. Two ways of displaying the colony inventory are available (list and detail).

line_colony -> list cage inventory

This item displays all cage inventory records.

line_colony -> list animal inventory

This item displays all animal inventory record.

line_colony -> new inventory

This item allows the BA to create a new animal or cage inventory for any number of selected colonies for a given time span. These are the records displayed in the above two menu commands (see "Inventory and Quotas," on page 62.).

line_colony -> display colonies by department

This item displays all mutant colonies in the database grouped according to the department to which the colonies belong.

line_colony -> search lines

This calls the query editor for a custom search of the colonies.

line_colony -> delete colony

This allows the BA to delete a colony from the database. This deletion is permanent so be sure you know what you are doing! If there are cages, litters or offspring associated with the colony, they will also be deleted if you confirm the deletion. You will also be asked whether you want to delete the line record corresponding to the colony. It is possible to delete only the colony and leave the line for future use or reference. In many cases, you may be better served by just marking the colony as inactive instead of deleting it. This permits you the reactivate the colony at a later date if necessary.

line_colony -> delete line

Lines can also be deleted from the database. If there is an associated colony, you cannot delete the line.

line_colony -> show colony use

This item allows the BA to check how often animals from a colony are being ordered. TierBase displays the ratio of the number of animals ordered vrs the number of animals eliminated. The BA can also specify a cutoff ratio

value below which the colony use should be flagged as needing attention. The use-ratio for those colonies with values below the cutoff value will be displayed with bulleted names. This provides an easy way for the BA to see which colonies are producing excessive animals.

line_colony -> modify colony access

This allows the BA to specify who has access to a particular colony. Since the BA has access to all colonies, he/she can give access of any colony to any user.

line_colony -> reset colony access

If this item is called, the colony access for all colonies in the database is reset to the ground state. This means that for the generic users (scientists), only the owner and the first and second responsible scientist will have access to the colony. As is always the case, these three people can provide access to other users in TierBase. As you can imagine, this command erases all colony access given to users by those responsible for the colonies.

Modifying colony records

Whenever colonies are being displayed, you will see a menu command called modify. In this menu are the menu items *sequentially* and *simultaneously*. These items allow the BA to modify a selection of colony records, either sequentially or simultaneously. This can be quite handy in several situations such as when an animal tech is replaced by a new coworker and many colonies have to be assigned to the new tech. Simply select all the colony records to be modified, call the *modify-> simultaneously* menu item. A modification dialog will be presented and you can fill in the name of the new animal tech and click the save button. Thats it!

Inventory and Quotas

A database like TierBase lends itself well to situations where the number of animals and/or cages need to be regularly monitored. Perhaps the breeding resources are limited and need to be optimally distributed among the users. Perhaps invoices need to be made, including cage or animal holding costs. Whatever the reason, the ability to take an inventory is very useful. In addi-

tion, there may be some situations where it is also useful to set an upper limit or quota on the number of cages or animals maintained at the institute. This can be useful for the Breeding Administrator (BA) to keep track of how many animals are present, how many cages are in use and who is using which fraction of the breeding unit space.

TierBase allows the quota to be set, either per colony or per user. Once set, the quota can be checked whenever an animal or cage inventory is created. Colonies or users exceeding the quota are displayed and e-mails can be sent to those responsible. It is not mandatory to use quotas or create inventories, but if they are set, the BA usually chooses to follow either cage or animal totals, but rarely both.

It is important to realize, that in either case, automatic calculation of cage or animal inventories is only possible for colonies where the analysis environment is active. If you do not know what the analysis environment is, you should go the corresponding chapter in the TierBase Handbook.

The use of cage inventories and quotas is more demanding than animal inventories in terms of animal technician data-management. This is because the calculation of a cage inventory requires that all cages for a colony (holding and mating) are always kept up-to-date. For example, if 2 males in a holding cage are separated because they are fighting, a new holding cage must be created in the database. Since TierBase does not require that all animals are put in cages but it does keep track of whether an animal is alive or not, it is often easier to use animal inventories and quotas. In this case, the number of living animals in the colony is calculated and compared with the animal quota set for the colony. In the case of user quotas, the number of living animals in all colonies owned by the user is compared with the user animal quota specified for this user.

How to set the quota (available only for the BA):

Colony quotas are set on the second page of the colony input form. The colony record also stores the last values for the number of cages and animals counted the last time a colony inventory was created (see making an inventory, "line_colony -> new inventory," on page 64).

User quotas are displayed on the third page of the user input form and are specific for each breeding environment. Only one cage and animal quota is possible for one breeding environment. The BA can modify the quotas by

clicking the “modify” button on the user input form. A list of all quota records belonging to the current user is displayed. New quotas can be created by clicking the “new” button at the bottom of the form. Existing records can be modified by double clicking. To delete a quota record, double click it and click the “delete record” button on the form.

How to check quotas (available only for the BA):

Quotas are checked in conjunction with creating an inventory. To make an inventory, call “line_colony -> new inventory”.

line_colony -> new inventory

This item allows the BA to create either an animal or cage inventory for a selection of colonies. This means that for an animal inventory, all living animals for each selected colony are counted and the result is stored as an animal inventory record. The total is also stored in the colony record for comparison with the animal quotas entered there (if any). Likewise, a cage inventory involves counting the number of holding and mating cages for the selected colonies. As was the case for the animal inventory, the cage totals are stored in a cage inventory record and in the colony record. The inventory records also contain the duration of the inventory which is just the number of days between the current inventory and the previous one. This means that by creating inventory records regularly, you will have a record of your animal and cage stocks which can be used to create invoices and/or to follow the occupancy of the breeding facilities.

When the new inventory menu item is chosen, the inventory setup form is presented.

Cage / Animal Inventory

1 colony selection and
 or

all active accessible colonies

department

breeding environment

room

line name 0 colonies

colony owner 0 colonies

2 select colony records selected

3 inventory type min. age (days) of
offspring to include in
animal inventories

colony cage animal

user quota user cage quota user animal quota

4 results

colony display colony inventory result

user quota display only

send e-mail to user with all quota results

send e-mail to user only if quota is exceeded

5

The “Cage/Animal Inventory Dialog is presented. You must first specify which colonies you would like to include in the inventory. When the form is first presented, the default setting is all colonies where the analysis area is active (remember, you don’t have to use the analysis-area for a colony if you do not want to. If you are not sure what the analysis area is, see the description of this in the generic user chapter.). If this is OK, just click the

“Select” button and the number of colonies selected will be displayed. If you would like to restrict the inventory to only certain colonies, you can do this by specifying the colonys according to owner, department, etc. Don’t forget to click the “Select” button to generate the colony selection you want to work with.

After specifying which colonies should be checked, go to area 3 and specify the type of inventory to be made. If you only want to check user quotas, check the user animal quota or user cage quota check box, depending on the kind of quota you have set. Next, go to area 4 and specify whether you just want to display the results (default) or whether you would like to send an e-mail to the colony owners with the inventory results, either for all breeding environments, or just for those that exceed the quotas.

Next, click the calculate button. If you have chosen to check user quotas, the results will be displayed and possibly e-mails will be sent. When completed, you will be notified of how many inventory records were created.

Caution: Depending on the number of users and colonies selected, you could be requesting that TB send a large number of e-mails. This could take several minutes to complete.

line_colony -> colony report

This item allows the BA to display the current cage and animal totals for a collection of colonies in two different ways, a list report or a detailed report. In both cases, the totals are not stored in the database for future reference. To save the totals, create a cage or animal inventory, see “The use of cage inventories and quotas is more demanding than animal inventories in terms of animal technician data-management. This is because the calculation of a cage inventory requires that all cages for a colony (holding and mating) are always kept up-to-date. For example, if 2 males in a holding cage are separated because they are fighting, a new holding cage must be created in the database. Since TierBase does not require that all animals are put in cages but it does keep track of whether an animal is alive or not, it is often easier to use animal inventories and quotas. In this case, the number of living animals in the colony is calculated and compared with the animal quota set for the colony. In the case of user quotas, the number of living animals in all colonies owned by the user is compared with the user animal quota specified for this user.,” on page 63. The colony report is used to get an overview

of the cages and animals present at the moment the report is calculated. When the menu item is called, a setup dialog is displayed.

The image shows a software dialog box titled "Colony Report". It is divided into several sections. At the top, under "select colony", there is a checkbox for "all active accessible colonies" which is checked. To the right of this section are two radio buttons: "and" (selected) and "or". Below these are five input fields, each with a "clear" button: "department", "breeding environment", "room", "line name" (with a value of "0"), and "colony owner" (with a value of "0"). A "select" button is located below these fields, followed by a text field showing "0 selected colonies". A horizontal line separates this section from the next. Below the line, there is a label "min. age (days) of offspring to include in report summary" with a value of "10". At the bottom, under the heading "view", there are three buttons: "detail", "summary", and "done".

Select the colonies to be analyzed using the buttons in the upper part of the window. Then click either the list or detail button, depending on the type of report desired. The colony report menu item is also available to the generic user group (ie. scientists). In this way, they can create their own reports for the number of animals or cages they have. Generic users can create reports for all colonies belonging to their department.

Inventory

available lines

user 11 selected lines

page	name	number	manipulated Gene	owner	avail.
1 / 2	<input type="radio"/> Bob1	0363/1		nielsen	✓
<input type="button" value="→"/> <input type="button" value="←"/>	<input type="radio"/> SRp20	0367/2		nielsen	✓
	<input type="radio"/> CD28	0362		nielsen	
	<input type="radio"/> SRp20/lokCre	0368/2		nielsen	
	<input type="radio"/> SRp20/CD19	0367		nielsen	
	<input type="radio"/> Po-cre	0364		nielsen	
	<input type="radio"/> 1.5-Bob	0365		nielsen	
	<input type="radio"/> CD11-cre	0366		nielsen	
	<input type="radio"/> slp-65	0370/2		nielsen	✓
	<input type="radio"/> Bob-slp	0359		Nielsen	✓

selected line

full name	<input type="text" value="Nielsen"/>		
working name	<input type="text" value="Bob-slp"/>	responsible scientist	<input type="text"/>
number	<input type="text" value="0359"/>	responsible caretaker	<input type="text"/>
owner	<input type="text"/>	breeding environment	<input type="text"/>
department	<input type="text"/>	breeding room	<input type="text"/>

view

	cages	litters	offspring
total	<input type="button" value="matings"/> 0	<input type="button" value="all"/> 0	<input type="button" value="all"/> 0
current	<input type="button" value="mate L"/> <input type="button" value="mate O"/> 0	<input type="button" value="current"/> 0	<input type="button" value="current"/> 0
	<input type="button" value="holding"/> 0		<input type="button" value="living"/> 0

Breeding units -> new unit

This is the command given when the BA would like to create a new breeding unit. Recall, all colonies must specify which breeding unit it belongs to. Animal techs can also specify which breeding unit they work in, so that they only get the jobs for their unit.

Breeding units -> list all

Displays a list of all breeding units.

Job Types

TierBase provides the user with the ability to submit several types of jobs to the breeding facilities of the institute. A list of job types available and their abbreviations is shown below.

TABLE 1. Job Types

	Description	Abbrev.
1	animal maintenance (a separate record for each species)	am
2	animal orders (a separate record for each species)	ao
3	cage maintenance (separate records for species, location etc.)	cage
4	cryoconservation	cc
5	cryoconservation with strain elimination	cce
6	animal elimination	elm
7	strain elimination	elmStr
8	embryo transfer	et
9	immunization (separate recs. for species and primary imm, secondary imm. etc)	imnz
10	microbiological tests	mictst
11	mating start	mst
12	mating stop	mst
13	staged pregnant females (for embryos)	pf
14	project inventory	proj
15	send animals to another insitute (separate records for different types)	send
16	recipt from other institutes (separate records for different types)	recpt
17	transgene or ES cell injection	tgES
18	tissue samples (blood, tail biopsy, etc)	tio
19	extra jobs (separate records for each job type)	xtra

The Breeding Administrator can add and modify job types, including the cost for each job. It is VERY IMPORTANT that the abbreviation for the job

type exactly matches the table above. If not, the job will not be recognized. For those job types that have multiple records (cage, immz, etc) the breeding administrator can specify the priority of the job type records. This is useful when one of the job type records should be used as the default record when a list of job type records is created. For example, if the priority of the "cage maintenance of mice outside of the SPF" job type record is set to 1 and the other cage job type records have priorities >1, then the "cage maintenance outside of SPF" will be offered as the default type whenever a new cage inventory record is being created.

Job Type menu items

Job Type -> show all

This item displays all job types entered in TierBase.

Job Type -> new treatment

This item displays the job type input form for entering a new job type.

Job Type -> modify selection

This allows the BA to modify job type records. The records can also be modified by simply double clicking on the record when it is displayed, for example by the *Job Type -> show all command*.

Job Type -> refresh treatment arrays

This command modifies popup buttons which display the job types. This is needed when a new job type has been added to the list and the BA has not logged out of TierBase. The popups are loaded at the time the user logs into the database.

Job Type -> export treatment selection

This item allows the BA to export a selection of job types to a text file on disk. This file can then be imported to a table calculation or text processing application for further use.

Job Type -> list extra jobs

This item allows the BA to list the existing extra job type records. This is all job types where the abbreviation is "xtra".

Job Type -> add new extra job type

This item allows the BA to add extra job type records. These are job types for special services which are typically used only if invoices are to be written. If you are not charging the users for services provided, you probably will not need the extra job types.

Invoices

Periodically, the Breeding Administrator can create a billing invoice for each account number with a listing of the associated jobs. This invoice can be given to each account owner. It is also possible to create an invoice which does not list the individual jobs but just lists the totals for each job category. The cost of each job is determined by the job type record and the animal line ordered. The cost of each job type can be viewed by choosing the "all records" from the job type menu. The cost factor for each line can be found by viewing the details of the line record. For the calculation of cage costs, the costs can be entered in the job type record either in the units of cost per day, per week, per month or per job.

Invoice Menu Items

Invoice -> show all records

This item displays all existing invoices.

Invoice -> select invoices

This item calls the query editor to allow the user to create a selection of records.

Invoice -> calc job invoices

7. Specify whether the calculation should be saved or not. If you specify “create invoice record”, the corresponding job and inventory records are marked when the invoice calculation is made, so that they will not be used again for a new invoice . This means that you should not check the “create invoice” button unless you are sure you want to save the results.
8. Specify whether the results should be displayed on the screen. To print invoices without viewing the calculation results, just click the print check box in the setup dialog and uncheck the display check boxes.
9. Click the calculation button. The program will sum the costs and present the results. Regardless of whether you create invoice records or not, the grand total cost for all invoices in one calculation is displayed in a dialog window at the end of the calculation.

You can always create invoice records without printing them and then print them later.

Projects

The Breeding Administrator can view (but not modify) all animal ethics projects in the database. This is done by selecting the *Projects -> all projects* menu item.

Users

users -> active users

Displays all active users.

users -> inactive users

Displays all inactive users.

users -> update user var

Updates the user variables when a change was made to global variables. This is usually not necessary.

users -> modify colony access

Allows the BA to set the colony access for any user in the database.

users -> list project for user

Displays all projects accessible to a selected user.

users -> modify your user record

Allows user to modify their user record.

users -> add new user record

Like the Database Administrator, the BA has the ability to create new user records. These records specify user data such as telephone number, e-mail address, account number, preferred language, etc. Every TierBase user must have a user record in order to work in the database. The user record should not be confused with the user password account (contains the user name and password) which can only be created by the Database Administrator.

users -> delete users

The BA and database administrator (DbA) can delete user records from the database. This may be useful for discontinued user records which have no current jobs associated with them.

ba_utilities

ba_utilities -> check job consistency

This item runs an internal datacheck to verify that there are no inconsistencies in the job records. If inconsistencies are detected, they are displayed and the BA can correct them. Inconsistencies can result from a variety of sources such as network or server hardware problems, programming

errors, etc. They should be very rare. If this is not the case, you should inform the TierBase Designer. Please include specifics about what kind of inconsistencies were detected.

ba_utilities -> standing orders

A standing order can be created for any combination of the five working days and for any frequency of weeks from every week to every fourth week. Standing orders are also visible for animal techs from the *jobs -> standing orders* menu item. The standing orders generate "daughter" jobs at the appropriate intervals, as specified by the job and the database preferences set by the BA. The preferences specify the number of days in advance that a daughter job is created from a standing order. When the animal techs view new jobs, daughter jobs are marked with a check mark in the output form and the job number is red.

ba_utilities -> to Navigator

Displays the Navigator (startup) window

ba_utilities -> to animal tech environment

The BA can move between the BA and the animal technician environment. In this way, the BA has access to all functions available to the animal techs. The BA can also switch between the BA and the animal technician environments by clicking the "admin" button in the upper left-hand corner of the navigator.

ba_utilities -> preferences

The BA can set default values for the following parameters:

- institute name and address
- animal ethics officer
- breeding administrator
- currency
- default animal ordering parameters
- default job and project parameters

- strain use defaults (the length of time to consider a colony as not used and the ordered vrs eliminated ratio cutoff) see “line_colony -> show colony use,” on page 61
- default name for colonies accessible to all users
- age of animals in days to begin counting in inventory
- default names for mating cage parents when offspring are transferred from one colony to another

ba_utilities -> edit lists

The BA can edit the lists used to display site-specific variable such as departments, immunization methods, cause of death, species, etc. For a description of the lists, see the database administrator chapter.

ba_utilities -> job availability

This item allows the BA to inactivate specified job types for a specified period of time. A setup dialog is displayed where various job types can be inactivated.

job type access						
job type	active	inactive	date range		dd.mm.yy	
			start	stop		
animal orders	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
elimination	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
tissue order	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
cryo-conservation	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
mating start	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
mating stop	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
animal shipment	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>
embryo transfer	<input checked="" type="radio"/>	<input type="radio"/>	00.00.00	<input type="text" value="-"/>	00.00.00	<input type="button" value="message"/>

ba_utilities -> delete old records

The BA can delete old job, inventory or invoice records. Deleting old records helps to keep the data-file small and this in turn makes the database faster. However, this deletion is PERMANENT, so be sure you know what you are doing. (At least make a backup before you start the deletion.)

ba_utilities -> display log

Many activities performed by TierBase are logged. This allows the BA or DbA to monitor the database for work loads and for errors. The logged activities includes e-mails, sentinel activities, and user logins, project warnings, etc.

ba_utilities -> display statistics

This menu allows the BA to check the overall database use. It displays the number of records stored in the various tables.

Sentinel

TierBase has the ability to perform a variety of functions automatically. This offers considerable advantages to maintain data integrity and consistency. It also saves work for the database administrator, the breeding administrator and the animal safety officer. This section describes the functions integrated into the database and how to access them.

The ability to manage jobs and data automatically is controlled by the Sentinel. The database administrator and the breeding administrator are the only groups that have access to this function in the Sentinel menu. There are 5 commands in this menu, *Start*, *Stop*, *configure*, *display log* and *show requests*. When *Start/Stop* Sentinel is called, the sentinel is turned on or off. When *configure* Sentinel is called, a dialog is presented where the desired parameters for the sentinel can be specified. The *log* command displays an activity log for the sentinel. There, it is possible to see which kinds of requests the sentinel has performed and whether the execution was successful or not. The *show requests* menu item lists the requests and their status.

If the sentinel is switched on with the Start Sentinel command, the sentinel will not run unless it has been configured with the configure Sentinel command. If the sentinel has previously been configured and then turned off, turning it back on will automatically use the previous configuration. If the configure Sentinel command is given and functions are activated, the sentinel is automatically turned on when the configuration is saved

The table below describes the functions included in the sentinel.

TABLE 2. Sentinel Functions

	Function	Description
1	project expiry	This function checks the current animal projects for the expiry date. If a project is found that is nearing expiry, an e-mail is automatically sent to the project leader. If a project has expired, the project is stopped and an e-mail is also sent to the project leader. The number of days before starting to warn the leader and the number of days between warnings can be specified by the BA in the preferences dialog.
2	project quota	This function checks the current animal projects for animal use. If the animals used in a project is nearing the maximal number of animals allowed, an automatic e-mail is sent to the project leader. If a project has reached its quotas for all animal species approved, the project is stopped and an e-mail is also sent to the project leader. The % of the quota used before starting to warn the leader and the number of days between warnings can be specified by the BA in the preferences dialog.
3	job confirmation	If a user has been asked to confirm a job (this happens often when the animal technicians have created a tio job for tail biopsy's and are waiting for the results) the user can automatically be reminded after a specified time, to confirm the job if this function is activated. The user is also told that if the job is not confirmed within a specified time, it and the associated animals will be deleted.
4	rejected jobs	Rejected jobs can be automatically deleted after a specified time interval. There are no warnings or messages for this action.

TABLE 2. Sentinel Functions

	Function	Description
5	standing order activation	When this function is activated, the Batch Workstation checks once per day whether a daughter job should be generated from a parent standing order. If so, the job is generated so that it is available for the animal technicians.
6	data integrity	This functions checks the internal integrity of the records from the job and orders table. If a discrepancy is noted (eg, inconsistent status, delivery date, species etc) the breeding administrator is notified.
7	cage quotas	This function makes a cage inventory of all colonies in the database and stores the result in the colony record. If cage quotas have been entered, the sentinel checks whether the quota has been exceeded. If so, an e-mail is sent to the BA and the responsible scientist.
8	animal quotas	This function makes an animal inventory of all colonies in the database and stores the result in the colony record. If animal quotas have been entered, the sentinel checks whether the quota has been exceeded. If so, an email is sent to the BA and the responsible scientist.

Items 1, 2 ,3, 6, 7 and 8 require that the SMTP server have been specified so that e-mails can be sent. Items 4 & 5 do not require e-mail capability. This is done by the DbA.

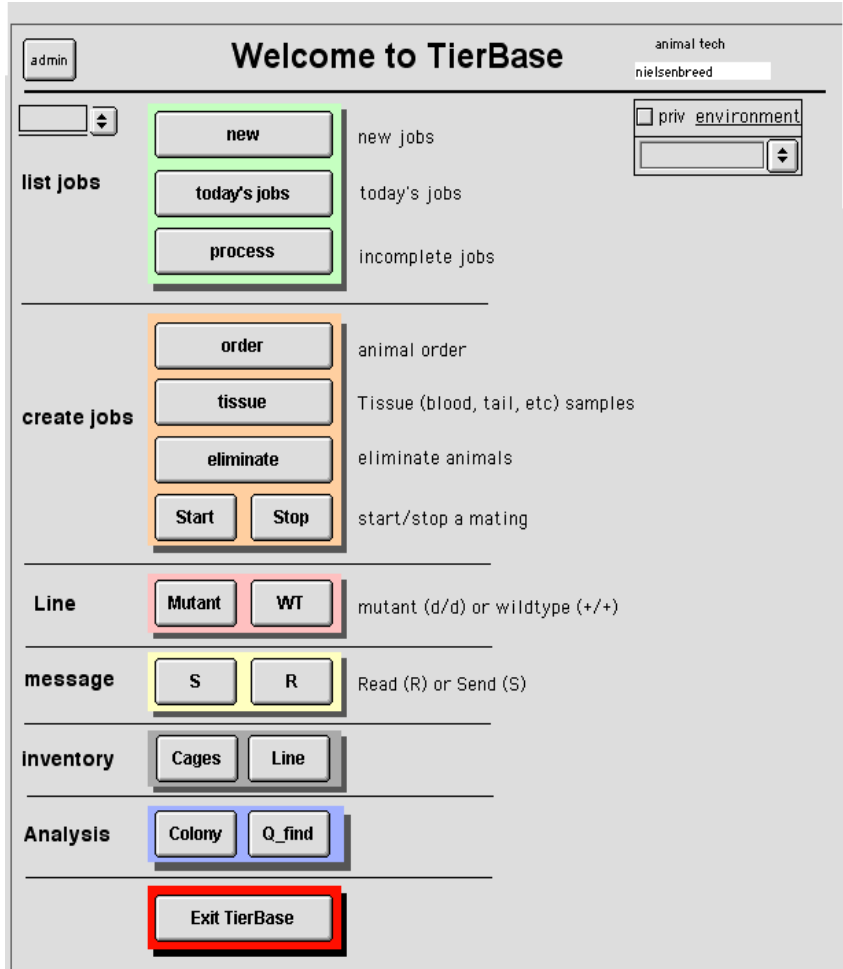
Introduction

Animal Technicians are one of the most important groups of people involved in a well functioning breeding facility. They are directly responsible for the successful and humane production of experimental animals. They also have the difficult job of responding to requests from others for a variety of activities associated with animal breeding and experimentation. This can range from animal orders for an experiment, to setting up matings, to sending animals to other institutes, and so forth. Much of TierBase has been designed with the animal technicians in mind. The guiding principle was to create an easy to use interface, which provides the animal tech with an overview of what has to be done and when. This focus of this guide is on the features of TierBase which are of particular interest to the animal technicians.

It is highly recommended, that the animal technicians also read the “Getting Started” and “Generic User” chapters of the TierBase handbook. This will help to give a well rounded idea of how TierBase works.

Animal Tech-Navigator

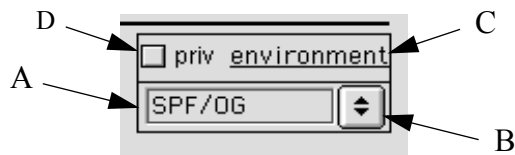
After logging in, the animal tech is presented with a Navigator window which contains buttons for the most frequently used functions.



The upper buttons (the green area) deal with the processing of jobs and the middle area (orange) deals with the creation of new jobs. These functions

are probably most often use by the animal techs. Lets go through these two areas in more detail.

Before we do that, however, it is important to consider the concept of the breeding environment. If you look carefully in the upper right hand corner of the navigator, you will see a small boxed area entitled environment.



This area displays the currently selected breeding environment. This means that if an environment is selected (SPF/OG in the example above, A), only the jobs for that environment will be displayed. You can change the environment by using the popup button on the right (B). By clicking on the word “environment” (C), you can clear the current breeding environment. The result is that jobs from all environments will be displayed. The small box labelled “priv” (D) is the private colony toggle. If this is clicked, only the private colonies and jobs will be listed.

Jobs

Job processing

What does job processing mean? TierBase provides a means for the orderer (for example, a scientist who needs animals for an experiment) to communicate with the animal techs via a job order. When a job is created, it has the status “submitted”. During the processing of the job by the animal techs, the status is changed to “received”, then to “running” and finally to “completed”. Jobs can also be given the status “rejected” or “to confirm” if necessary. By changing the status of a job, the animal techs keep track of

what has to be done and when. There is also the added bonus that the person who submitted the job can see at any time whether there are problems with the job or not. When the button in the green area labelled “new” is pressed, all new jobs (status “submitted”) are displayed. The jobs are grouped according to type. For example, all the new animal orders are displayed first.

animal order										04.05.2002	dd.mm.yy
										15:47:52	
job#	#	Line	number	age				delivery	note to caretaker		
16446	0229	129/Sv	female	0	6-8w	user	gumenschei	Tierausgabe BT X			
order date	01.02.02		male	0		project	Fr-3	animal			
Deliv. date	04.02.02		irr	30	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	injection w/o			
16493	0120	Balb/c	female	1	5-8w	user	bessler	Tierausgabe BT X			
order date	01.05.02		male	0		project	EA	animal			
Deliv. date	02.05.02		irr	0	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	killing			
16457	0120	Balb/c	female	0	6-8w	user	Jumaa	Tierausgabe BT X			
order date	01.02.02		male	0		project	MPI-ZH	animal			
Deliv. date	04.02.02		irr	2	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	breeding			
16492	0120/s	Balb/c schw	female	10	10-20w	user	haidl	Tierausgabe BT X		Verpaarung Di-M,	
order date	01.05.02		male	0		project	Ei-TO2	animal		Ausgabe Do	
Deliv. date	02.05.02		irr	0	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	killing			
16491	0120/s	Balb/c schw	female	10	10-20w	user	haidl	Tierausgabe BT X		Verpaarung Mo-Di,	
order date	30.04.02		male	0		project	Ei-TO2	animal		Ausgabe Mi	
Deliv. date	01.05.02		irr	0	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	killing			
16490	0120/s	Balb/c schw	female	5	10-20w	user	ketteler	Tierausgabe BT X		Verpaarung Mi-Do,	
order date	30.04.02		male	0		project	KLI-TO	animal		Ausgabe Mi	
Deliv. date	01.05.02		irr	0	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	killing			
16496	0120/s	Balb/c schw	female	10	10-20w	user	haidl	Tierausgabe BT X		Verpaarung Mo-Di,	
order date	16.04.02		male	0		project	Ei-TO2	animal		Ausgabe Mi	
Deliv. date	17.04.02		irr	0	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	killing			
16495	0120/s	Balb/c schw	female	5	10-20w	user	ketteler	Tierausgabe BT X		Verpaarung Mi-Do,	
order date	16.04.02		male	0		project	KLI-TO	animal		Ausgabe Mi	
Deliv. date	17.04.02		irr	0	f\$Q/vDA	status	submitted				
without	<input type="checkbox"/>	with	<input type="checkbox"/>	superov.	age	0	treatment	killing			
16487	0030/s	C57Bl/6schw	female	11	10-20w	user	steimle	Tierausgabe BT X		14,5 Tage tragend.	
order date	25.04.02		male	0		project	St-TO	animal		Ausgabe Freitag.	

status modify query subS all print cancel

If you click the “print” button, the job list is printed and the status is automatically changed to received. If you click the “cancel” button, no modification of the job status is made.

The next button on the navigator, “today’s jobs”, displays only the jobs that are due today, or earlier.

The “process” button in the green area displays all jobs which are not yet completed. In this list, all uncompleted jobs are displayed together, irrespective of their type. It is important that you learn the various job type abbreviations. They are:

Job Types

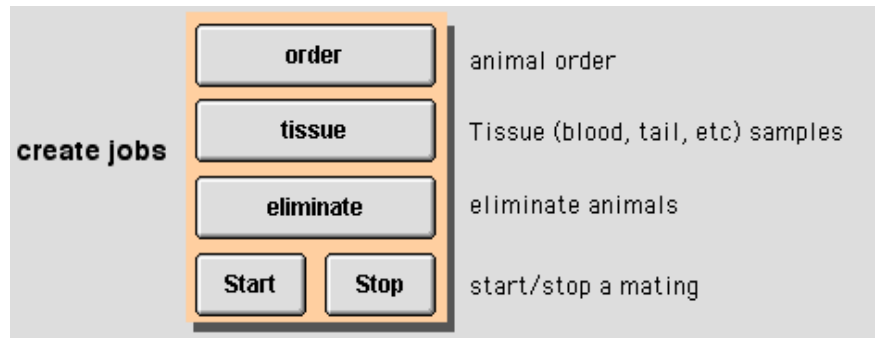
TierBase provides the user with the ability to submit several types of jobs to the breeding facilities of the institute. A list of job types available and their abbreviations is shown below.

TABLE 1. Job Types

	Description	Abbrev.
1	animal maintenance (a separate record for each species)	am
2	animal orders (a separate record for each species)	ao
3	cage maintenance (separate records for species, location etc.)	cage
4	cryoconservation	cc
5	cryoconservation with line elimination	cce
6	animal elimination	elm
7	strain elimination	elmStr
8	embryo transfer	et
9	immunization (separate recs. for species and primary imm, secondary imm. etc)	immnz
10	microciological tests	mictst
11	staged pregnant females (for embryos)	pf
12	project inventory	proj
13	send animals to another institute	send
14	receipt from other institutes (separate recs for EU, non-EU etc)	recpt
15	transgene or ES cell injection	tgES
16	tissue samples (blood, tail biopsy, etc.)	tio
17	extra jobs	xtra

After a short time using TierBase, you probably will have all the job type abbreviations memorized. That is all you need to quickly categorize the jobs when they are displayed together. You can also view the jobs using the job monitor. This is a small floating window that allows you to quickly switch between different job types. To learn how to use the job monitor, read the description in the main part of the handbook.

Create jobs



The buttons in the orange area of the navigator have to do with the creation of new jobs. The animal technician group can create jobs for any user in the database and for any available line. This can be handy when, for example, excess animals from a colony are to be eliminated. By creating an elimination job using the name of the scientist responsible for the colony, the animal tech insures that the animals bred in the facilities are registered and that the colony owner will be charged for the animals bred, even if they were not ordered for an experiment.

Animal orders (ao and pf)

When the "order" button is clicked, the animal order input form is presented.

04.05.2002 16:32:53 **Animal order form** A Order # 16494 page 1

User Name B UserID: 0 Lab:
 Project Name ProjectID: 0 Tel:
 Account number
 Line name
 #
 colony
 room

Mouse Rat Rabbit
 animal source

Animal numbers (, or -)

Quantity Females Males Unimportant total
 Age d w min. max.
 embryos - Superov. + Superov. 0.5 days (from vag. plug)

Use:
 Kill for..... Bone Marrow Spleen Blood
 other:
 Treatment : category
 duration (days) <1 1-7 8-30 >30

Notes to caretaker D

To fill out the form, begin with the user name (A). When the first letter of the user to receive the animals is typed, TierBase searches its list for users beginning with that letter and presents the first name found. If the name is correct, use the tab key (or the mouse) to move to the next field. If the name is not correct, continue typing until the name is found. You cannot place an order for a user who is not registered in TierBase. Enter the project name

using the grey popup button to the right of the project name field (B). The account number for the user must also be entered (this is usually done automatically when you tab out of the orderer field). Next, enter the line name (C) (make sure that you spell the name correctly). When you tab out of the name input area, TierBase looks for the line in the database. You are allowed to order lines not listed in TierBase. In this case, an alert window will open and ask you to confirm that the animals are to come from outside the institute. You can also enter the line by going to the line number input area and typing the number. If the line was found, several fields will be automatically filled in and you can continue to the area where you enter the number of females, males required and their ages. Next, you must specify what the animals are being ordered for. This is specified by the treatment popup button (D). The treatments available depends on the project selected. You must also specify the duration of the experiment. If you have selected a project of the type “notification” rather than of the type “approval”, you do not need to enter the treatment. Notification type projects are for orders where the animals are used as a source of organs or tissues. In this case the treatment is automatically set to “elimination without treatment”. To complete the order form, go to the second page: fill in the delivery date and delivery location and click the “submit” button.

Tissue jobs (tio)

Tissue jobs are often created by the animal techs when animals are weaned and tail biopsies are taken. Scientists can also create tissue jobs when necessary (for example to order blood samples). To create a tio job, click the “tissue” button. The tissue job input form is displayed.

The upper part of the form is similar to other input forms. You must fill out the information for the user, account number and colony. When you enter the colony, the next offspring number is displayed in the first row. Next, you enter the number of tissue samples (offspring being weaned) in the area just above the number column (A). A tio form can hold up to 50 samples.

Create jobs

date 05.05.2002
time 18:33:44

Tissue Samples

Job 16494

Orderer:

Account number:

UserID:

Lab:

Tel:

Mod. by:

page print: 1 2 Page 1

Status: confirm

Line # breeding source room complete job

colony ID# -1 increment generation deliv. date 00.00.00 dd.mm.yy
comp. date 00.00.00

sex: female (F) male (M) (?)

0

birth date: CW: 17 > <

mating display: m=mating # C=coage

test results: +(N)=wild type T=transgene d=defective p=loxP

use: retain/behalten (r) eliminate (e) mate/verpaar (m)

tissue: (t) tail (h) heparin blood (b) blood (e) ear (o)

mFemale1_Female2_X_Male:

number	sex	B-date	charact	parents	genotype	use	comments
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16							
17							
18							
19							
20							
21							
22							
23							
24							
25							

comment >
print
auto print
cancel
save

	number	sex	B-date
1	3001		
2			
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
13			
14			

After filling in the number of animals, click the column heading labelled “number” (B). The numbers of the samples should be incremented in the number column. Next, enter the sex of the first animal by clicking on the corresponding button above the sex column (throughout the database, the sexes of the animals are designated by F, M or ?). Here too, if you click on the column heading labeled “sex”, the value for the animal in the selected row will be used to fill the sex field for all samples below the selected row (the selected row is marked on the extreme left). The birthdate is filled in by first selecting the date (the current calendar week is the default but this can be changed by clicking on the arrow buttons, the popup button, or by entering the date by hand in the date area. Clicking on the “B-date” column header fills the birthdate from the selected row downwards, using the date displayed in the date entry area.

When you are finished, this area of the form should look something like this:

		sex	birth date
		female (F) <input type="checkbox"/>	CW: 12 <input type="checkbox"/>
		male (M) <input type="checkbox"/>	> <
		(?) <input type="checkbox"/>	25.03.2002
#	8		
number	sex	B-date	
1	3001	F	25.03.2002
2	3002	F	25.03.2002
3	3003	F	25.03.2002
4	3004	F	25.03.2002
5	3005	M	25.03.2002
6	3006	M	25.03.2002
7	3007	M	25.03.2002
8	3008	M	25.03.2002
9			
10			
11			
12			
13			
14			

If you have more than 25 samples, you access and fill out the second page of the form by clicking the “page” button at the upper right corner of the form. When you are finished with the data entry, save the form by clicking the “save” button at the bottom of the form.

When tio jobs are created by the animal tech group, the status is automatically set to “confirm”. In addition, an e-mail is sent to the scientist, informing her that a tio job must be confirmed and that tissue samples may need to be picked up. The scientist usually needs to analyse the tail biopsies to determine the genotypes of the animals. Then he/she must modify the tio job by specifying what should happen with the animals (the choices are retain, eliminate or mate) and then confirm the job by clicking on the confirm box next to the status area of the input form (upper right). When the tio job is confirmed, the status changes to “running” and the animal techs can process the job. Processing a tio job just means setting the status to completed if all the information is correctly filled out. When the tio job is completed, TierBase automatically creates the necessary elimination and mating jobs as specified by the scientist during the confirmation process.

Elimination (elm)

Elimination jobs are either created by the animal tech group when surplus animals are eliminated from a colony or when a scientist decides that certain animals are no longer needed. The tech creates the job by clicking the “eliminate” button. The elm job input form is displayed for data entry. This includes the colony, the person responsible, the account number and the number of animals. If the analysis area is active for the selected colony, the names of the animals must be entered in the area called “animal numbers” (A).

The image shows a screenshot of the Elimination (elm) job input form. The form is divided into several sections. At the top, there are fields for 'Line name' (containing 'Bob1'), '#', 'colony' (containing 'SPF/06'), and 'room' (containing 'R 6'). Below these is a section for 'animal numbers' with a 'check' button and a text input field. The 'total animals' field contains '0'. There is a checkbox for 'mark offspring' which is checked. A 'notes to caretaker' text area is below that. At the bottom, there is a section for 'elimination date' (containing '00.00.00' and 'dd.mm.yy') and 'Status' (containing 'completed').

Annotations A through E point to specific parts of the form:

- A**: Points to the 'animal numbers' input field.
- B**: Points to the 'check' button.
- C**: Points to the 'notes to caretaker' text area.
- D**: Points to the 'Status' field.
- E**: Points to the popup button next to the 'Status' field.

The “check” button can be clicked to check if the entered animals are present in the database. If the animals are reserved or dead, they cannot be put in the elimination job. The status of elm jobs created by the animal techs are automatically set to “completed” (D). As is the case for most other job input forms, the status can be changed by clicking on the popup button (E). For colonies with active analysis areas, the offspring are marked as dead when elimination jobs are completed..

Mating start (mst)

Mating start jobs are usually created by scientists to tell the animal techs to setup the mating but animal techs can also create mst jobs. Filling out the mst input form is fairly straight forward. For colonies with active analysis areas, a mating cage record is created and the offspring are marked as being in a mating when a mst job is completed.

Mating stop (msp)

Mating stop jobs are usually created by scientists to tell the animal techs to stop an existing mating. Filling out the msp input form is fairly straight forward. After entering the name of the user and selecting the colony, two pop-ups are filled with information which makes it easy to fill in the parental information.

The screenshot shows a software interface for creating a Mating Stop (msp) job. The form is divided into several sections:

- parents**: A section with a sub-label *F1, F2, xM*. It contains a 'name (geno)' field and three input boxes labeled 'female 1', 'female 2', and 'male'. A large 'X' is positioned between the 'female 2' and 'male' boxes. To the right is a 'mating #' field with the value '-1'.
- mating selection**: A section with a sub-label **** parents**. It contains a table with columns 'mate#' and 'date'. Below this are two sub-sections:
 - start mat. jobs**: A list of recent start mating jobs. An arrow labeled 'A' points to this section.
 - cage recs.**: A list of current mating cage records for the selected colony. An arrow labeled 'B' points to this section.

The first popup is a list of recent start mating jobs (A). If the scientist submitted a mst job and the mating was setup, you can select the mst job and the parents will automatically be filled into the msp input form. For colonies with active analysis areas, the second popup is filled with the current mating cage records for the selected colony (B). Selecting one of them automatically fills in the information for the parents. The corresponding mating cage record is marked as discontinued and the offspring records are marked as no longer being in a mating when a msp job is completed.

Tips for Animal Techs

For ao, elm and cage inventory entry forms, you have a short-cut for filling out the user name in the form. If no user name is entered when you fill out the line name or number and tab out of the field, the responsible scientist is automatically filled into the user field.

Orders cannot be placed for discontinued users.

Messages

In order to support the communication between the animal technician group and the rest of the database users, TierBase has two integrated message systems. The first is used when the animal techs would like to send a message to a scientist. Provided the SMTP server has been set by the database administrator (DbA), the techs can send an e-mail which is then read by whatever e-mail program the scientist uses (Eudora®, Outlook Express®, etc.). The second message system contained within TierBase does not involve sending an e-mail. This system is primarily used by the scientists when communicating with the animal techs. The message is sent to a breeding unit so that anyone there can read it. This can be useful when animal techs are absent because of illness or are rotated through different breeding units.

Sending an e-mail

To send an e-mail to one or more scientists, click the “S” button in the message area of the navigator or chose the *File->send_e-mail* menu item. The message input form is displayed.

The screenshot shows a dialog box titled "E-mail Message". It has two tabs: "general" and "available animals". The "general" tab is selected. The dialog contains the following elements:

- Recipient***: A text input field, a "select" button, and a counter showing "0".
- Subject***: A text input field.
- Message**: A large, empty text area for composing the email body.
- attachment**: A text input field, a "file" button, and a dropdown arrow.
- * mandatory**: A note indicating that the recipient and subject fields are required.
- Buttons**: "Cancel" and "send" buttons at the bottom right.

First select the recipients, either by typing the name in the field or by clicking the “select” button. If you would like to send the same e-mail to several users, use the “select” button and command-click the user records displayed. The number of selected recipients will be displayed to the right of the select button. Next, enter the subject and the message text. You can also include an attachment document by clicking the “file” button. If you are sending the mail from a Mac to Mac, you do not need to encode the document. If you are sending from Win to Win or Win to Mac, use base64 encoding. When you are finished, click the send button.

Reading animal tech messages

The message title in the navigator will have a grey background if there is a new message. To read it, just click the “R” button. You will be presented with a list of messages. You can read one simply by double-clicking on the record.

Modifying your user record

The first time you login to TierBase, you may be asked to enter some user information. TierBase needs to know your telephone number, e-mail address, preferred language, etc. If you need to modify any of this information, you can do this at any time by calling the *users -> modify your user record menu item*. (see xx)

Access to the Analysis Area

Animal technicians have access to the analysis area for all colonies where the analysis area has been activated. Activation is done either by the BA or by the scientist themselves. When the analysis is active, TierBase creates mating cages, litter and offspring records when appropriate. For example, when the scientist sends a mating start job (mst) to the animal techs, the names of the parents are filled in the job form. When the animal tech completes the job, TierBase looks for the parents in the offspring list. If they are found, a mating cage is created and the parents are marked as being in the new mating. Almost every job involves this type of communication between the job area and the analysis area. To get a better idea about how the information is stored in the analysis area, the animal techs should read about using the analysis area in the Generic User chapter of the handbook.

Animal Ethics Officer Guide

Introduction

In most cases where animals are being bred for experimental purposes, it is necessary to obtain permission from the governmental authorities before the breeding facilities or animals from the facilities can be used. It is also necessary to have a designated Animal Ethics Officer (AEO), who is responsible for insuring that the applicable laws pertaining to animal rights are observed. In addition, the AEO serves as the coordinating link between the breeding facilities, the scientific “end users” and the governmental authorities. TierBase has a variety of features which simplify and organize the duties of the AEO. This guide describes the features of TierBase which are specific for the animal ethics officer.

This chapter is not intended as an alternative to the other chapters in the handbook. They should also be carefully studied by the animal safety officer.

The Animal Ethics Group is responsible for maintaining the list of animal experimentation projects in use at the institute. They are also responsible for creating summaries of animal used for a project or for the institute. These summaries must be submitted to the authorities on a regular basis. Because all breeding and experimental use of animals are stored in Tier-Base with the jobs submitted to the breeding facilities, the AEO has an easy way of viewing the current animal use at the institute. With only a few simple commands, a complete listing of animal use can be created. This listing is formatted in such a way that it can be directly submitted to the governmental authorities.

AEO Navigator

After logging in, the AEO is presented with a Navigator window which contains buttons for the most frequently used functions.

The screenshot displays the 'Welcome to TierBase' interface. At the top right, it shows 'Animal Safety Group' and the user 'nielsenSAFE'. A 'privB' checkbox is visible. The main content is organized into sections:

- Projects:** Includes buttons for 'all', 'active', 'enter new', 'report', and 'edit project prefs'. Descriptions include 'list/modify projects', 'enter new project', 'calculate totals for projects and print them out if desired', and 'modify project preferences and list of treatments approved for projects'.
- Users:** Includes buttons for 'project leaders' and 'user'. Descriptions are 'show project leaders' and 'show all users'.
- Line:** Includes buttons for 'Mutant' and 'WT'. Description is 'show mutant or wild type lines present in the institute'.
- Inventory:** Includes buttons for 'Cages' and 'Line'. Description is 'show all jobs or just orders'.
- Exit TierBase:** A prominent button at the bottom.

Animal Ethics Projects

In most countries, it is not possible to perform experiments on animals at a research facility without first obtaining permission for the experiments from the governmental authorities. In Germany, two types of animal ethics projects (appreviated “projects” in this Guide) are typically granted. The first requires approval of the experiments planned. The second common project

type requires only notification of the animal user and does not involve experimentation on the animals. Projects must specify, in detail, not only the types of experiments approved, but also the names of the people performing the experiments and their qualifications, the number of animals approved, and the length of time over which the experiments will be performed. All of this information is stored in TierBase. TierBase also keeps a running total of the number of animals used in each project so that project leaders and animal ethics or safety officers can follow animal use and apply for new projects in a timely fashion.

Creation and modification of projects

Entry of new projects into the database can only be done by members of the animal safety group. Likewise, activation, inactivation or modification of projects can also be done only by this group. To create a new project, click the “enter new” button on the Navigator. The project input form will appear and the information can be entered.

When entering the names of the project leader and alternate leaders, a warning will appear if the name entered is not found in the list of registered users in TierBase. This should be a warning to check your spelling. Only users whose name matches exactly the entry in the project input form will be recognized as leaders or alternate leaders. The easiest way to enter the name is to click on the underlined project leader and alternate leader labels. A list of TierBase users will be presented and you can select the project leader from the list. Don't forget to enter the authorized treatments and the authorized users on the second and third pages of the input form. Click on the tabs at the top of the form to move between the various form pages. The project type is specified by clicking on the popup-box to the right of the project type field. If nothing appears when the box is clicked, the project type list has not been created. Cancel the project input form and do this now. (see the Figure , "Modify Project Preference Lists," on page 103)

Tips for Project Nomenclature

To make the management of projects easier, you might want to consider the following suggestions for naming the projects.

- Projects should have a short, easy to remember title consisting of the abbreviated name of the project leader.
- Projects could be given an extension to discriminate between approval and notification projects. For example, a numbered extension (eg. Mo-1) could designate projects requiring approval by the governmental authorities. Projects with a letter as extension (eg. ki or to) could indicate the notification projects. These projects are to be used only for ordering animals which will undergo no treatment before being painlessly killed.
- The reference number for approval projects could begin with an "A". If the A is followed by an "e" (extension), this could indicate projects which are an extension of a previously approved project and cannot be extended again. (Project leaders take note!).

Project leaders are allowed to view the current project information for which they have access. This includes the running totals and maximum number of ordered animals permitted for the project, when the project expires, etc. At any time, project leaders can also view a summary of animal orders associated with each of their projects for a specified time-span. They cannot change project information.

Project treatments

Part of the information stored with animal ethics projects in TierBase includes the treatments and the users approved by the governmental authorities. If you have used previous version of TierBase, the treatments (called project treatments here) were "hard-coded" and included things like irradiation, infection, operation with terminal anaesthesia, etc. Beginning with TierBase version 388, it is possible for the animal ethics officer (AEO) to specify the project treatments herself. This allows more flexibility in specifying the projects. In addition, each project treatment has an associated severity grade which also can be specified. In Switzerland, for example, all treatments fall into 3 severity classes (1-3), 1 being the least severe. At the end of the year, the AEO is required to send a report to the authorities with totals of animal used in each project for each severity class. If the country in which you are working does not have this rule, you can just enter 1 as the

severity and your report will contain only one severity class. It is probably wise to formulate the project treatments in such a way that they can be used again and again. This will prevent the yearly project report from being too long. For example, instead of creating project treatments titled “infection with virus a”, “infection with virus b”, etc. , it is better to create the more generic treatment “viral infection”. This is simpler and in most cases should be accepted by the authorities (an exact description of the virus and the protocol is contained in the project description with the authorities have anyway).

Modify Project Preference Lists

To create or modify project treatments, the AEO has a button on the navigator called “edit project prefs.”.

TierBase Project Preferences

Treatments

Default treatment for elimination
kill w/o treatment

Default treatment severity
1

experimental treatments	severity
animal shipment	0
behavioral restriction	1
bleeding	1
breeding	1
embryos without superovulation	1
immunization	1
infection	1
injection w/o disease	1
irradiation	1
kill w/o treatment	1
operation w/ term. anaesth	1
operation w/ trans. anaesth	1
operation w/o anaesth	1
other treatment	1
pain induction	1
superovulation	1
terminal bleeding w/ anaesth	1
toxicity test	1
tumor inoculation	1

Project Types

notification

MPI-ZH default project for elimination jobs

Mo-11-IM default project for immunizations

-EA Title suffix for projects used to send animals (<4)

-ZH Title suffix for projects used to breed animals (<4)

After clicking this button, a dialog is displayed with a list of the treatments stored in the database. To modify one or more of the treatment entries, click the button “edit” in the upper area of the dialog. Each of the treatments displayed can be modified by double clicking on them. A new treatment is created by clicking the “new record” button at the bottom of the form. Don’t forget to specify the severity class associated with the treatment. It can be chosen from the pop-up button to the right of the severity field. To modify the project type list, click the “edit project types” button. To specify default

projects for some job types, click the corresponding buttons in the bottom part of the dialog. Click the “Save” button to save your changes.

Project Report

To calculate the total number of animals used in any set of projects, click the “report” button in the yellow area of the navigator. You must first make a selection of projects that you would like to include in the totals. All animals used in all projects selected will be added together. After selecting the projects, you must specify the jobs you would like to use as a basis for summing the animals used. You specify the job status and the start and stop dates to be included. In this way, it is easy create a summary of animals and experiments used at an institute for a given time span. The report consists of a series of records summed according to the criteria given in the Report area. The animal use can be calculated by project, animal source, treatment and severity.

Project Report niensensafe

1 Project Selection

status active inactive all

type

select subset

selected projects

2 Job Selection

status

submit date start > dd.mm.yy

stop <

select subset

selected jobs

3 Report Title

project separate combine

animal source separate combine

treatment separate combine

severity separate combine

display with print no print

4 sum the animal use for the selected projects

These dates are used to select all jobs which were completed within this time range. By clicking the “OK” button, the animals are summed and displayed for printing.

Currently, only jobs of the type ao, pf and elm are included in the totals.

Database Administrator Group

Introduction

The TierBase database administrator (DbA) is typically a user who is involved in setting up the database so that it can be used by the other groups. The DbA usually is not involved in animal experiments, animal ethics project management or management of animal breeding. This chapter describes the functions available to the DbA. In addition, it is probably a good idea if the DbA has some perception of how TierBase is organized. Reading other chapters in this handbook will help.

The DbA is usually responsible for :

- installing and maintaining the server and client software necessary to run TierBase
- installing and maintaining the TierBase structure and data files. Maintenance includes creating backups and checking for/ and repair of data corruption.
- creating new user accounts with passwords
- putting users into appropriate user groups

- creating and maintaining data lists which are used throughout the database. These include lists such as: departments, species, cause of death, etc. These lists are usually configured when TierBase is first installed but can be modified at any time.
- collecting reports of database bugs and user suggestions.

Install Server/Client Software

TierBase can be used on a single computer as stand-alone application, or in a multi-user server/client environment. For a server/client environment, the 4D server software must be installed on the server hard drive and the 4D client software must be installed on a computer which has a network connection to the server. For instructions on installation of the 4D Server or Client software, refer to the installation instructions supplied on the 4D installation CD.

Install TierBase

The TierBase database consists of two files called the structure and the data files. On windows© operating system, the structure and data files are split into two files each.

To install TierBase for the first time, follow the steps below:

- Copy the structure file to hard disk. On Mac©OS, the structure file is called TBxx without an ending (the xx refers to the version number of TierBase). On Windows©OS, the structure file consists of 2 files which end in .4DB and .RSR. Unless you need to use data created by another TierBase application, it is recommended that you create a new data file. An empty data file is supplied on the TierBase install CD. To use the supplied data file, copy the data file to your disk. On MacOS, the data file has the ending data. On Windows©OS, the data file is actually 2 files ending in .4DD and .4DR. If you are using Windows©OS, please be aware of the fact that when you copy a file from a CD to your hard drive, the copied file may have the status Read only. To add new data or modify existing data, you must first change the status of the structure and data files to Read/Write before you begin to use TierBase.

- Start the server by double-clicking on the server icon
- Follow the instructions for setting up the server (license number)
- Login to TierBase as the administrator from a client computer.
- Enter the TierBase license number.
- Enter data for various lists to setup the working environment. To do this, call the “edit Lists” menu item.

TABLE 1. Lists

List name	Description	Example
analysis method	a list of methods used to analyze the animals	PCR, FACS, ELISA, Southern
breeding requirements		sterile bedding, antibiotics, filter cap cage
breeding room	a list of breeding rooms for the animal strains	R101, R102, R103
cause of death		wasting, tumor, infection, sold
delivery location		
department	a list of departments associated with users and animal strains	
sc_	a list of possible physical strain characteristics (sc) which can be associated with the offspring of a given strain	sc_coat color, sc_body form
species	a list of species from which the animal strains are chosen (must be english)	mouse, rat, rabbit
standard strains	a list of standard animals strains often used	BALB/C, C57BL/6, NMRI, 129Sv

- Enter new users and passwords by calling “new user account” from the user menu. Users may have to be put in a group in order that they have privileges or access to functions which are appropriate to that group. The relevant groups are the breeding administrator, animal technician and animal ethics groups. Users not put in a group will be classified as a generic user. These are the scientists. The DbA should read the chapters in this handbook corresponding to these groups to learn more about the functions of these groups.

Install a TierBase Update

When a new version of TierBase becomes available, it is easy for the DbA to incorporate the new version while using existing data. Basically, the update consists of three steps:

- Save the user accounts.
- exchange the structure files
- import the user accounts

To perform a TierBase update:

- Login to TierBase as the administrator
- Save the users accounts by choosing the “new password account” menu item. In the password editor, call the menu item “save groups”. This will store the information for users, passwords and groups to a file on your hard disk.
- Log off
- If you are running a Client/Server environment, stop the TierBase application on the server.
- Navigate to the folder containing your database and remove the structure file. (If you are using a server, this file will be on the server hard drive.) On MacOS®, the structure file is called TBxx without an ending. On Windows®, the structure file consists of 2 files which end in .4DB and .RSR. It would probably be safer to archive the structure file(s) but you can also just discard them.
- Copy the new TierBase structure file(s) to the database folder.
- If necessary, rename the datafile(s) so that it exactly matches the prefix name of the structure file prefix. For example, if your structure file is

called TB3 (TB3.4DB and TB3.RSR on Windows©), then the datafile should have the name TB.data (TB3.4DD and TB3.4DR on Windows©).

- On Windows©, make sure that all files are set to Read/Write and are not Read only.
- If appropriate, start the server.
- Login to TierBase as the database administrator from a client computer.
- Invoke the password editor window and load the groups you saved at the beginning.