Genetix

QSoft Data Tracking

Application Guide

www.genetix.com

08MAN1074.A0
Effective Date: 11-Feb-10

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QSoft Data Tracking

What is QSoft Data Tracking?

QSoft Data Tracking is a database system for storing details of biological samples that have been manipulated by the modules available for Genetix robots and instruments. These modules currently include: Colony Picking, Gridding, Rearraying, Replicating, Microarraying, Liquid Handling and Yeast-2-Hybrid.

The system consists of a database and a user interface for querying this database to identify the contents of a given receptacle (well plate, bioassay tray, slide or filter).

The database stores information about each sample - including the receptacle that each sample exists in. The Data Tracking system will also allow you to store details of colony properties such as size, average intensity (useful for GFP analysis), and location.

The system does not currently store details of processes such as DNA sequencing which has been performed by non-Genetix robots. However samples can be annotated manually if required. The system is designed as an efficient mechanism for collating, storing and querying sample information as samples pass through Genetix robots.

Each run of a Genetix robot module generates a set of log files, the one that is relevant to Data Tracking is an XML file with a filename in the following format:

QSoft Log Date Time DT.XML

This file contains details of each receptacle accessed during the run and the movement of samples between receptacles (e.g. from well plates to filters during Gridding). These files are then imported into the database to reflect the changes made during the run.

Data Tracking relies on being able to uniquely identify each receptacle for which information is stored. This is achieved by applying a barcode to each receptacle. The database can be queried by entering a barcode to view all of the samples contained in that receptacle (arranged by location). Multiple samples can be stored in a given location if required e.g. where samples have been pooled or in Yeast-2-Hybrid experiments where each colony represents a bait and prey.

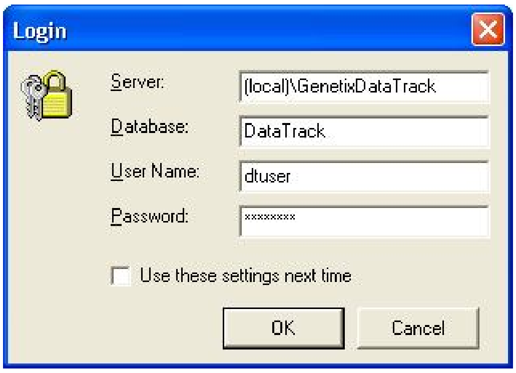
QSoft Data Tracking Software

Overview

Start the application by double-clicking the **QSoft Data Tracking** icon on your Windows® desktop.

Figure 1: QSoft Data Tracking Icon

The first time that you run Data Tracking you will be prompted to connect to a database using the login screen.



Server: (local)\GenetixDataTrack

Database: DataTrack

User Name: dtuser

Password: ********

☐ Use these settings next time

Figure 2: Login Dialog

Enter the required details as described below.

Server

Displays the location of the database to log into. The default is the data tracking database on the local machine as shown in the screen above – you will only need to change this if a separate data tracking server exists on your network.

Database

The database name defaults to “DataTrack” – you will only need to change this if you are using another database that exists on a separate data tracking server on your network.

User Name

Allows login to the database – enter **dtuser** as shown in the screen above. There is currently no facility to change the user name.

Password

Allows login to the database – enter **dtuserpw**. Please note that the password is case sensitive so type it exactly as shown. There is currently no facility to change the password.

Use these settings next time

Tick this box to override the password security. If this box is ticked you will not be prompted to log in every time you run Data Tracking.

If you want to display this dialog again you can access it by opening the **File** menu and choosing **Select Database.**

QSoft Data Tracking Application Window

The setup window is very similar in layout to many typical Microsoft® Windows applications. The setup window is split into 2 panes.

Commands can be selected by dropping down the appropriate menu or clicking the relevant button on the toolbar.

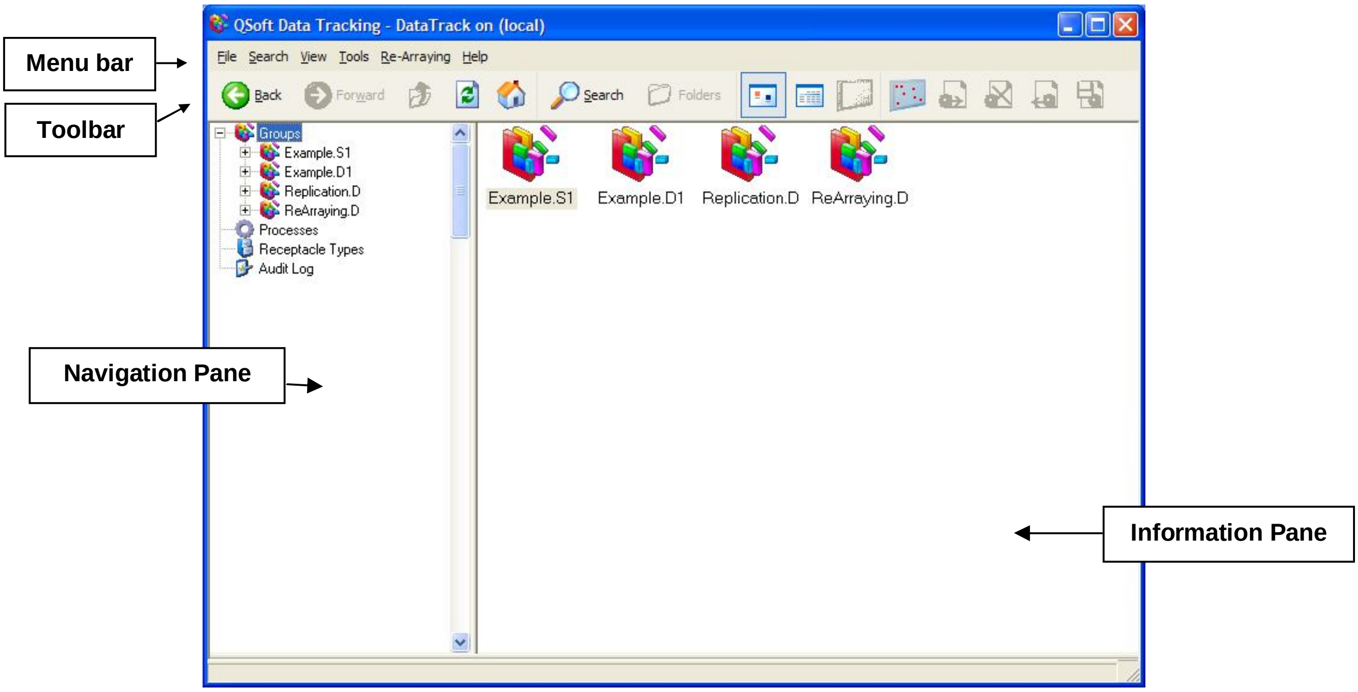


Figure 3: Data Tracking Opening Screen

Title Bar

The topmost section of the setup screen is the title bar, it displays the name of the current database.

Menu Bar

The menu bar commands are described in detail in the section headed **The Menu Options** (below).

Toolbar

The toolbar provides shortcuts for the most commonly used commands. All have equivalent options in the menus.

Navigation Pane

The navigation pane is on the left-hand side of the screen.

Groups

Displays a list of the groups of receptacles in the database.

Highlight the **Groups** icon, a list of the groups in this database will be displayed in the Information pane.

Display Receptacles

Double-click a group name in the Information pane to show all receptacles within that group.

Display Samples

Double-click a receptacle name in the Information pane to show all samples in the selected receptacle.

For each sample this lists the location (as a grid co-ordinate or well location), accession number and name (if allocated) as well as a brief description and any annotation that has been stored.

Display Sample History

Double-click a sample name in the Information pane to show all processes that have involved this sample – every source and destination location along with the dates and times that the transfers took place.

Display Processes

If you double-click a history item, the Processes list is displayed with a highlight to indicate this items position in the order of **all** the processes imported into Data Tracking.

Processes

Displays a list of the processes that have been imported into the current database. Typically a process might be a routine previously performed on the data such as Picking, Gridding etc. (by importing the Data Tracking XML file) or an import from QSoft Library Manager into a Data Tracking database.

Receptacle Types

Select this to display all types of receptacles used in the current database. Receptacles are containers such as well plates, bioassay trays, slides and filters.

Audit Log

Shows the date and time of all changes that have been made to the database.

Information Pane

The Information Pane is the right-hand section of the screen. Details of the selected item are displayed in this pane.

The data displayed here can be sorted by field (column), to do this click the relevant column header.

Summary information about the selected item is shown on the left hand side of this pane.

The Menu Options

QSoft Data Tracking contains drop down menus that can be accessed by pointing with the mouse and clicking the left mouse button.

File

The File menu contains facilities for data file operations.

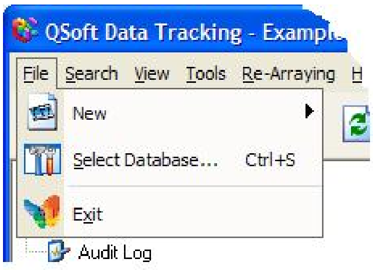
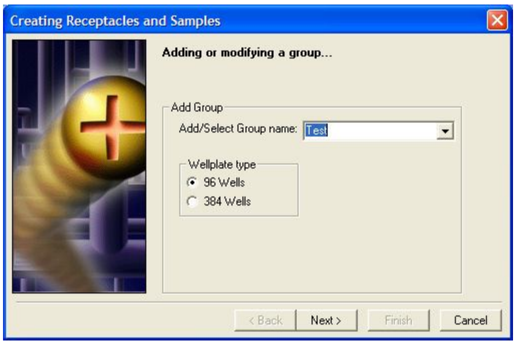


Figure 4: File Menu

New

New Data – Allows the addition of more plate(s). Either add the plates to an existing group or create a new group. A wizard will guide you through the steps for adding new data. The first dialog prompts you to select a group name from the list or type in a new group name. Next, select the correct plate type.



Adding or modifying a group...

Add Group

Add/Select Group name: Test

Wellplate type

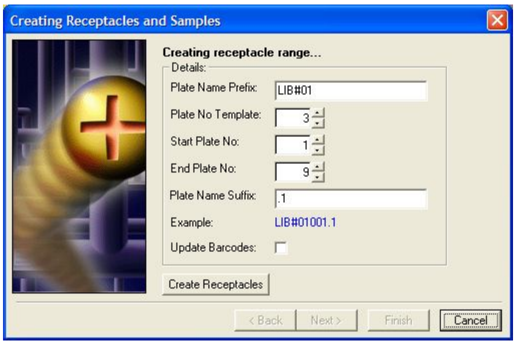
● 96 Wells

○ 384 Wells

Figure 5: Add or Select Group

Click Next then,

Click the Plate Range button.



Creating receptacle range...

Details:

Plate Name Prefix: LIB#01

Plate No Template: 3

Start Plate No: 1

End Plate No: 9

Plate Name Suffix: .1

Example: LIB#01001.1

Update Barcodes: ☐

Figure 6: Enter Range Details

Plate Name Prefix - You can either accept the default plate name prefix or create your own.

Plate No Template – There are six predefined templates for plate name styles, however custom templates can be defined.

Note - Defined templates will overwrite an existing template.

To define a custom template:

- select the template number to overwrite
- type in the custom prefix
- set values for start and end plates
- type in the custom suffix
- click OK

Start Plate No - Define the first plate number to add.

Note: If plates have previously been added to the library, the number entered must be greater than the number of the last existing plate.

End Plate No – Define the end of the range by specifying a plate number.

Plate Name Suffix - Either accept the default, predefined, plate name suffix or create a suffix.

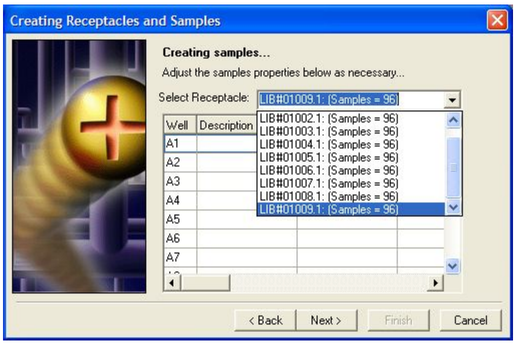
Note: An example of what has been defined appears at the bottom of the screen. The template option saves what has been defined, so by selecting the template the defined settings for that number will appear.

Update Barcodes – This check box will create a barcode matching the plate name.

Note: Barcodes cannot be generated for an existing range of plates. If creating barcodes was omitted then the range will need to be deleted and re-created with the **Update Barcodes** option checked.

Create Receptacles – Click this button when satisfied with the plate settings.

Click **Next** to display the following dialog.



Creating Receptacles and Samples

Creating samples...

Adjust the samples properties below as necessary...

Select Receptacle: LIB#01009.1: (Samples = 96)

LIB#01002.1: (Samples = 96)
LIB#01003.1: (Samples = 96)
LIB#01004.1: (Samples = 96)
LIB#01005.1: (Samples = 96)
LIB#01006.1: (Samples = 96)
LIB#01007.1: (Samples = 96)
LIB#01008.1: (Samples = 96)
LIB#01009.1: (Samples = 96)

Well	Description
A1	
A2	
A3	
A4	
A5	
A6	
A7	

Figure 7: Populate Plate Details

Drop down the list of Receptacles and select each one to populate the list of wells for that plate.

If required, other information can be entered for each well e.g. Description, Accession number.

Click **Next** then click Export Samples.

When the Export process has finished, click **Finish** to close the wizard.

Select Database

Displays the login dialog to allows connection to a different database or login as a different user.

Exit

Click this to quit the application.

Search

The Search menu opens a dialog in the Navigation pane which offers the facility to locate a receptacle or sample according to a specific barcode or keyword with optional restrictions on the search criteria.

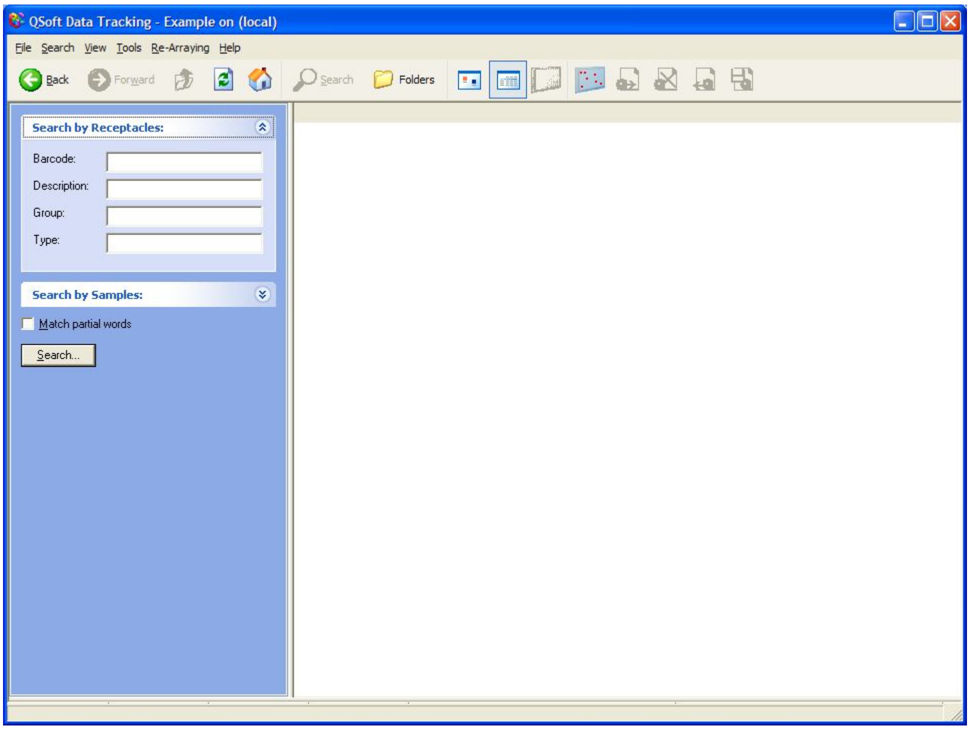


Figure 8: Search by Receptacles

Search by Receptacles

Barcode

Enter either a complete barcode or part of a barcode.

Description

Enter text known to be in a container’s description field.

Group

Enter a known Group name.

Type

Enter a receptacle type such as **Genetix Plate 96X6010.**

Search by Samples:

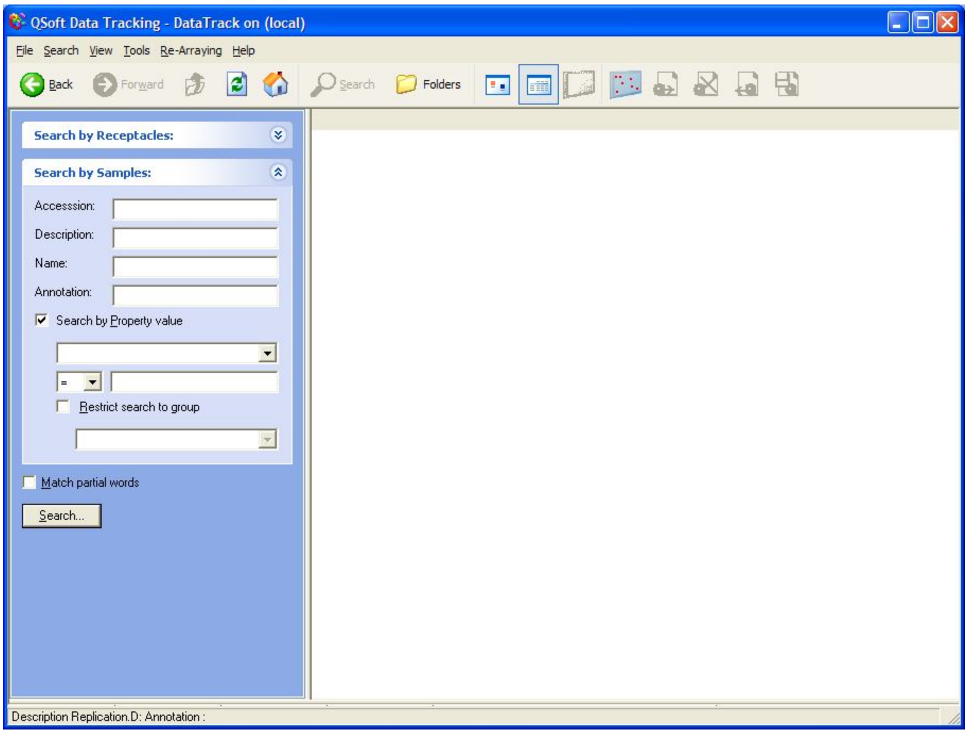


Figure 9: Search by Samples

Accession

Enter a known accession number.

Description

Enter text known to be in a sample’s description field.

Name

Enter text known to be in a sample's name field.

Annotation

Enter text known to be in a sample's annotation field.

Search by property value

Search for samples containing properties of interest. Select a custom property from the drop-down list, choose a comparison operator from the list and enter the search criteria.

Restrict search to group

Tick this box to limit the search to one specific group, then choose the group from the drop-down list.

Match partial words

Tick this option to allow the search to locate samples using a given set of characters within any string. For example, if **Genetix Plate** is entered**,** all receptacles of Type **Genetix Plate** will be listed.

Search

Click this button to activate the search based on the given criteria.

View

The View menu enables selected items to be viewed and shows how library information is displayed.

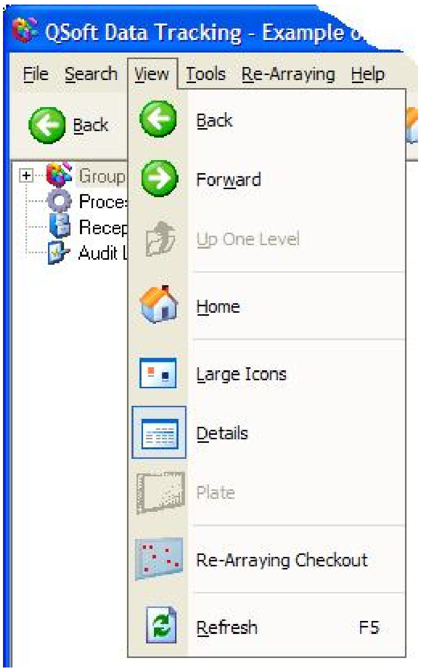


Figure 10: View Menu

Back

Click this to revert to the previous view, continue to click it to move through previously viewed screens in sequence.

Forward

Click this to move up through the screens in sequence to the most recently displayed one.

Up One Level

Moves the current view to the next level up in the hierarchy.

Home

Select this option to close the search window and return to “Groups” view.

Large Icons

Default view, groups or receptacles are displayed as icons with the name underneath.

Details

Receptacles or Wells and associated information are displayed in table format.

Plate

Available if a plate is selected in the Navigation pane. The plate layout is displayed in the Information pane, as you click on a well location, information about the well is shown in the status bar at the bottom of the window.

Rearraying Checkout

Samples that have been selected for inclusion in a rearraying file are listed in a separate pane in the lower part of the Data Tracking window (see Rearraying below).

Refresh

Updates the screen display.

Tools

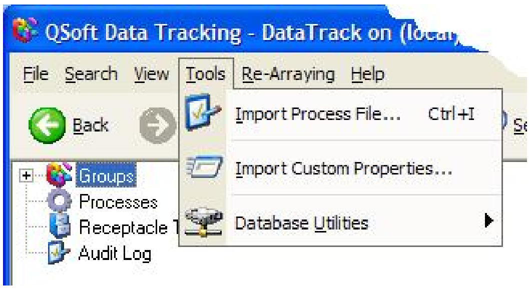
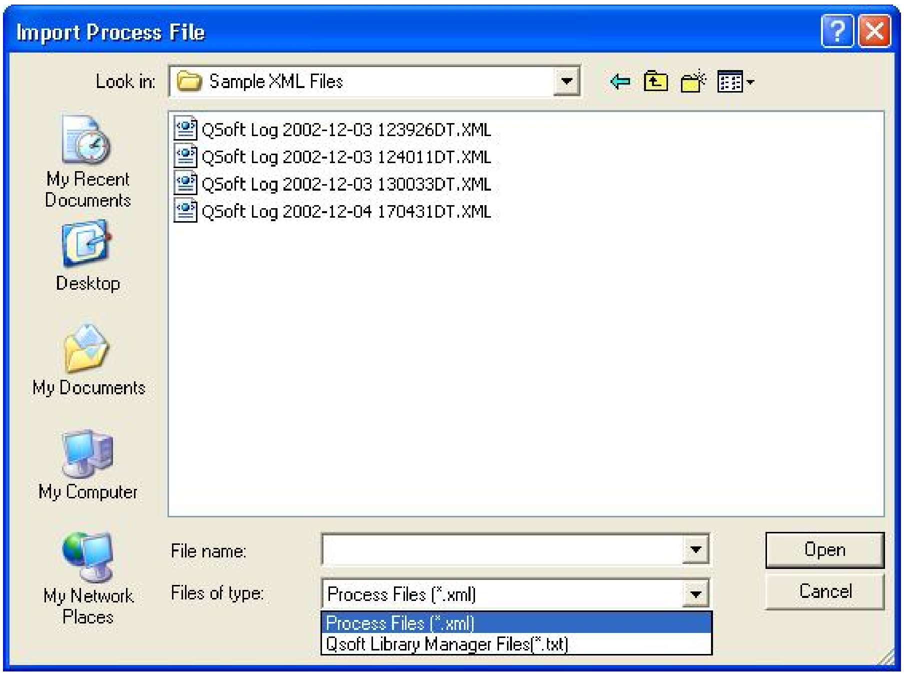


Figure 11: Tools Menu

Import Process File

Import either – a Data Tracking process file (in XML format), which is the result of a process previously carried out by your Genetix robot (e.g. Picking, Gridding etc.) – or a QSoft Library Manager file (which has a .txt extension). The QSoft Library Manager file format can be used to import data from an external source such as LIMS or Excel. For an example of the Library Manager file format, see Appendix A of this manual.

A Windows Open File dialog box is displayed to allow you to browse to the folder where the import file is located.



Look in: Sample XML Files

QSoft Log 2002-12-03 123926DT.XML
QSoft Log 2002-12-03 124011DT.XML
QSoft Log 2002-12-03 130033DT.XML
QSoft Log 2002-12-04 170431DT.XML

File name:

Files of type: Process Files (*.xml)

Figure 12: Import Process File

Drop down the “Files of Type” list and select the required file format then choose the file to be imported.

Import Custom Properties

Custom properties are values that can be applied to samples at a given location. For example, a plate reader can be used to obtain a set of readings for the samples in a well plate. If these values are imported into QSoft Data Tracking, they can later be used in searches to identify samples of interest. There are very few restrictions on the values that can be used for custom properties; for full details and for information about the format of the custom properties file, see Appendix B.

Database Utilities

Backup

Creates a copy of the database, a dialog will prompt for a unique name to be entered for the backup.

Restore

Will recover a previously backed up database file.

Delete

Allows old database backups to be deleted.

Purge Database

This will clear all user data from the database.

To limit the risk of accidently purging the database, log in as the System Administrator to use this option:

- The default user name is **sa**
- The default password is **genetixsapw**

Rearraying

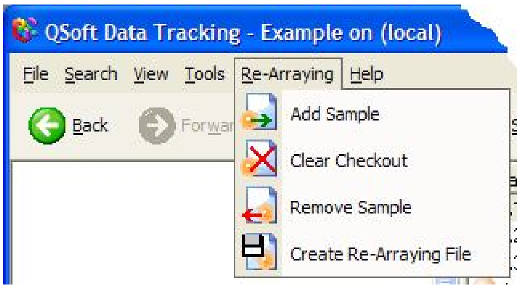


Figure 13: Rearraying Menu

Add Sample

Click this option to Add the highlighted sample(s) from the currently selected plate to the Rearraying checkout. Select several contiguous samples by holding down the Shift key, clicking the first sample in a block then clicking the last sample in the block. To select several non-contiguous samples, hold down the Control key as you click each sample.

Clear Checkout

Will clear all samples from the rearraying checkout.

Remove Sample

This will remove selected samples from the rearraying checkout. Several samples can be removed at once by selecting them with Shift+click or Control+click in the same way as for adding samples.

Create Rearraying File

Select this option to write the contents of the Rearraying checkout to a text file. You will be prompted to enter a filename with a .IMP extension. The data from this file can then be used as input to a Rearraying routine on a Genetix robot.

The Toolbar

The toolbar provides shortcuts for the most commonly used commands. All have equivalent options in the menus:

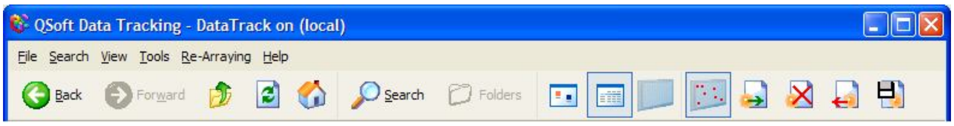


Figure 14: Toolbar

Hold the mouse over any of the toolbar buttons for a few seconds and a "Tooltip" will be displayed to indicate the name of the button.

Using QSoft Data Tracking

Flow of Sample Data

The diagram in Figure 15 describes the role of QSoft Data Tracking in the processes performed on sample data. This is described in more detail below.

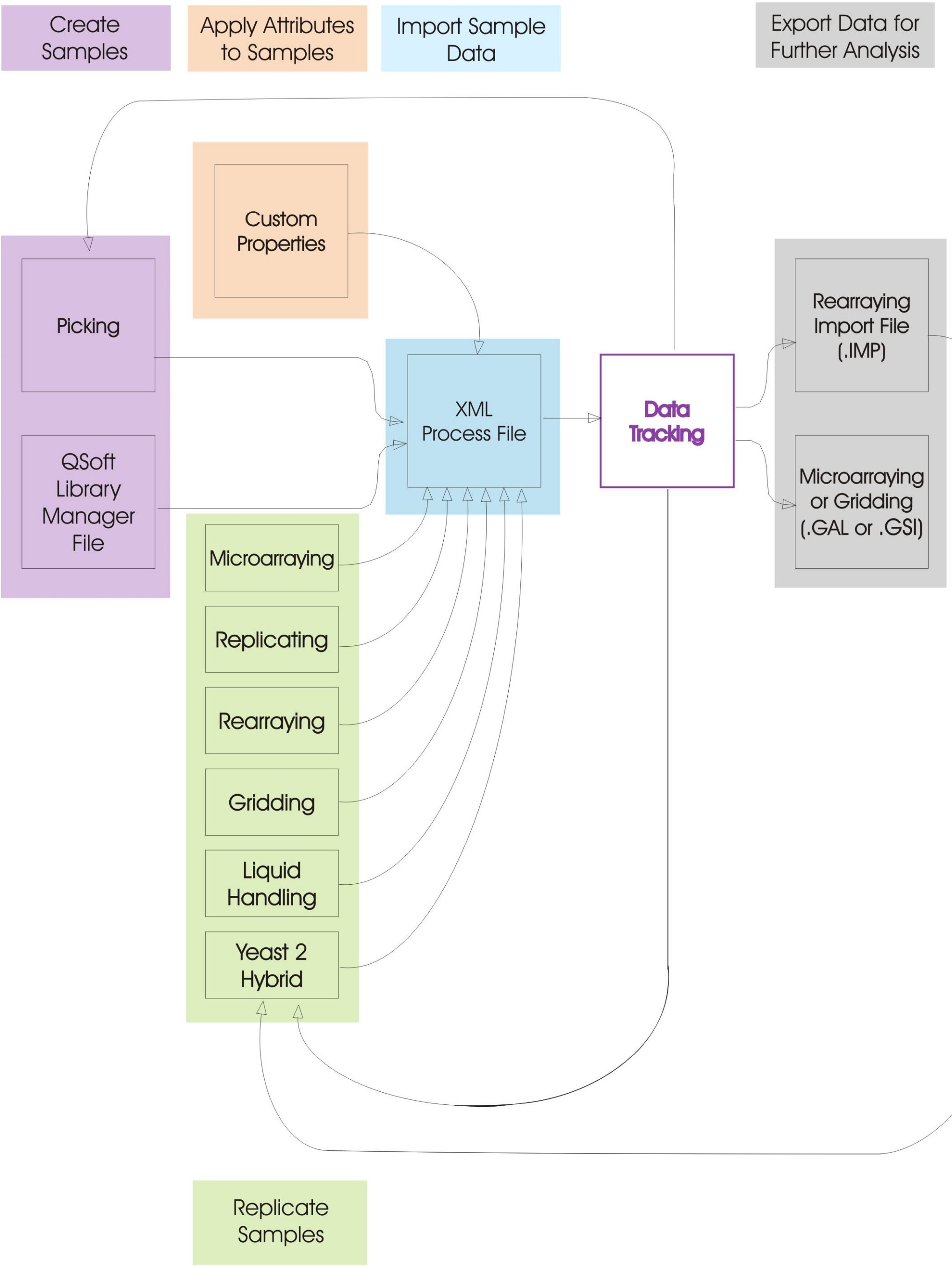


Figure 15: Flow of Sample Data

Create Samples

The samples can be entered into Data Tracking via one of two routes, either automatically - from a Picking run on a Genetix robot or manually - imported from another data source.

QSoft Picking software tracks the samples replicated from bioassay trays to well plates. This tracking information is stored in a process file in xml format (with a filename which ends DT.XML). The file contains information which uniquely identifies every sample with each individual replication carried out.

Apply Attributes to Samples

It is possible to create a Custom Properties file to contain searchable attributes about specific samples. This is a comma-separated text file with user-defined fields which hold values for each sample well e.g. A plate reader may generate some data for a well which can then be imported to the database.

The format of the Custom Properties file is described in Appendix B.

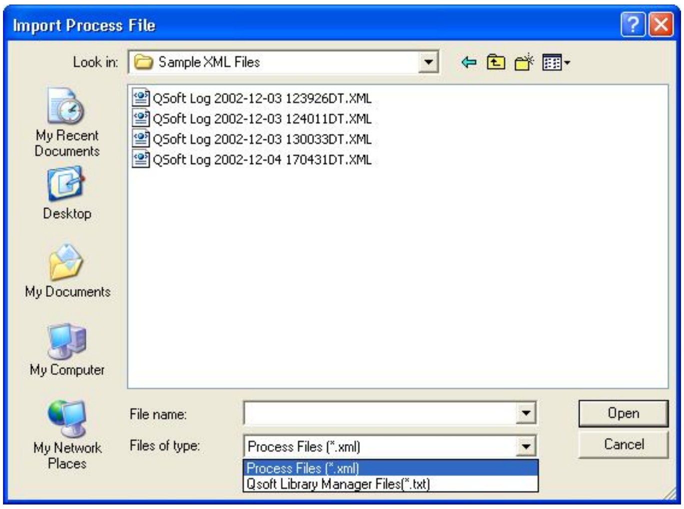
Import Sample Data

The xml process file is imported into QSoft Data Tracking.

It is possible to manually import a process file created using QSoft Library Manager (the predecessor of QSoft Data Tracking) or by converting a file from an external source (such as LIMS or Excel) into Library Manager file format. This file will be converted to XML format by the Data Tracking software.

For an example of the Library Manager file format, see Appendix A of this manual.

To import a process file, open the **File** menu and select **Import Process File**.



Look in: Sample XML Files

QSoft Log 2002-12-03 123926DT.XML
QSoft Log 2002-12-03 124011DT.XML
QSoft Log 2002-12-03 130033DT.XML
QSoft Log 2002-12-04 170431DT.XML

File name:

Files of type: Process Files (*.xml)

Process Files (*.xml)
Qsoft Library Manager Files(*.txt)

Figure 16: Import Process File

Browse to the location of the process file and select the file type from the drop down list. Highlight the import file name and click **Open**.

Process/Interrogate the Data

To locate a sample, either browse through the groups in the Navigation pane of the application window or use the Search facility. For detailed information of the search facility, see the section headed **Search** on page 11.

To view or edit the properties of a sample, right click with the mouse on the selected sample. The following shortcut menu is displayed.

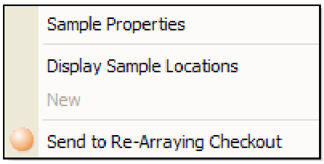
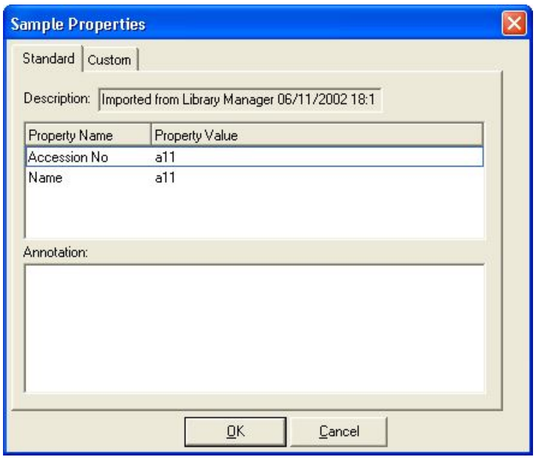


Figure 17: Sample Shortcut Menu

Sample Properties

A dialog similar to this one will appear.



Description: Imported from Library Manager 06/11/2002 18:1

Property Name	Property Value
Accession No	a11
Name	a11

Annotation:

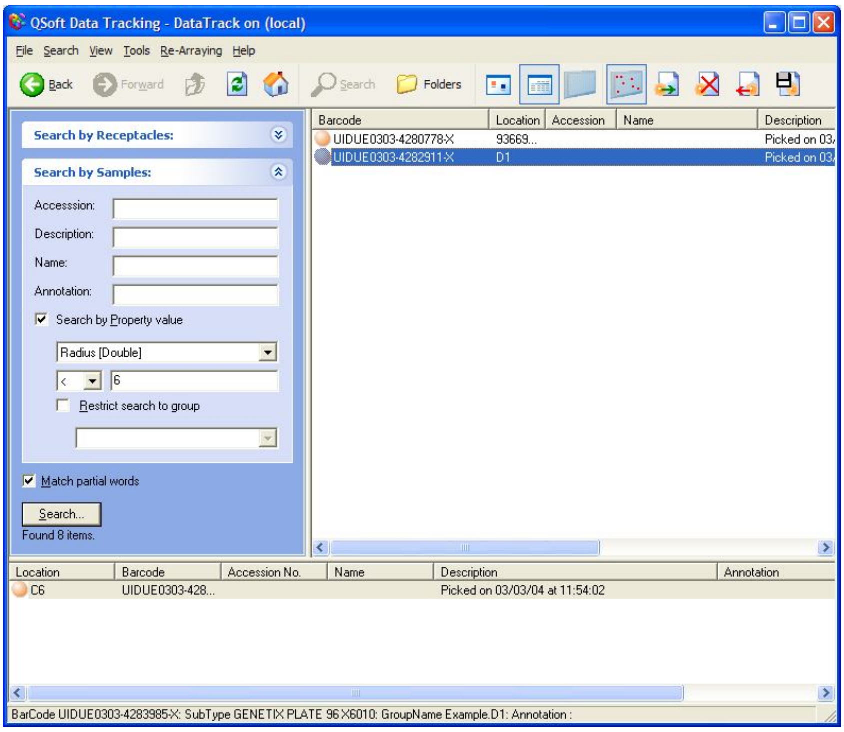
Figure 18: Sample Properties

To edit a property value, double-click the relevant item and type in the new value. Add or amend the annotation associated with the sample.

Click OK to store the information.

Export the Data for Further Processing

The resulting data from a Sample Search by Property Value can be written to a Rearraying Import file for further processing. To do this, either right-click a sample and select **Send to Rearraying Checkout** from the shortcut menu (see Figure 17 above) or highlight (select) a sample from the list and use the options in the Rearraying menu (as described in the section describing the Rearraying menu on page 16).



Accession:
Description:
Name:
Annotation:
☑ Search by Property value
Radius [Double]
< 6
☐ Restrict search to group
☑ Match partial words
Found 8 items.

Barcode	Location	Accession	Name	Description
UIDUE0303-4280778-X	93669...			Picked on 03/
UIDUE0303-4282911-X	D1			Picked on 03/

Location	Barcode	Accession No.	Name	Description	Annotation
C6	UIDUE0303-428...			Picked on 03/03/04 at 11:54:02	

BarCode UIDUE0303-4283985-X: SubType GENETIX PLATE 96 X6010: GroupName Example.D1: Annotation :

Figure 19: Example Search

Add samples using the options from the Rearraying menu and create the Rearraying file as described on page 16.

Glossary of Terms

Array

Nylon filter or slide on which the clones are immobilized or array of DNA/protein spots on a glass slide.

Arrayed

Distribution of colonies or samples into known positions from 96 or 384 well plates.

Base Class

Blueprint for the properties of an object.

Bioassay Tray (QTray)

22x22 cm clear plastic tray from which colonies/phage are picked.

Bioassay Tray Holder

Perspex holder fitted to the robot bed for holding two Bioassay trays in place whilst carrying out a Picking routine.

Block

A pattern of clones or spots immobilized within an array produced by one pin.

Blue/White

Blue White selection protocol for visualization of colonies expressing β-galactosidase.

CCD Camera

Charge Coupled Device Camera. A cooled digital camera for capturing high-resolution images with a wide dynamic range.

Clone

A particular DNA moiety contained within a DNA vector and propagated in a host cell.

Compressing

Converting 4 x 96 well plates into 1 x 384 well plate etc.

Custom Property

A custom property is a value that you can apply to samples at a given location in order to use later in the Data Tracking search facility.

Datum Point

A series of X, Y, Z co-ordinates that define a set position on the Robot bed.

Destination Plate Holders

Holders for microplates located on the bed of the robot. The number of Plate Holders available depends on which robot is being used.

DMF

Dimethyl formamide.

Expanding

Converting 1 x 384 well plate into 4 x 96 well plates etc.

Field

An array is divided into fields. The field is the area covered by the head.

Filter Block

Solid blocks onto which gridding membranes are placed (2 per QPix).

GFP

Green Fluorescent Protein. Used to monitor subcellular protein localization, analyze differential gene expression. Protein interactions and cell transfection efficiency.

Gridding head

Head used for gridding and replicating. Available in 96 pin or 384 pin formats, either sprung or gravity.

Guide Spot

A reference spot created by the user, in order to make grids (arrays) easier to read.

Hybridization intensity

(as judged by pixel intensity) is a measure of gene activity.

I/O

Inputs / Outputs.

IPTG

Isopropyl-thio-β-D-galactoside.

LB

Luria-Bertani Medium.

LIMS

Laboratory Information Management System

MADGE

Microplate Array Diagonal Gel Electrophoresis.

Marker Spot

A reference spot created by the user, in order to make grids (arrays) easier to read.

Multi-spot pin

Microarray pin which is loaded with a volume of sample which is then dispensed in aliquots.

Phage

Bacteriophage.

Picking Tray

See Bioassay Tray Holder.

Probe

A labeled DNA or RNA used to hybridize to an array .

Process (Data Tracking)

A routine performed on the data or an import from a file in QSoft Library Manager format.

QSoft Library Manager

This is the predecessor of QSoft Data Tracking.

QSoft.DLL

ActiveX software component housing all the functionality of robot software.

Rearraying

Redistribution of selected colonies into new plates performed with picking head.

Receptacle

Container used in Data Tracking - such as well plate, bioassay tray, slide or filter.

Replicating

To copy, compress or expand 96 or 384 well plates.

Script

Listing of all moves needed to complete a routine.

Spot

Corresponds to a visual hybridization imprint of a clone with a probe.

SSC

Sodium Chloride/Sodium Citrate buffer.

Sub-Grid

(See Block)

X Drive

Axis running from back to front of the QArray Mini bed or right to left on any other bench-top robot.

XML

Extensible Markup Language. A simple text format derived from SGML Originally designed to meet the challenges of large-scale electronic publishing, XML is also used in the exchange of a wide variety of data on the Web.

Y Drive

Axis running from left to right across the QArray Mini bed or back to front on a bench-top robot.

Y2H

Yeast 2-Hybrid. Screening of ‘prey’ proteins encoded by cDNA libraries for interaction with a particular ‘bait’ protein.

Z Drive

Axis running vertically on the Robot bed.

Appendix A

QSoft Library Manager

Export a file from QSoft Library Manager

To export a file from QSoft Library Manager, open the File menu and select Export Data – QSoft Library Manager will prompt you for a file name (with a .txt extension). A message will confirm that the Export operation was successful.

QSoft Library Manager File Format

Comment lines can appear anywhere in the file and must be prefixed with //

The first meaningful statement specifies the group name

e.g.

LibraryName: Example One

The next meaningful statement specifies the plate type in this library

e.g.

PlateType: Genetix 96

Subsequent lines describe Plate/Well information in the following format

LibraryPlateName,Barcode,WellName,SampleID,AccessionNo,Comment

e.g.

EXAMPLE_PLATE_1,98765432,A1,Tomato,XX0099P11,Meaningful remark

Barcode, Sample ID, Accession no. and Comments are optional fields and therefore may be omitted however the comma separators must still be present

e.g.

EXAMPLE_PLATE_1,,A1,,,

Example QSoft Library Manager File

```
//GENETIX LIBRARY MANAGER FILE
//
//Comments are prefixed //
//Note: this file must consist of the following format:
//LibraryName: Test Library
//PlateType: Genetix 96
//
//Plate/Well format as follows:
//LibraryPlateName, Barcode, WellName, SampleID, AccessionNo,Comment
//
LibraryName: EXAMPLE ONE
PlateType: Genetix 384
//
```

```
EXAMPLE_PLATE_1.1,98765432,A1,Tomato,XX0099P11,Descriptive remark
EXAMPLE_PLATE_1.1,98765432,A2,Cress,ZZ9900X22,
EXAMPLE_PLATE_1.1,98765432,A3,,
EXAMPLE_PLATE_1.1,98765432,A4,Barley,
EXAMPLE_PLATE_1.1,98765432,A5,,
EXAMPLE_PLATE_1.1,98765432,A6,,
EXAMPLE_PLATE_2.1,,B7,,
EXAMPLE_PLATE_2.2,,B9,,
EXAMPLE_PLATE_2.3,,H6,Tomato,
EXAMPLE_PLATE_2.4,,H11,Red Pepper,
EXAMPLE_PLATE_6.1,,,,
EXAMPLE_PLATE_7.1,,,,
```

Appendix B

Example Custom Properties file

This is a comma-separated text file. The Barcode field and the Location field are required and must be the first 2 fields respectively. Subsequently there must be at least one more user-defined field to store custom properties. Data Tracking will automatically determine the data type stored in a user-defined field (string, floating point number etc). It is possible to add several hundred user-defined fields if required.

The first row of the file contains the field names separated by commas. Subsequent rows contain the data for each field. The **Barcode** field and the **Location** field must not be left blank, any user defined field may be left blank but the comma to indicate the division between fields must still be present. See example below.

Barcode,Location,Positive,Name,Age

25/02/2002 10:41:59:1,A1,TRUE,well a1,5

25/02/2002 10:41:59:1,B4,,,23

25/02/2002 10:41:59:1,D2,FALSE,well d2,56.4

25/02/2002 10:41:59:1,F6,,,2

25/02/2002 10:41:59:1,E14,TRUE,well e14,19

25/02/2002 10:41:59:1,C2,,,2

Appendix C

XML Schema

XML (Extensible Markup Language) (XML) is a simple, flexible text format derived from SGML. Originally designed to meet the challenges of large-scale electronic publishing, XML is also playing an increasingly important role in the exchange of a wide variety of data on the Web and elsewhere.

XML Schemas express shared vocabularies and allow machines to carry out rules made by people. They provide a means for defining the structure, content and semantics of XML documents.

Below is the schema used by Genetix for data exchange, this can also be found at the following web page www.genetix.com/schemas/genetix-process-1.0.xsd

```
<?xml version="1.0" encoding="UTF-8" ?>
   <xs:schema xmlns:xs="http://www.w3.org/2001/XMLSchema" elementFormDefault="qualified">
      <xs:element name="annotation" type="xs:string" />
      <xs:element name="description" type="xs:string" />
      <xs:element name="process">
         <xs:complexType>
            <xs:sequence>
               <xs:element ref="description" />
               <xs:element name="starttime" type="xs:dateTime" />
               <xs:element name="robotname" type="xs:string" />
               <xs:element name="modulename" type="xs:string" />
               <xs:element name="softwareversion" type="xs:string" />
               <xs:element name="operator" type="xs:string" />
               <xs:element name="runnumber" type="xs:integer" />
               <xs:element name="group" type="xs:string" />
               <xs:element name="createsamples" type="xs:boolean" />
               <xs:element name="contents">
                  <xs:complexType>
                     <xs:choice minOccurs="0" maxOccurs="unbounded">
                        <xs:element name="receptacle">
                           <xs:complexType>
                              <xs:sequence minOccurs="0">
                                 <xs:element ref="description" minOccurs="0" />
                                 </xs:sequence>
                                 <xs:attribute name="subtype" type="xs:string" use="required" />
                                 <xs:attribute name="columns" type="xs:integer" use="required" />
                                 <xs:attribute name="rows" type="xs:integer" use="required" />
                                 <xs:attribute name="barcode" type="barcode" use="required" />
                                 <xs:attribute name="type" type="xs:string" use="required" />
                                 <xs:attribute name="group" type="xs:string" use="required" />
                           </xs:complexType>
                        </xs:element>
                        <xs:element name="sample">
                           <xs:complexType>
                              <xs:sequence minOccurs="0">
                                 <xs:element ref="description" minOccurs="0" />
                                 <xs:element ref="annotation" minOccurs="0" />
                                 <xs:element ref="property" minOccurs="0" maxOccurs="unbounded" />
                              </xs:sequence>
                              <xs:attribute name="barcode" type="barcode" use="required" />
                              <xs:attribute name="location" type="location" use="required" />
                              <xs:attribute name="accessionnum" type="xs:string" use="required" />
                              <xs:attribute name="name" type="xs:string" use="required" />
                           </xs:complexType>
                        </xs:element>
                        <xs:element name="replicate">
                           <xs:complexType>
                              <xs:attribute name="srcbarcode" type="barcode" use="required" />
                              <xs:attribute name="sourcelocation" type="location" use="required" />
                              <xs:attribute name="destbarcode" type="barcode" use="required" />
```

```
                           <xs:attribute name="destlocation" type="location" use="required" />
                        </xs:complexType>
                     </xs:element>
                     <xs:element name="location" minOccurs="0" maxOccurs="unbounded">
                        <xs:complexType>
                           <xs:sequence minOccurs="0">
                              <xs:element ref="property" minOccurs="0" maxOccurs="unbounded" />
                           </xs:sequence>
                           <xs:attribute name="barcode" type="barcode" use="required" />
                           <xs:attribute name="location" type="location" use="required" />
                        </xs:complexType>
                     </xs:element>
                  </xs:choice>
               </xs:complexType>
            </xs:element>
            <xs:element name="finishtime" type="xs:dateTime" />
         </xs:sequence>
         <xs:attribute name="guid" type="xs:string" use="required" />
      </xs:complexType>
   </xs:element>
   <xs:element name="property">
      <xs:complexType>
         <xs:simpleContent>
            <xs:extension base="xs:anySimpleType">
               <xs:attribute name="name" type="xs:string" use="required" />
               <xs:attribute name="type" type="xs:string" use="required" />
            </xs:extension>
         </xs:simpleContent>
      </xs:complexType>
   </xs:element>
   <xs:simpleType name="barcode">
      <xs:restriction base="xs:string">
         <xs:minLength value="1" />
      </xs:restriction>
   </xs:simpleType>
   <xs:simpleType name="location">
      <xs:restriction base="xs:string">
         <xs:minLength value="1" />
      </xs:restriction>
   </xs:simpleType>
</xs:schema>
```

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