I-SPY
USER'S GUIDE

Version 1.0
DRAFT

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Center for Bioinformatics

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TABLE OF CONTENTS

About This Guide

This section introduces you to the *I-SPY User's Guide*. It includes the following topics:

Purpose

This guide provides an overview of I-SPY. This book is organized into chapters that parallel I-SPY's workflow.

Audience

This guide is designed to assist researchers and investigators using the I-SPY Analysis Portal application.

Topics Covered

If you are new to I-SPY, read this brief overview, which explains what you will find in each chapter.

- *Chapter 1* provides an overview of the I-SPY program.
- *Chapter 2* provides instructions to start using I-SPY.
- *Chapter 3* describes how to search on patient or sample identiers. The results show the patients that fulfill the criteria.
- *Chapter 4* describes how to perform a clinical and an IHC (Immunohistochemistry) query.
- *Chapter 5* extends the basic knowledge of the previous chapters and shows you how to work with class comparisons, hierarchical clustering, principal component analysis, a correlation scatter plot, and a box-and-whisker plot.
- *Chapter 6* describes how to view all the results generated from searches and high order analyses.
- *Chapter 7* describes how to manage user-defined and study-defined patient and gene identifier lists.

Text Conventions Used

The following table explains conventions used in this guide. The various typefaces represent interface components, keyboard shortcuts, toolbar buttons, dialog box options, and text that you type.

Convention	*Description*	*Example*
Bold	Highlights names of option buttons, check boxes, drop-down menus, menu commands, command buttons, or icons.	Click **Search**.
URL	Indicates a Web address.	http://domain.com
text in SMALL CAPS	Indicates a keyboard shortcut.	Press ENTER.
text in SMALL CAPS + text in SMALL CAPS	Indicates keys that are pressed simultaneously.	Press SHIFT + CTRL.
Italics	Highlights references to other documents, sections, figures, and tables.	See *Figure 4.5*.
Italic boldface monospace type	Represents text that you type.	In the **New Subset** text box, enter ***Proprietary Proteins***.
Note:	Highlights information of particular importance	**Note:** This concept is used throughout the document.
{ }	Surrounds replaceable items.	Replace {last name, first name} with the Principal Investigator's name.

Table Documentation conventions

CHAPTER

1

ABOUT I-SPY 1.0

This chapter introduces you to I-SPY and provides an overview of I-SPY functions.

Topics in this chapter include:

About I-SPY

The NCI Center for Bioinformatics (NCICB), in collaboration with physicians, researchers, and cooperative groups, has designed I-SPY. Clinical trials are critical to identifying markers and mechanisms of resistance in therapy, and I-SPY is a multi-center clinical trial for women undergoing neoadjuvant chemotherapy from breast cancer. I-SPY is a web-based system which supports correlative data analysis and centralized reporting of results to catalyze the transition from uniform to tailored care.

I-SPY facilitates collaboration, provides an infrastructure for data management, analysis and communication, and develops a commitment to sharing information and developing data standards.

About I-SPY Functions

Users can perform a variety of tasks in I-SPY. *Table 1.1* describes each I-SPY task.

Task	Description
Perform a Patient or Sample Identifier Lookup	Search the database for patient or sample identifiers. Display, download, and save the data associated with the search criteria. For more information, see *Conducting an Identifier Lookup* on page 9)
Perform a Search	Perform one of the following types of queries: • Clinical query • IHC query For more information, see *Conducting Searches* on page 13.
Perform a High Order Analysis	Run the following types of higher order analyses: • Class comparisons • Hierarchical clustering • Principal component analyses • Correlation scatter plot • Categorical plot analysis. For more information, see *High Order Analysis* on page 21.
View Results	View Search and High Order Analysis results. For more information, see *Viewing Results* on page 33.
Manage Lists	Manage user-defined or study-defined patient or gene identifier lists. You can use them to filter queries or perform analysis. For more information, see *Managing Lists* on page 47).

Table 1.1 I-SPY user tasks

CHAPTER

2

GETTING STARTED WITH I-SPY 1.0

This chapter introduces the I-SPY interfaces, navigation, and common features used on I-SPY pages.

Topics in this chapter include:

Launching I-SPY

To launch I-SPY, follow these steps:

1. Go to the I-SPY portal on the NCICB website:

   http://ispy-analysis-stage.nci.nih.gov

The I-SPY login page appears *(Figure 2.1).*

Figure 2.1 I-SPY login page

Creating a User Account

Each I-SPY user is given a unique user name and password. The user name and password you are assigned determines your access rights for the software. To set up a user account, you must:

- Contact NCICB Application Support:
  - NCICB@pop.nci.nih.gov
  - 888-478-4423 (toll-free) or 301-451-4384 (local)

OR

- Go to the NCICB I-SPY login page and click the **request username/password** link to send an e-mail requesting a username and password to NCICB Application Support.

Logging In

To log into I-SPY, you need your username and password assigned to you by the I-SPY Administrator.

1. On the login page, enter your **username** and **password**.

Figure 2.2 I-SPY login

Note: If you would like to offer feedback via e-mail to the I-SPY development team, click the **feedback** link.

2. Click the **Submit** button. If your login is successful, the Legal Rules of the Road page appears *(Figure 2.3).*

Accepting I-SPY Provisions

Once you log in, the Legal Rules of the Road page appears. After reading the provisions, click the **CLICKING HERE** link *(Figure 2.3)* in the lower right-hand corner.

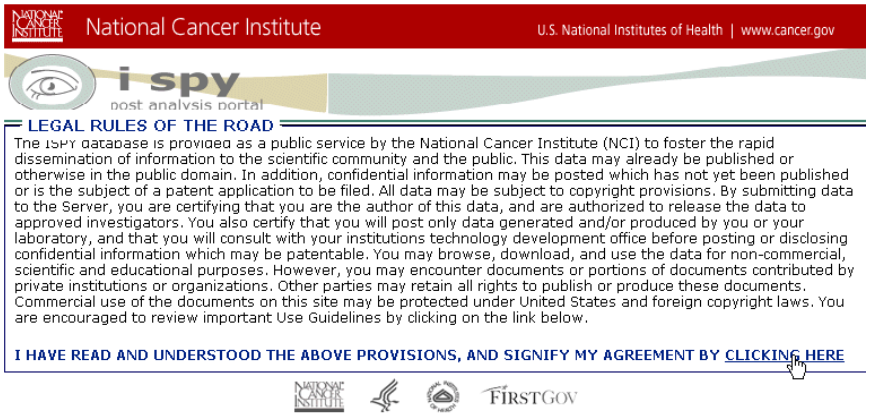


Figure 2.3 Legal Rules of the Road page

The I-SPY workspace appears (*Figure 2.4*).

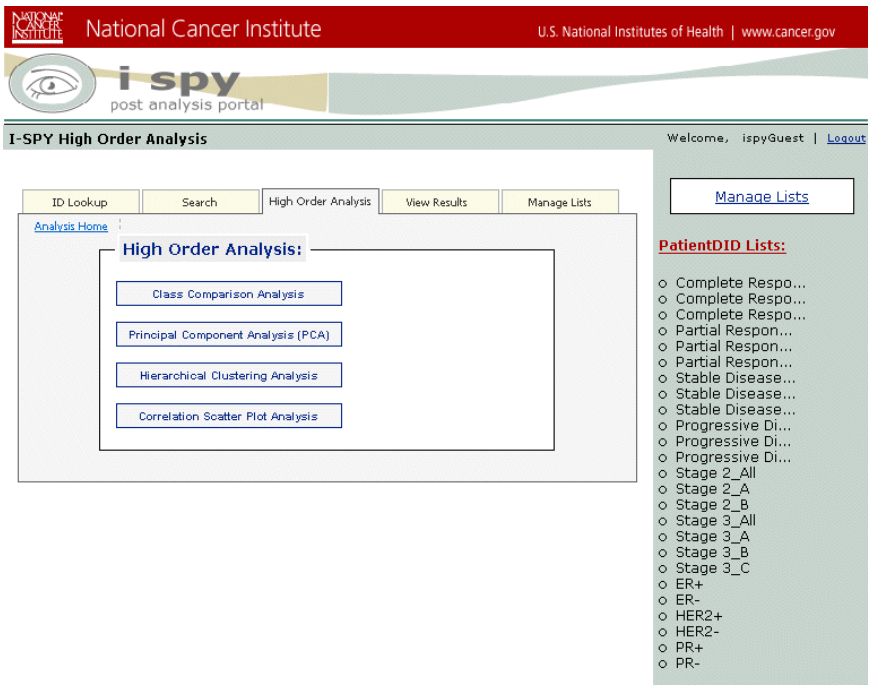


Figure 2.4 The I-SPY workspace

Welcome to I-SPY 1.0

The I-SPY workspace comprises a set of five tabs, a blue panel, help links, and a logout link. The five tabs enable you to perform the following functions:

1. Perform an ID lookup.
2. Perform complex searches.
3. Perform higher order analyses.
4. View results of the searches and analyses.
5. Manage lists.

The blue panel displays pre-defined patient identifier lists and the default gene identifier list. As you add your own lists, the new lists will appear in red.

Getting Help

Will this be the same as REMBRANDT?

Information about how to use I-SPY is easily accessed from I-SPY's menu (*Figure 2.5*) in the top left of the I-SPY workspace.

Figure 2.5 I-SPY's menu

Table 2.1 describes each item on the I-SPY toolbar.

Help	***How to Access***
Complete online help	To access the complete version of online I-SPY help, click the **help** link located in the I-SPY menu. For complete page-level help, click  on any I-SPY page. For brief field help, click  .
Application support	To obtain support for I-SPY, click the **support** link located under the I-SPY menu.
Tutorials	To access I-SPY tutorials, click the **tutorials** link located under the I-SPY menu.
User's Guide	To access a pdf version of the *I-SPY User's Guide*, click the **user guide** link located under the I-SPY menu.

Table 2.1 Getting help with I-SPY

Application Support

You can find additional support at the NCICB Applications Support Web site. To access the site, do the following:

Click the **support** link in the I-SPY menu. The NCICB Applications Support Group page appears.

Logging Out

To log out of I-SPY, follow these steps.

1. On the I-SPY workspace, click the **logout** link (*Figure 2.6*) in the upper right-hand corner.

Figure 2.6 Logout link

You are logged out of I-SPY.

Will this be changed as it is in REMBRANDT?

CHAPTER

3

CONDUCTING AN IDENTIFIER LOOKUP

This chapter describes how to use I-SPY to lookup patient identifiers or sample identifiers.

Topics in this chapter include:

ID Lookup Overview

The ID Lookup function enables you to find information about samples for a given patient by entering either sample or patient identifiers. Once you perform the lookup, you can also perfrom the following tasks:

- Display patient sample information
- Download patient sample information
- Save multiple patients' data to an I-SPY PatientIDID list

Note: You can use a PatientDID list to filter I-SPY queries and perform data analysis.

Looking Up a Patient or Sample Identifier

When you search for a patient identifier, I-SPY displays the patient along with all the samples associated with the patient. If you search for a sample identifier, I-SPY displays the patient associated with the sample identifier. To perform an ID lookup, follow these steps:

1. From the ID Lookup page (*Figure 3.1*), enter a valid patient identifier, such as `1001`, or enter a valid sample identifier, such as `209512`.

   Note: To enter multiple identifiers, separate the identifiers with commas. For example, enter `1001,1002`.

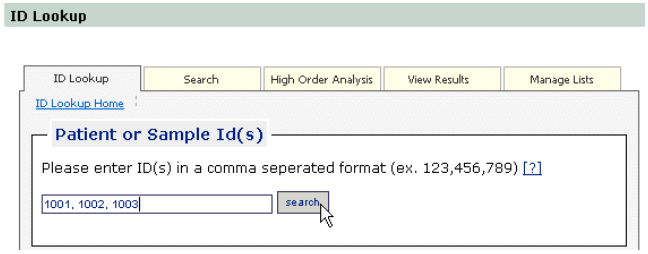


Figure 3.1 Entering identifiers

2. Click the **Search** button.

   The patients associated with the identifier(s) appear below the **Search** button (*Figure 3.2*).

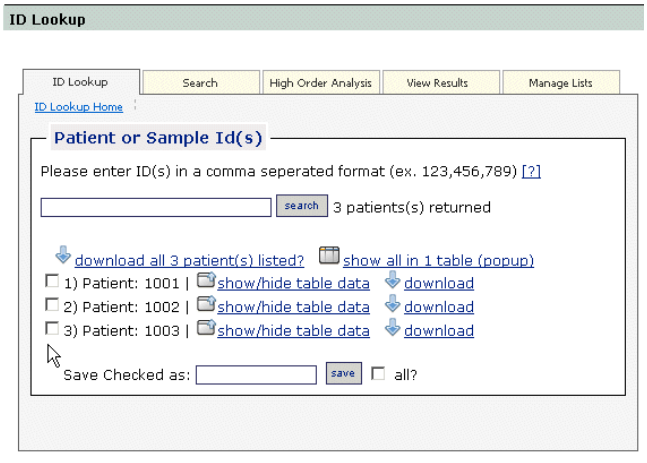


Figure 3.2 Found patients

Displaying/Hiding the Patient Sample Information

Once you perform an ID Lookup, you can display sample information for either an individual patient or multiple patients. Follow these steps:

1. To display all the samples collected for an individual patient click next to the patient's row.

   The table highlights the lookup criteria (*Figure 3.3*).

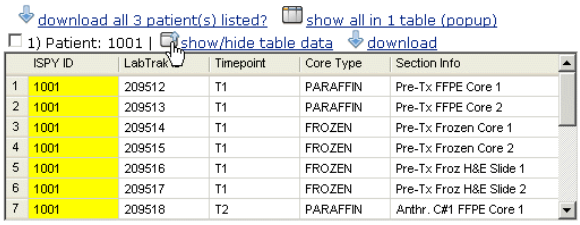


Figure 3.3 Patient table data

Table 3.1 describes the sample information associated with the patient.

Item	*Special Instructions*
ISPY ID	The identifier for the patient.
LabTrak ID	The identifier for the sample collected.
Timepoint	The timepoint when the sample was collected. • **T1** • **T2**: Early treatment day 1, cycle 2 • **T3**: Inter-regimen • **T4**: Prior to surgery for response evaluation forma and sample post-surgery
Core Type	The type of substance used to store the sample.
Section Info	

Table 3.1 Understanding the patient table data page

Note: To hide the table, data click .

2. To display data for multiple patients in one table click above the list of patients.

   All the patients' data are shown in one table listed in descending order by patient identifier.

   Note: To hide the table data, close the window.

Downloading Patient Sample Information to an Excel File

From the ID Lookup page, you can download one patient's sample data to a file or download all the listed patients' data to the same file. Follow these steps.

To download an individual patient's data to an Excel file, follow these steps:

1. Click next to the patient for which you want to download data.
2. Name the file and select a location.

   The individual patient's data is saved to the Excel file.

If you searched for *multiple* patients, to save all the patients' data to the same Excel file, follow these steps.

1. Click above the list of patients to download all the patient sample information to one file.
2. Name the file and select a location.

   All the patients' data is saved to the same Excel file listed in descending order by patient identifier.

Creating a PatientDID List with the ID Lookup

From the ID Lookup page, you can save multiple patients' data to a PatientDID list (see *PatientDID Lists*). You can use PatientDID lists to further filter a query or analyze data. To create an I-SPY PatientDID list, follow these steps.

1. Select the box next to each patient to be saved to the PatientDID list (*Figure 3.4*) or select the **All** box to select all of the patients.

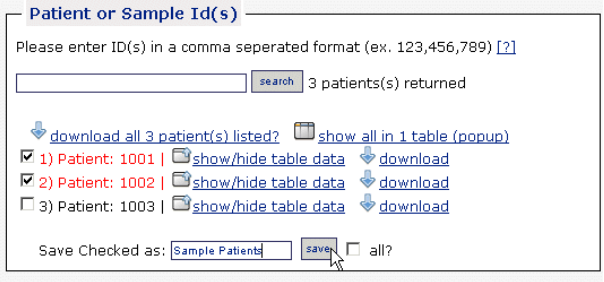


Figure 3.4 Saving to a PatientDID list

2. Name the list.
3. Click the **save** button.

   The list name appears in red in the blue panel at the bottom of the PatientDID Lists.

   Note: To further modify the new PatientDID list, see *Managing Lists*.

CHAPTER

4

CONDUCTING SEARCHES

This chapter describes how to perform advanced queries to generate customized reports.

Topics in this chapter include:

Search Overview

The Search function enables you to perform advanced queries from the following categories:

- Clinical Query
- IHC Level of Expression Query
- IHC Loss of Expression Query

Performing a Clinical Query

A *clinical query* enables you to generate clinical reports using customized search criteria. The search criteria filter the report based on clinical, MR, or pathology parameters. For example, you can create a clinical query that finds patients between the ages of 31 and 50 and had a complete response within timepoints T1 and T2.

To define a clinical query, follow these steps:

1. On the Clinical Query Form page, you are required to fill in at least one search criteria (*Figure 4.1*).

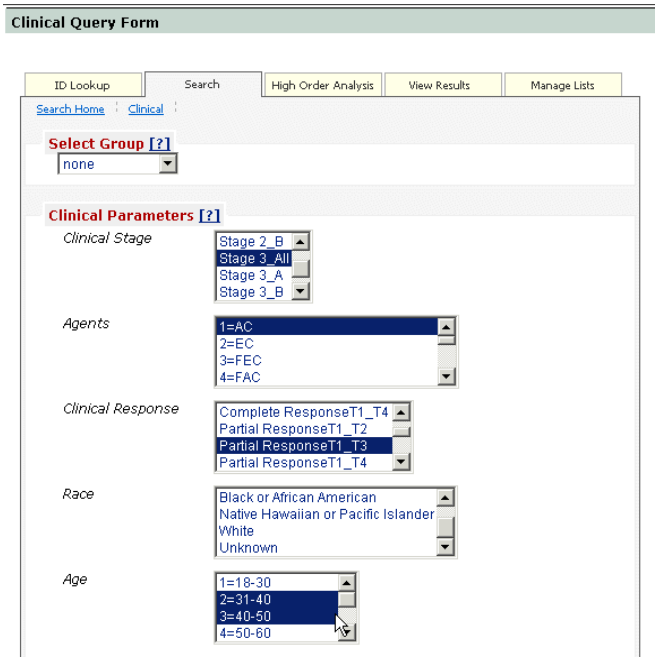


Figure 4.1 Clinical Query Form page (top portion)

2. *Table 4.1* lists the available search criteria:

Note: To select more than one option in a list box, SHIFT-click or CTRL-click.

Criteria	*Item Name*	*Special Instructions*
Select Group	Select Group	A *group* is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Select a group to filter the query to a collection of patients. Lists that you created appear in red.
Clinical Parameters	Clinical Stage	Select a clinical stage to further filter the query: • **Stage 2_All** • **Stage 2_A** • **Stage 2_B** • **Stage 3_All** • **Stage 3_A** • **Stage 3_B**
	Agents	Select an agent to further filter the query.

Table 4.1 Clinical Query search criteria instructions

Criteria	*Item Name*	*Special Instructions*
	Clinical Response	Select one or more clinical responses and the appropriate timepoint range. • **Complete Response** • **Partial Reponse** • **Stable Disease** • **Progressive Disease** For more information, see *PatientDID Lists*.
	Race	Select one or more races.
	Age	Select one or more age ranges.
MR Parameters	Morphology	Select an MRI parameter to further filter the query based on the radiologist measurement.
	Percent LD, Decrease	This group of options enables you to specify the percentage of LD (Longest Diameter) change in the size of the tumor between two timepoints. Select the timepoint range in which to analyze the percentage of LD change: • **PERCENT_LD_CHANGE_T1_T2**: The specified percentage change in LD occurred between timepoints T1 and T2. • **PERCENT_LD_CHANGE_T1_T3**: The specified percentage change in LD occurred between timepoints T1 and T3. • **PERCENT_LD_CHANGE_T1_T4**: The specified percentage change in LD occurred between timepoints T1 and T4. Select the greater than/equal to (**>=**) or less than/equal to (**<=**) indicator and enter the percentage of LD change to search for in the selected timepoint range.
Pathology	Pathology Tumor Size	Specify the tumor size and associated biomarkers to filter the query. Select the greater than/equal to (**>=**) or less than/equal to (**<=**) indicator and enter a value in centimeters of the tumor size.
	Status	Specify the Pathology Status: **ER+**: Estrogen receptor positive **ER-**: Estrogen receptor negative **PR+**: Progesterone receptor positive **PR-**: Progesterone receptor positive **HER2+**: HER2 positive **HER2-**: HER2 negative

Table 4.1 Clinical Query search criteria instructions

3. Once you fill in at least one search criteria, you are required to enter a name for the clinical query. The name must be unique among all the queries in the current session.

   To clear all the entries on the page, click the **Clear** button.

4. To submit the query and generate the Clinical report, click the **Submit** button.

   The Clinical report will be listed on the View Results page. From the report, you can save all or some of the patients' data to an I-SPY PatientDID list. You can use PatientDID lists to further filter a query or perform analysis. See *Clinical Reports*.

Performing an IHC Level of Expression Query

An *IHC (Immunohistochemistry) Level of Expression* query enables you to filter a search with one or more timepoints, biomarkers, and stain characteristics. The report results list records that satisfy the specified search criteria.

To perform a IHC Level of Expression query, follow these steps:

1. On the IHC Level of Expression Query Form page, the following search criteria are available to filter the query (*Figure 4.2*).

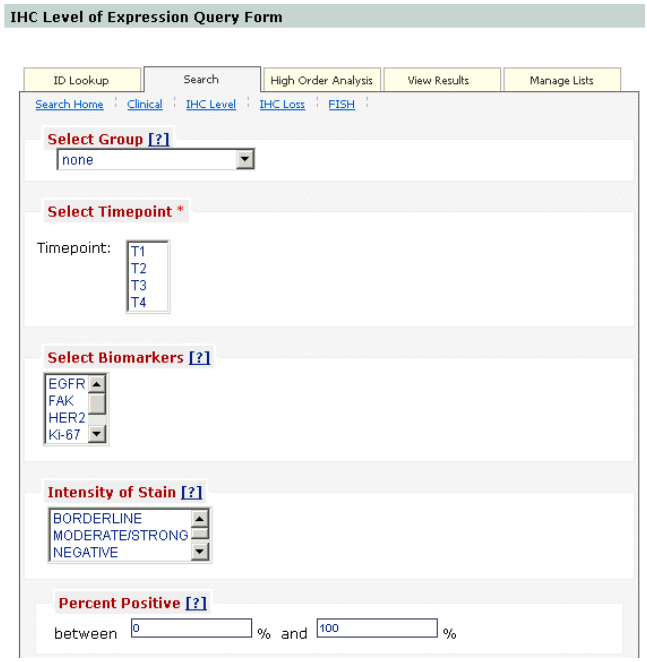


Figure 4.2 IHC Level of Expression Query Form page (top portion)

Table 4.2 lists the available search criteria:

Note: To select more than one option in a list box, SHIFT-click or CTRL-click.

Criteria	*Special Instructions*
Select Group	A *group* is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Select a group to filter the query to a collection of patients. Lists that you created appear in red.
Select Timepoint	You are required to specify at least one timepoint during which the selected criteria are fulfilled. **T1**, **T2**, **T3**, **T4**
Select Biomarkers	Select one or more biomarkers to filter the query: • **P27** • **Ki-67** • **EGFR** • **CCND1** • **P53** • **HER2** • **BCL2** • **FAK**
Intensity of Stain	Select an option that best describes the intensity of stain: • **Negative** • **Borderline** • **Weak** • **Moderate_Strong** • **Unevaluable**
Percent Positive	Enter the percent positive range to filter the query.
Localization of Stain	Select an option that best describes the localization of stain: • **None** • **Membrane** • **Nucleus** • **Cytoplasm** • **Membrane_and_Cytoplasm** • **Nuclear_and_Cytoplasm** • **NA** or Not Applicable
Distribution of Stain	Select an option that best describes the distribution of stain: • **None** • **Homogenous** • **Heterogenous**

Table 4.2 IHC Level of Expression Query search criteria instructions

2. Once you fill in the search criteria, you are required to enter a name for the IHC query. The name must be unique among all the queries in the current session.

   To clear all the entries on the page, click the **Clear** button.

3. To submit the query and generate the IHC Level of Expression report, click the **Submit** button.

   The IHC Level of Expression report will be listed on the View Results page. From the report, you can save all or some of the patients' data to an I-SPY PatientDID list. You can use a PatientDID list to further filter a query or perform analysis. For more information, see *IHC Level of Expression Search Results*.

Performing an IHC Loss of Expression Query

An *IHC (Immunohistochemistry) Loss of Expression* query enables you to filter a search with one or more timepoints, the P27 biomarker only, and invasive and benign range characteristics. The report results list records that satisfy the specified search criteria.

To perform a IHC Loss of Expression query, follow these steps:

1. On the IHC Loss of Expression Query Form page, the following search criteria are available to filter the query (*Figure 4.2*).

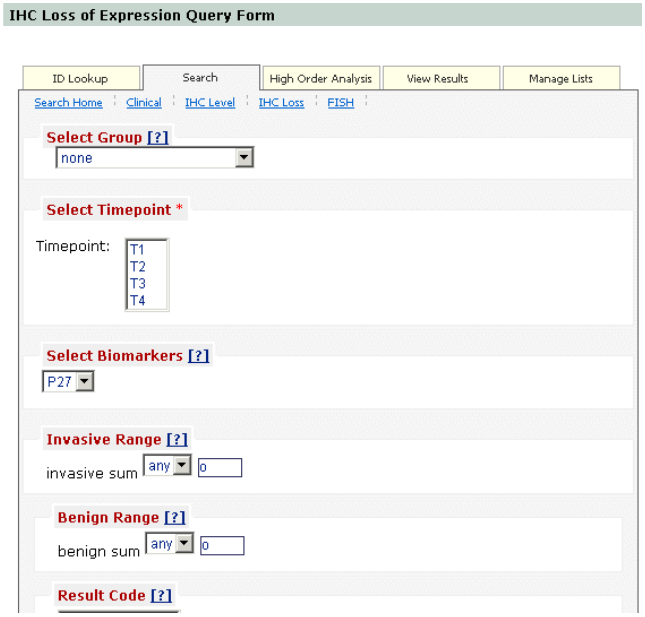


Figure 4.3 IHC Loss of Expression Query Form page (top portion)

Table 4.2 lists the available search criteria:

Note: To select more than one option in a list box, SHIFT-click or CTRL-click.

Criteria	*Special Instructions*
Select Group	A *group* is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Select a group to filter the query to a collection of patients. Lists that you created appear in red.
Select Timepoint	You are required to specify at least one timepoint during which the selected criteria are fulfilled. **T1**, **T2**, **T3**, **T4**
Select Biomarkers	IHC Loss of Expression data is available only for biomarker **P27**.
Invasive Range	Specify equal to, greater than, or less than to define the range invasive sum: • = • >= • <= Specify the value for the invasive sum.
Benign Range	Specify equal to, greater than, or less than to define the range benign sum: • = • >= • <= Specify the value for the benign sum.

Table 4.2 IHC Loss of Expression Query search criteria instructions

2. Once you fill in the search criteria, you are required to enter a name for the IHC query. The name must be unique among all the queries in the current session.

   To clear all the entries on the page, click the **Clear** button.

3. To submit the query and generate the IHC Loss of Expression report, click the **Submit** button.

   The IHC Loss of Expression report will be listed on the View Results page. From the report, you can save all or some of the patients' data to an I-SPY PatientDID list. You can use a PatientDID list to further filter a query or perform analysis. For more information, see *IHC Loss of Expression Search Results*.

CHAPTER

5

HIGH ORDER ANALYSIS

This chapter describes how to use I-SPY to run higher order analyses.

Topics in this chapter include:

High Order Analysis Overview

The *High Order Analysis* function enables you to perform the following analyses:

- Class Comparison Analysis
- Principal Component Analysis (PCA)
- Heiarchical Clustering AnalysisCorrelation Scatter Plot AnalysisCategorical Plot Analysis

Report results are listed on the View Results page.

Performing a Class Comparison

A *Class Comparison* alows you to identify genes and reports that are differentially expressed between two groups. To perform a Class Comparisons, follow these steps:

1. The Class Comparison Analysis Form page *(Figure 5.1)* enables you to define the criteria to perform a class comparison.

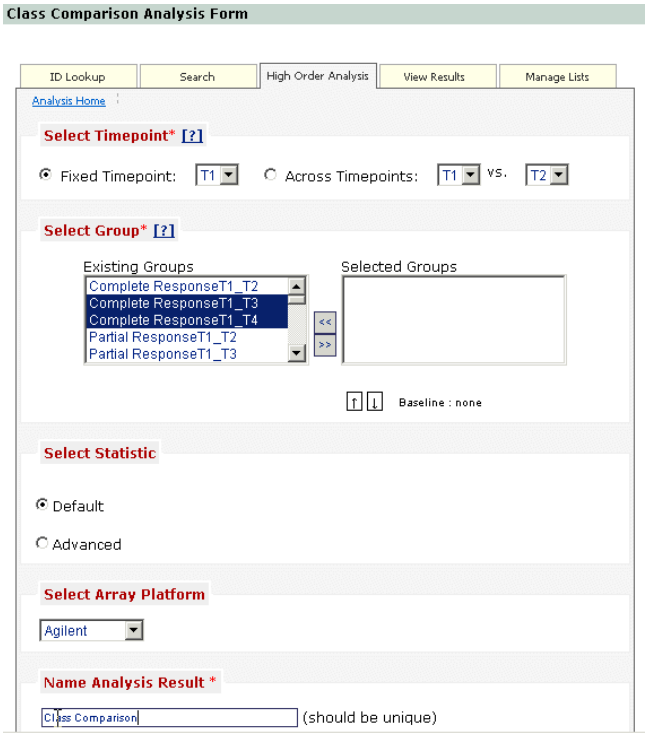


Figure 5.1 Class Comparison Analysis Form page

2. You are required to complete at least one criteria for the class comparison. *Table 5.1* lists the available criteria:

Criteria	*Item Name*	*Special Instructions*
Select Timepoint	Fixed Timepoint	Select a timepoint in which to perform the analysis. This option compares two groups at the same timepoint.
	Across Timepoints	Select a range of timepoints in which to perform the analysis. This option analyzes one group at different timepoints.

Table 5.1 Class Comparison criteria instructions

Criteria	*Item Name*	*Special Instructions*
Select Group	Existing Groups Selected Groups	A *group* is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Select a group to filter the query to a collection of patients. Lists that you created appear in red. For a *Fixed Timepoint* analysis, select two groups (compares two groups at the same timepoint). For an *Across Timepoints* analysis, select one group (analyzes one group at different timepoints).
	Baseline	For a *Fixed Timepoint* analysis, the baseline is determined by the second group in the **Selected Groups** box. For an *Across Timepoints* analysis, the baseline is determined by the first timepoint in the chosen range. The **(baseline)** appears in red next to your selection.
Select Statistic	Default	Select to perform a default statistical analysis.
	Advanced	Select to define additional statistical analysis options.
	• Statistical Method	Select the appropriate statistical method: • **T-test: Two Sample Test** to identify genes showing statistically significant differences between two samples. • **Wilcoxon Test: Man-Whitney Test** is the non-parametric test analog to the independent two-sample t-test. This test is used in place of a two-sample t-test when the populations being compared are not normal.
	• Multiple Comparison Adjustment	Family-wise Error Rate (FWER): Bonferroni False Discover Rate (FDR): Benjamini-Hochberg
	• Fold Change	The default is >=2. Specify the threshold for the differential regulation. This returns differential expression ratios between tumor and non-tumor samples for a particular reporter.
	• p-value	The probability for obtaining the differences in expression values between tumor (or a subtype of tumor) and non-tumor samples. The default is <=0.05.
Select Array Platform	Select Array Platform	Select the array platform.

Table 5.1 Class Comparison criteria instructions

3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.

4. To submit your criteria and create a Class Comparison report, click the **Submit** button.

Performing a Principal Component Analysis

A *Principal Component Analysis* is a dimensionality reduction algorithm, which identifies clusters of samples that may have similar gene expression profiles. To perform a Principal Component Analysis, follow these steps:

1. The Principal Component Analysis (PCA) Form page *(Figure 5.2)* enables you to define criteria to perform a PCA.

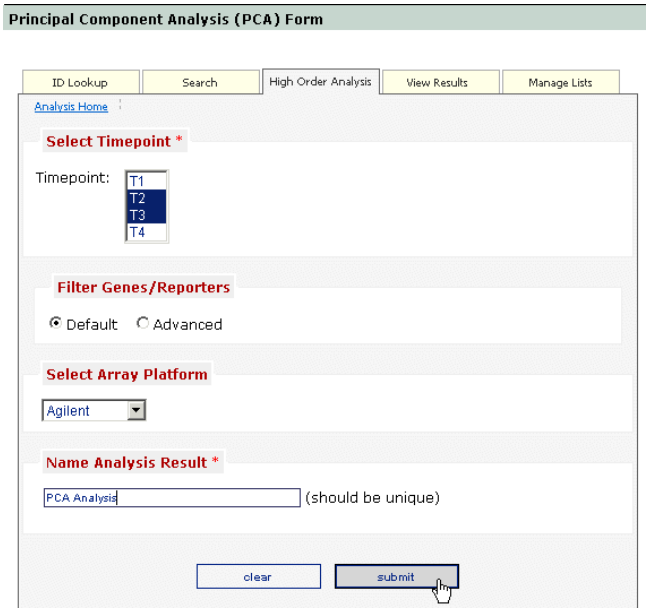


Figure 5.2 Selecting Principal Component Analysis criteria

2. You are required to complete at least one criteria for the Principal Component analysis. *Table 5.2* lists the available criteria:

Criteria	*Item Name*	*Special Instructions*
Select Timepoint	Timepoint	Select one or more timepoints in which to perform the analysis.
Filter Genes/Reporters	Default	Select to perform a default statistical analysis.
	Advanced	Select to define additional gene/reporter filters.
	• Constrain reporters by variance (Gene Vector) percentile: %	Enter a percentage which selects the reporters whose variances of the log ratio (or Log2 signals) across all experiments were among the top percentile of variance of all reports identified. For example, 70% chooses reporters with the top 30 (100 - 70) percentile of variance.
	• Constrain by GeneList	A *Gene list* is a pre-defined or user-defined list comprising pgenes with certain characteristics. Select a gene list to filter the query. Lists that you created appear in red. The default gene list is **defaultGene1**.
Select Array Platform	Select Array Platform	Select an array platform.

Table 5.2 Principal Comparison Analysis criteria instructions

3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
4. To submit your criteria and create a Principal Comparison Analysis report, click the **Submit** button.

Performing Hierarchical Clustering Analysis

Hierarchical Clustering analysis creates a dendrogram of the samples in the analysis. To perform a Hierarchical Clustering, follow these steps:

1. The Hierarchical Clustering Analysis Form *(Figure 5.3)* enables you to fill in criteria for a hierarchical clustering.

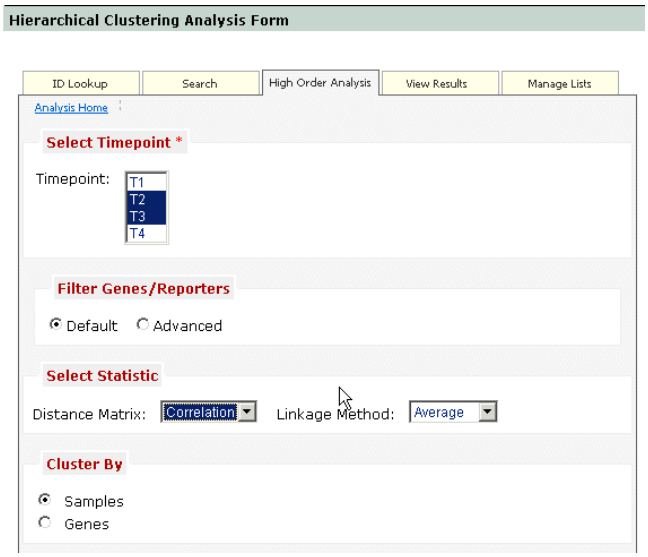


Figure 5.3 Selecting Hierarchical Clustering criteria

2. You are required to enter at least one step for the hierarchical clustering. *Table 5.3* lists the available criteria:

Criteria	*Item Name*	*Special Instructions*
Filter Genes/Reporters	Default	Select to perform a default statistical analysis.
	Advanced	Click to define additional gene/reporter filters.
	• Constrain reporters by variance (Gene Vector) percentile: %	Enter a percentage which selects the reporters whose variances of the log ratio (or Log2 signals) across all experiments were among the top percentile of variance of all reports identified. For example, 70% chooses reporters with the top 30 (100 - 70) percentile of variance.
	• Constrain by GeneList	A *Gene list* is a pre-defined or user-defined list comprising pgenes with certain characteristics. Select a gene list to filter the query. Lists that you created appear in red. The default gene list is **defaultGene1**.

Table 5.3 Hierarchical Clustering criteria instructions

Criteria	*Item Name*	*Special Instructions*
Select Statistic	Distance Matrix	Select a distance matrix option: • **Correlation** measures the relative shape of the gene regulations rather than the absolute levels. This is a natural choice, because it is widely used to measure gene correlations. • **Euclidean** distance is the most common distance measure. It measures the absolute level of gene regulation.
	Linkage Method	Select a linkage option to affect the shape of the resulting clusters: • **Average linkage** is the average of all pair-wise distances between members of the two clusters. • **Single linkage** is the minimum distance between two clusters. • **Complete linkage** is the maximum distance between two clusters.
Cluster By	Cluster by	Leave the default to cluster on **Samples** or cluster by **Genes**.
Select Array	Select Array Platform	Select an array platform.

Table 5.3 Hierarchical Clustering criteria instructions

3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
4. To submit your criteria and create a Hierarchical Clustering Analysis report, click the **Submit** button.

Performing Correlation Scatter Plot Analysis

A *Correlation Scatter Plot analysis* enables you to select two continuous variables and plot them against each other. The variables can be gene expression values or a clinical parameter like MRI percent longest diameter change.

The following lists examples of how you can use a Correlation Scatter Plot Analysis.

- **Cross platform validation**: Select the same gene on two different platforms and display the correlation between the expression values.
- **Interreporter validation**: Select the same gene (but different reporters) on the same platform.
- **Gene expression correlation**: Investigate the relationships between gene expression values for two different genes.
- **Clinical parameter and gene expression relationship**: Investigate the relationship between a clinical parameter and the gene expression values for a given gene.

To perform a Correlation Scatter Plot Analysis, follow these steps:

1. The Correlation Scatter Analysis Form *(Figure 5.3)* enables you to fill in criteria for generate a correlation scatter plot.

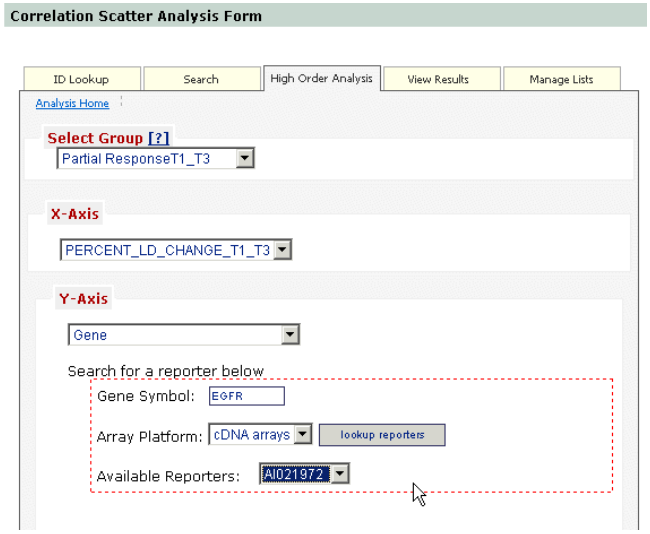


Figure 5.4 Selecting Correlation Scatter Plot criteria

2. You are required to enter at least one step for the correlation scatter plot. *Table 5.4* lists the available criteria:

Criteria	***Special Instructions***
Select Group	A *group* is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Select a group to filter the query to a collection of patients. Lists that you created appear in red.
X-Axis	Enter gene information or select an LD_CHANGE option to show the correlation between the X- and Y-axis items.
• Gene	Select **Gene**. Note that to generate the plot, you must select a gene symbol for one axis. • Enter a gene symbol. • Select an array. • Click the **Lookup Properties** button. • Select a reporter.

Table 5.4 Correlation Scatter Plot criteria instructions

Criteria	*Special Instructions*
• PERCENT LD_CHANGE	This group of options enables you to analyze the percentage of LD (Longest Diameter) change in the size of the tumor. • **PERCENT_LD_CHANGE**: On the X-axis include all samples and compare against all PERCENT_LD_CHANGE values. • **PERCENT_LD_CHANGE_T1_T2**: On the X-axis display the percentage of LD change between timepoints T1 and T2. • **PERCENT_LD_CHANGE_T1_T3**: On the X-axis display the percentage of LD change between timepoints T1 and T3. • **PERCENT_LD_CHANGE_T1_T4**: On the X-axis display the percentage of LD change between timepoints T1 and T4.
Y-Axis	Same as the X-axis options.
Correlation	Select a distance matrix option: • **Pearson** correlation measures the relative shape of the gene regulations rather than the absolute levels. This is a natural choice, because it is widely used to measure gene correlations. • **Spearman** correlation is a non-parametric test for the strength of the relationship between pairs of variables. Spearman Rank Correlation measures the correlation between two sequences of values. The two sequences are ranked separately and the differences in rank are calculated at each position. The range of Spearman Correlation is from -1 to 1. Spearman Correlation can detect certain linear and non-linear correlations. However, Pearson Correlation may be more appropriate for finding linear correlations.

Table 5.4 Correlation Scatter Plot criteria instructions

3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
4. To submit your criteria and create a Correlation Scatter Plot report, click the **Submit** button.

Performing Categorical Plot Analysis

The *Categorical Plot analysis* enables you to select one or more groups of patients as defined in the I-SPY Manage Lists function, and view a Box-and-Whiskers plot of a continuous variable for the patients in the selected groups. These groups can be the pre-defined groups defined in I-SPY or groups that you create with the Manage Lists function. The following example describes how creating lists in the I-SPY Manage Lists function (see *Combining Existing Lists to Create a New List* on page 50) can generate categorical plots for specific needs.

- Using the I-SPY Manage Lists function, create two lists
  - A Triple Negative list combining the ER-, HER2-, PR- groups
  - A Triple Positive list combining the ER+, HER2+, PR+ groups
- Specify Categorical Plot criteria to compare the Percent Longest Diameter Change for timepoints T1 to T4 with values for patients in the Triple Positive group versus patients in the Triple Negative group.

Other general uses of Box-and-whisker plots include the following:

- Indicate whether a distribution is skewed and whether there are potential unusual observations (outliers) in the dataset.
- Perform a large number of observations.
- Compare two or more datasets.
- Compare distributions because the center, spread, and overall range are immediately apparent.

To perform a Categorical Plot Analysis, follow these steps:

1. The Categorical Plot Analysis Form *(Figure 5.3)* enables you to fill in the criteria to generate a categorical plot.

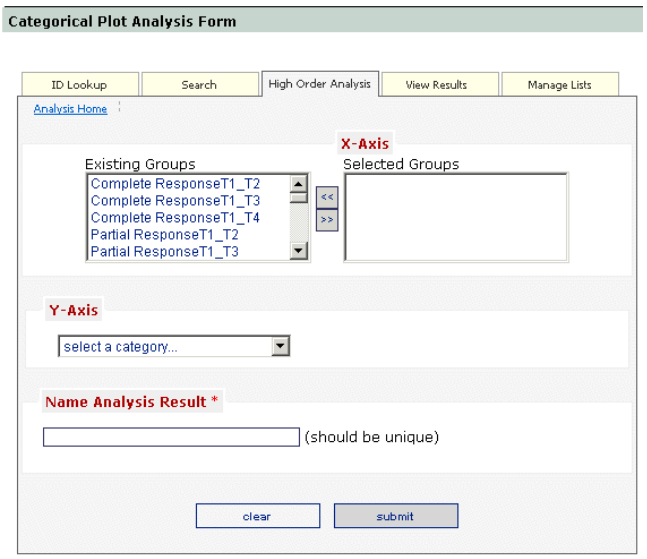


Figure 5.5 Selecting Categorical Plot Analysis criteria

2. You are required to complete an entry for the categorical plot. *Table 5.5* lists the available criteria:

Criteria	*Special Instructions*
Select Group (X-axis)	A *group* is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Select the groups for the X-axis to filter the query to a collection of patients. Lists that you created appear in red.
Y-axis	Enter gene information or select an LD_CHANGE option to show the correlation between the X- and Y-axis items.
• Gene	Select **Gene** for the X-Axis. • Enter a gene symbol. • Select an array. • Click the **Lookup Properties** button. • Select a reporter.
• PERCENT LD_CHANGE	This group of options enables you to analyze the percentage of LD (Longest Diameter) change in the size of the tumor. • **PERCENT_LD_CHANGE**: On the X-axis include all samples and compare against all PERCENT_LD_CHANGE values. • **PERCENT_LD_CHANGE_T1_T2**: On the X-axis display the percentage of LD change between timepoints T1 and T2. • **PERCENT_LD_CHANGE_T1_T3**: On the X-axis display the percentage of LD change between timepoints T1 and T3. • **PERCENT_LD_CHANGE_T1_T4**: On the X-axis display the percentage of LD change between timepoints T1 and T4.

Table 5.5 Correlation Plot Analysis criteria instructions

3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
4. To submit your criteria and create a report, click the **Submit** button.

CHAPTER

6

VIEWING RESULTS

This chapter describes reports and search results that I-SPY returns after advanced searches and high order analyses.

Topics in this chapter include the following:

Results Overview

The View Results page shows a collection of reports previously viewed in a particular user session. This allows you to compare reports by opening them in separate windows. You can view results generated with the Search function and the High Order Analysis function.

Search Results

The following results are generated from the Search function:

- *Clinical Reports*
- *IHC Level of Expression Search Results*
- *IHC Loss of Expression Search Results*

View Results (*Figure 6.1*) displays the query name and lists the output generated for the query.

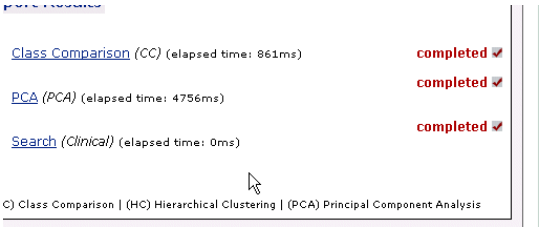
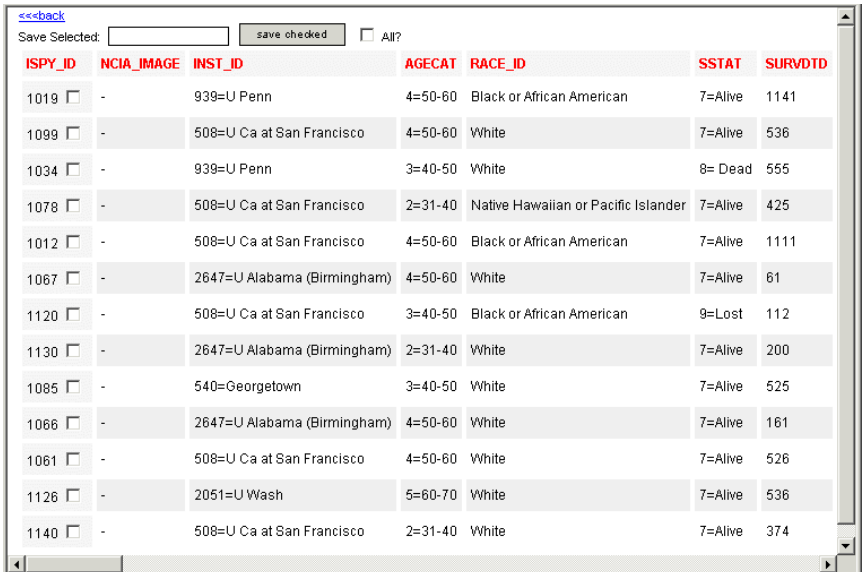


Figure 6.1 Search Results

Clinical Reports

A *Clinical report* displays the demographic, clinical, MR, and pathology data for a given set of patients (*Figure 6.2*). From any Clinical report in I-SPY, you can also create a PatientDID list to further filter a query or perform analysis. For more information, see the Related Topics.



ISPY_ID	NCIA_IMAGE	INST_ID	AGECAT	RACE_ID	SSTAT	SURVDTD
1019	-	939=U Penn	4=50-60	Black or African American	7=Alive	1141
1099	-	508=U Ca at San Francisco	4=50-60	White	7=Alive	536
1034	-	939=U Penn	3=40-50	White	8= Dead	555
1078	-	508=U Ca at San Francisco	2=31-40	Native Hawaiian or Pacific Islander	7=Alive	425
1012	-	508=U Ca at San Francisco	4=50-60	Black or African American	7=Alive	1111
1067	-	2647=U Alabama (Birmingham)	4=50-60	White	7=Alive	61
1120	-	508=U Ca at San Francisco	3=40-50	Black or African American	9=Lost	112
1130	-	2647=U Alabama (Birmingham)	2=31-40	White	7=Alive	200
1085	-	540=Georgetown	3=40-50	White	7=Alive	525
1066	-	2647=U Alabama (Birmingham)	4=50-60	White	7=Alive	161
1061	-	508=U Ca at San Francisco	4=50-60	White	7=Alive	526
1126	-	2051=U Wash	5=60-70	White	7=Alive	536
1140	-	508=U Ca at San Francisco	2=31-40	White	7=Alive	374

Figure 6.2 Clinical Report

Creating a PatientDID List from a Clinical Report

On any Clinical page, you can select and save patients to a PatientDID list.

1. There are two ways to select patients on the Clinical window:
   - To select an individual, select the box in the **I-SPY ID** column (*Figure 6.3*).

ISPY_ID	NCIA_IMAGE	INST_ID	AGECAT	RACE_ID	SSTAT	SURVDTD
1104 ☑	-	2527=U Texas SW Med Ctr	4=50-60	Black or African American	7=Alive	516
1128 ☑	-	508=U Ca at San Francisco	2=31-40	White	7=Alive	416
1053 ☑	-	372=U North Carolina at Chapel Hill	5=60-70	White	7=Alive	723
1009 ☑	-	508=U Ca at San Francisco	3=40-50	Asian	7=Alive	1021

Figure 6.3 Checking the I-SPY ID column

   - To select all of the patients, select the **All** box (*Figure 6.4*).

Figure 6.4 Selecting all of the samples on the Clinical window

   To clear all of the patients, uncheck the **All** box.

2. To save the patients to a PatientDID list, enter a name for the list (*Figure 6.5*). You can select PatientDIDs to further filter a query or perform an analysis.

Figure 6.5 Saving Selected Samples on the Clinical page

3. Click the **save checked** button. Sample List Saved appears.
4. Click the **OK** button.

   The new PatientDID list is now displayed in red in the blue panel at the bottom of the PatientDID names (*Figure 6.6*). Mouse over the name and the data items appear.

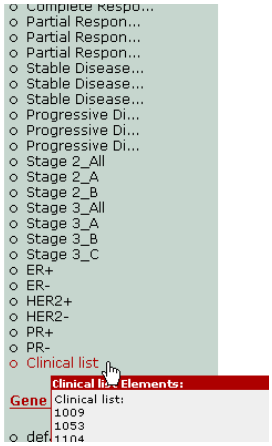


Figure 6.6 Saved PatientDID list

IHC Level of Expression Search Results

An *IHC Level of Expression report* displays the patients selected from the IHC Level of Expression search (*Figure 6.3*). On the IHC Level of Expression page, you can select and save patients to a PatientDID list.

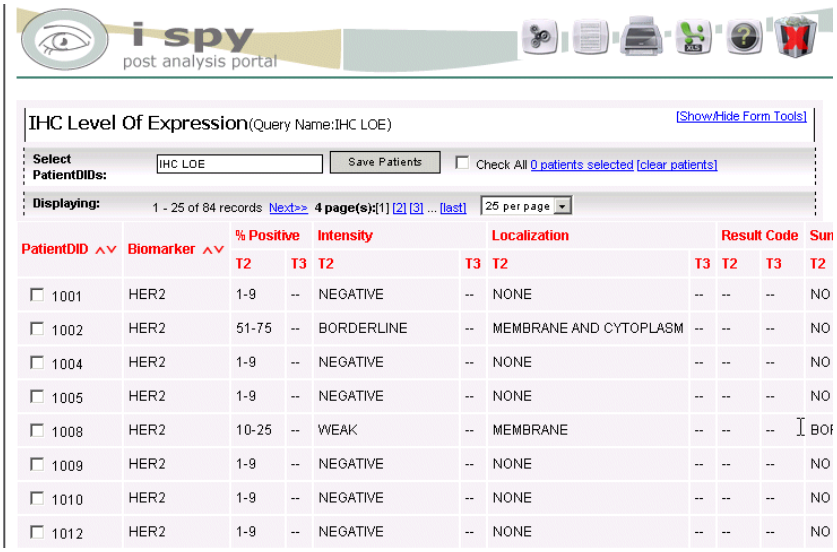


Figure 6.7 IHC Level of Expression Report

IHC Loss of Expression Search Results

An *IHC Loss of Expression report* displays the patients selected from the IHC Loss of Expression search (*Figure 6.3*). On the IHC Level of Expression page, you can select and save patients to a PatientDID list.

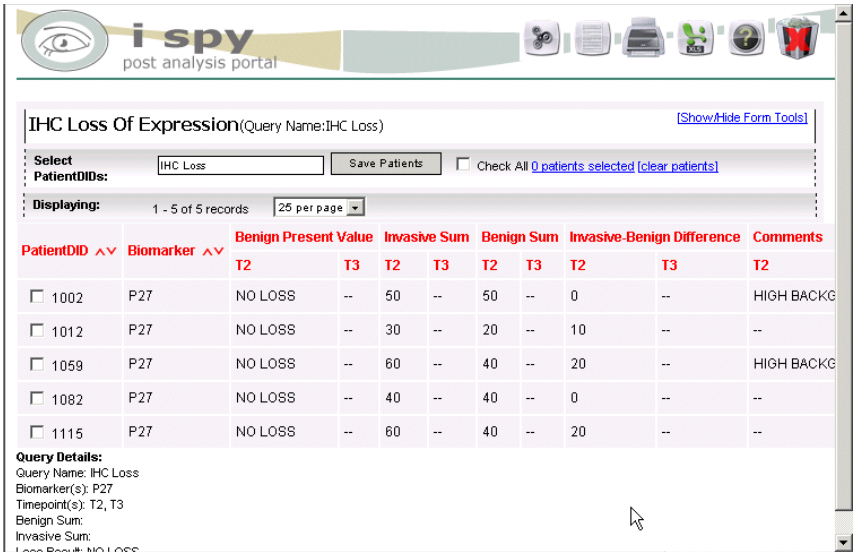


Figure 6.8 IHC Loss of Expression Report

High Order Analysis Results

The following reports are generated from the High Order Analysis function:

- *Class Comparison Report*
- *Principal Component Analysis Plot*
- *Hierarchical Clustering Report*
- *Correlation Scatter Plot*
- *Categorical Plot Analysis*

View Results (*Figure 6.9*) displays the query name and lists the output generated for the query.

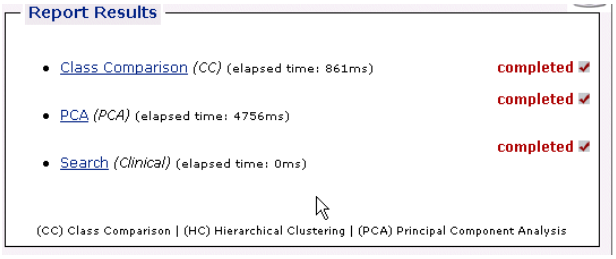


Figure 6.9 HOA Results

Class Comparison Report

The *Class Comparison* report (*Figure 6.10*) displays group average, fold change, and *p*-value based on the search parameters that you selected. For a **T-test** or **Wilcox** Statistical Method analysis (*Figure 6.10*), the Class Comparison report is as follows.

- The report displays the group average, where the numerator is the mean of log(base 2) expression signals from the samples in the first group. The denominator is the mean of log(base 2) expression signals from the samples in the second group.
- The fold change for the reporter between the selected groups appears along with *p*-value.
- Gene symbol annotations appear for each reporter. To obtain extensive annotations, click the Excel icon on the upper right-hand corner of the report.

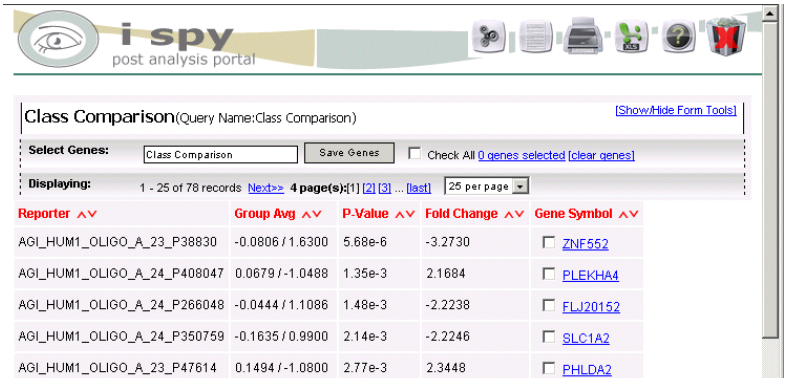


Figure 6.10 Class Comparison Report

Creating a Gene List (Select Genes toolbar)

On the Class Comparison page, you can select and save the genes to a Gene list. You can use a Gene list to filter a query or perform analysis. To create a Gene list, follow these steps (*Figure 6.11*):

1. To select all of the genes in result list, click the **Check All** box.
2. To select some of the genes, check the box in the Gene Symbol column.

   Note: To clear the selected genes, click the **clear genes** link.
3. To save the selected genes, enter a unique name for the file next to **Select Genes**, or maintain the current name, which varies based on the type of Statistical Method selected for the analysis.

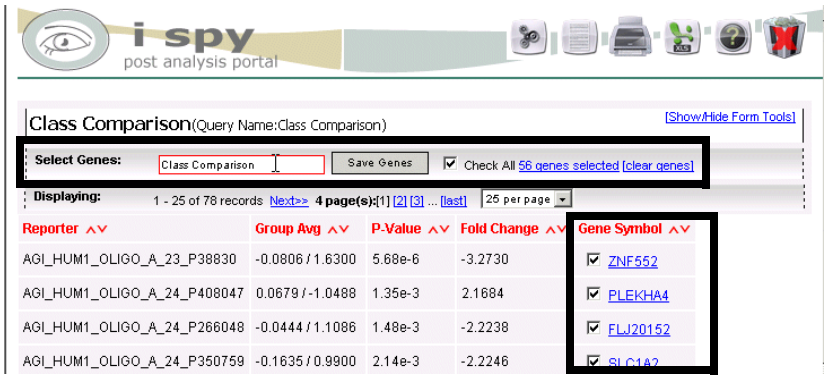


Figure 6.11 Selecting Genes instructions

4. Click the **Save Genes** button.

   The results are saved.
5. Click the **OK** button.

   The new Gene list appears in red in the blue panel at the bottom of the Gene Lists names. Mouse over the name and the data items appear.

Resorting Column Results

To sort a column in a report, follow these steps:

1. If a report column has red triangles pointing up and down next to the name, you can sort a column of numeric or alphabetical values (*Figure 6.12*).

Figure 6.12 Sorting column results

2. To sort a column in ascending order, select the red triangle pointing up. To sort a column in descending order, select the red triangle pointing down.

Showing Additional Information

When results are listed in a report, row or column items may appear as links. Click the link to display additional information about the item.

For example, to display more information about a gene, click the name link (*Figure 6.13*).

Figure 6.13 The Gene column

The Cancer Genome Anatomy Project (CGAP) browser opens.

Principal Component Analysis Plot

The *Principal Component Analysis plot* (*Figure 6.14*) is a two-dimensional graph which plots the various principal components from the analyses.

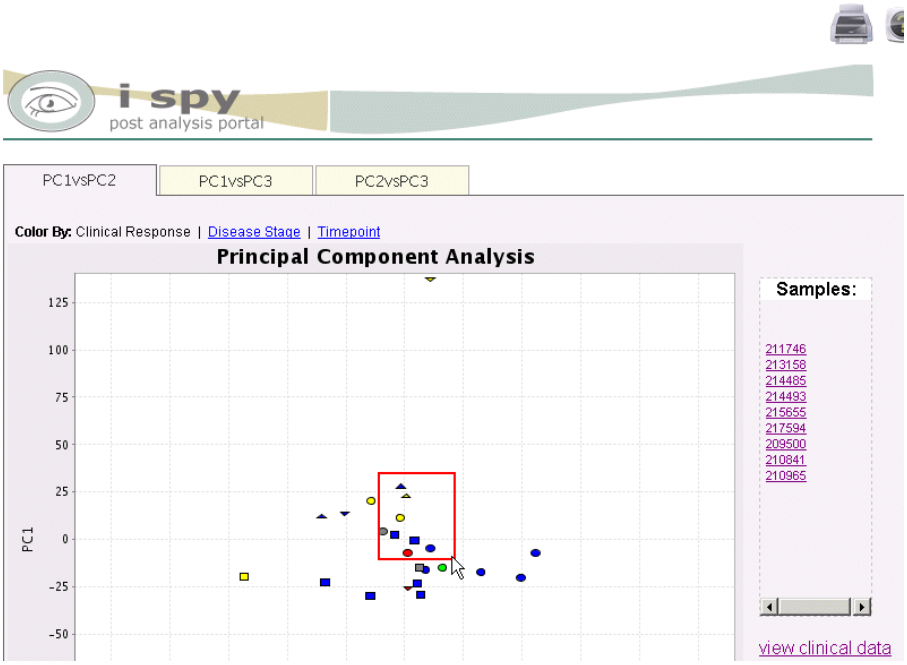


Figure 6.14 Principal Component Analysis Plot

Table 6.1 describes other areas in the plot:

Area	Description
Tabs	You can click on the three tabs at the top of the graph to display the following: • PC1vsPC2 • PC1vsPC3 • PC2vsPC3
Color By	Each point on the graph represents a sample, and by default, the samples are colored by **Clinical Response**. To color by **Disease stage** or **Timepoint**, click the appropriate link.
Legend	At the bottom of the graph, a legend defines how the different shapes on the graph indicate different survival ranges for patients.
Samples	The **Samples** area enables you to select, review, and display clinical data for samples in the plot (see *Selecting Samples of Interest in a Plot*).

Table 6.1 Areas of the Principal Component Analysis Plot

Selecting Samples of Interest in a Plot

To select the samples of interest in an I-SPY plot, follow these steps:

1. Click and drag a rectangle around the samples.

   A red rectangle appears around the samples, and the list of the samples appears on the right-hand side (*Figure 6.15*).

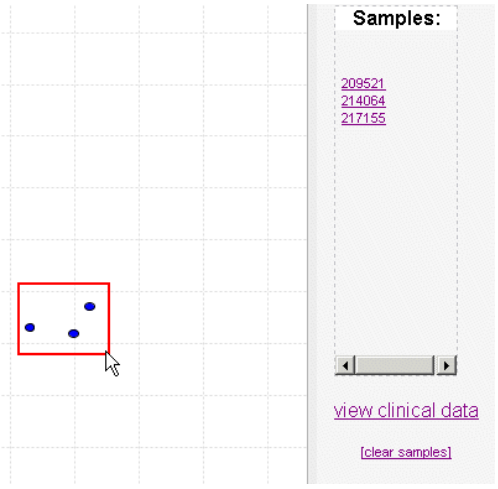


Figure 6.15 Sampling from a clinical plot

2. To help lasso the points on the plot and identify the location of these points, mouse over a sample name in the list.

   A yellow circle appears on the plot where the sample is located (*Figure 6.16*).

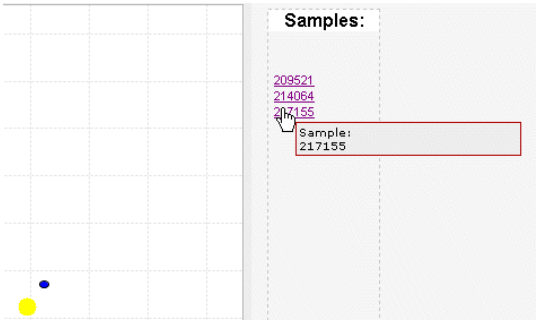


Figure 6.16 Lasso the points

3. To generate clinical data for the selected samples and save the samples, click the **view clinical data** link.

   To select another group of samples, click the **clear samples** link and start again.

Hierarchical Clustering Report

The *Hierarchical Clustering report* (*Figure 6.17*) displays the dendrogram from the hierarchical clustering analysis and a clinical report. The dendrogram is organized based on the gene expression profiles of the samples. Samples with similar profiles are placed closer together on the tree. To adjust the size of the graph, move the box on the **Image Control** bar in the top lefthand corner.

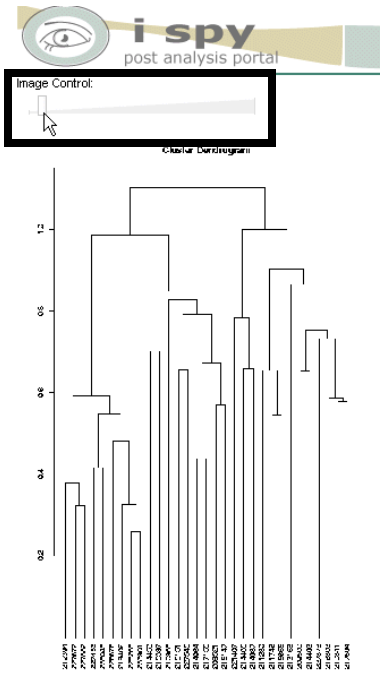
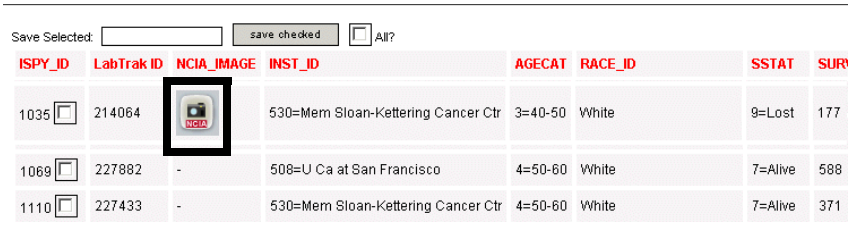


Figure 6.17 Hierarchical Clustering Dendrogram

A clinical report appears beneath the dendrogram where you can select patients and create a PatientDID list. You can also display an image associated with a patient. Click the NCIA icon in the **NCIA_Image** column (*Figure 6.18*), and the National Cancer Imaging Archive(NCIA) web site appears. As a first time user, register to obtain a username and password, and then you will have access to these images.



ISPY_ID	LabTrak ID	NCIA_IMAGE	INST_ID	AGECAT	RACE_ID	SSTAT	SUR
1035	214064		530=Mem Sloan-Kettering Cancer Ctr	3=40-50	White	9=Lost	177
1069	227882	-	508=U Ca at San Francisco	4=50-60	White	7=Alive	588
1110	227433	-	530=Mem Sloan-Kettering Cancer Ctr	4=50-60	White	7=Alive	371

Figure 6.18 Hierarchical Clustering Clinical Report

Correlation Scatter Plot

The *Correlation Scatter plot* (*Figure 6.19*) is a visualization used to compare two continuous variables. The X-axis represents the values for one of the variables and the Y-axis represents the values for the other variable.

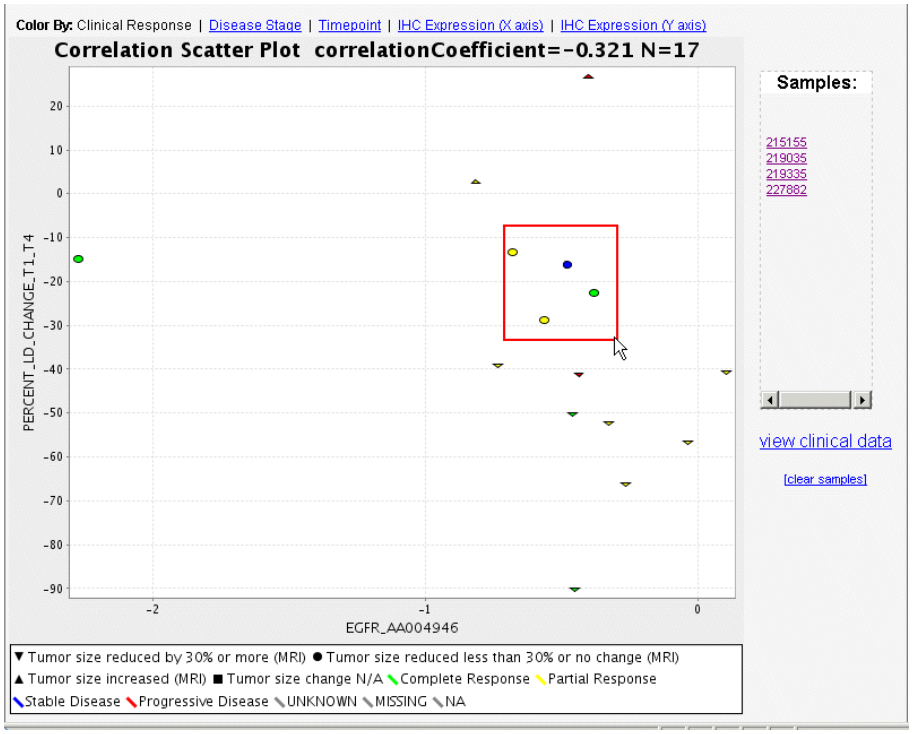


Figure 6.19 Correlation Scatter Plot

Table 6.1 describes other areas in the plot:

Area	Description
Color By	Each point on the graph represents a sample, and by default, the samples are colored by **Clinical Response**. To color by **Disease stage** or **Timepoint**, click the appropriate link. To plot IHC expression on the X- or Y-axis, click the **IHC Expression X axis** or **IHC Expression Y axis** link. For example, selecting color by **IHC Expression (X Axis)**, colors the points on the plot based on the IHC Expression of the gene on the X-axis. Selecting color by **IHC Expression (Y Axis)** colors the points on the plot based on the IHC Expression of the gene on the Y-axis.
Correlation Coefficient	Computed and displayed in the title. Correlation coeffients with values close to 1 are highly correlated. Values close to -1 indicate an inverse relationship. Values close to 0 indicate no correlation between the parameters. At the bottom of the graph, there is a legend defining how the different shapes on the graph indicate different survival ranges for patients.

Table 6.2 Areas of the Correlation Scatter Plot

Area	Description
Legend	At the bottom of the graph, a legend defines how the different shapes on the graph indicate different survival ranges for patients.
Samples	The **Samples** area enables you to select, review, and display clinical data for samples in the plot (see *Selecting Samples of Interest in a Plot*).

Table 6.2 Areas of the Correlation Scatter Plot

Categorical Plot Analysis

The *Categorical Plot analysis* (*Figure 6.20*) displays a Box-and-Whiskers plot of a continuous variable for patients in selected groups.

The following items in the graph indicate the following:

- **Black dot in the box** indicates mean value.
- **Horizontal line in the box** indicates the median value.
- **Circles** are potential outliers.
- **Triangles** are outliers beyond the graph.

Example uses of box and whisker plots include the following:

- Indicate whether a distribution is skewed and whether there are potential unusual observations (outliers) in the dataset.
- Perform a large number of observations
- Compare two or more datasets.
- Compare distributions because the centre, spread, and overall range are immediately apparent.

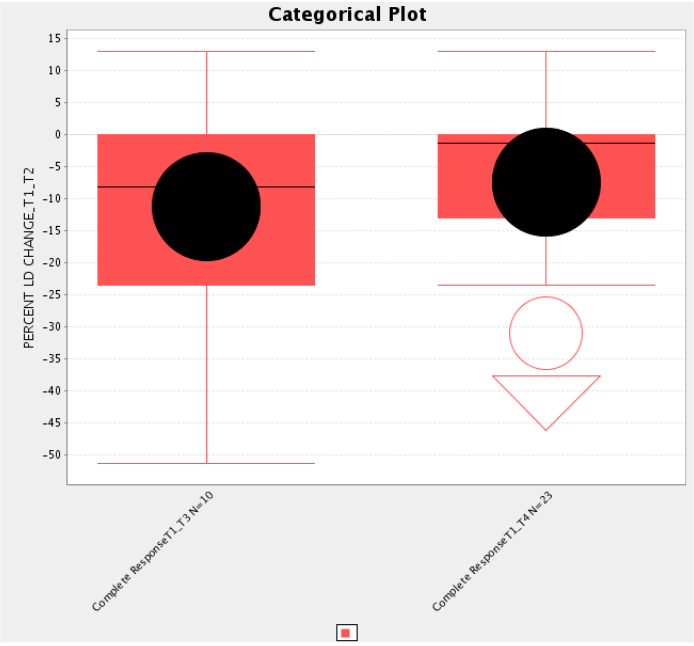


Figure 6.20 Categorical Plot

CHAPTER 7
MANAGING LISTS

This chapter describes how to manage patient and gene lists.

Topics in this chapter include:

Managing Lists Overview

The I-SPY Manage Lists function centralizes all activities pertaining to the creation and management of user-defined, as well as study-defined **PatientDID Lists** and **Gene Lists**. With these lists, you can further refine queries or facilitate analysis. Using the Manage List function, you can perform the following functions:

- View data items in a list
- Create new lists from existing lists
- Delete lists
- Add lists by uploading them or typing them

You can also create PatientDID lists from Clinical Search, IHC Search, and Hierarchical Clustering results. You can generate Gene Lists from Class Comparison results.

PatientDID Lists

An I-SPY *PatientDID list* is a list of patients with certain characteristics that you can use to filter a query or perform analysis. These lists are pre-defined in the Manage Lists function, or you can create your own lists throughout I-SPY. The blue panel displays all PatientDID lists. Mouse over a list name in the blue panel to display the list's data items. Note that user-defined lists appear in red type in the blue panel.

*Table 7.1*lists and describes the pre-defined PatientDID Lists available when you start using I-SPY.

PatientDID List Name	***Description***
Complete Response	
Partial Response	
Stable Disease	
Progressive Disease	
Stage 2	
Stage 3	
ER	Estrogen Receptor
HER2	
PR	Progesteron Receptor

Table 7.1 PatientDID List descriptions

Gene Lists

An I-SPY *Gene list* is a list of genes with certain characteristics that you can use to filter a query or perform analysis. The pre-defined gene list is **defaultGene1**, or you can create your own list with the Class Comparison function. The blue panel displays the names of the Gene lists. Mouse over a list name in the blue panel to display the list's data items. Note that user-defined lists appear in red type in the blue panel.

Viewing the Data Items in a List

To vie the individual data items on a list, follow these steps:

1. At the top of the Manage List page, click on the type of lists you would like to view (**PatientDID List** or **Gene List**).

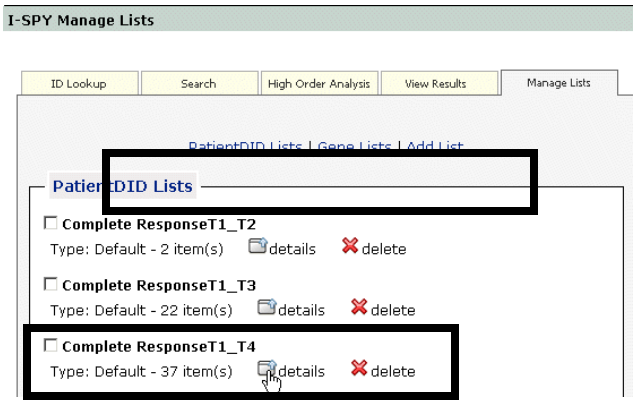


Figure 7.1 List types and Details

2. Find a list to be viewed, and click the **details** icon to display all of the items in the list.

   Note: You can also mouse-over the list name in the blue panel and the list's data item names appear.

3. To export the list, click the **export list** link at the bottom of the data item list.

Removing Data Items to Create a New List

You may delete items from an existing list, then view the new list or save the list on your computer. Follow these steps:

1. At the top of the Manage List page, click on the type of lists you would like to view (**PatientDID List** or **Gene List**).
2. Find the list you want to change, and click on the box next to the list name.
3. Click the **details** icon to display all the items in the selected list.

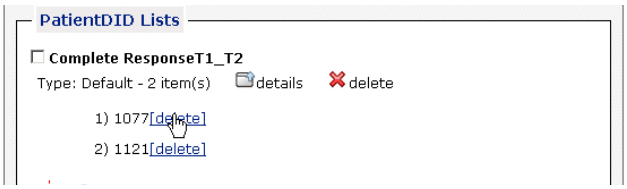


Figure 7.2 Deleting data items

4. Click the **delete** link beside the item you want to delete.The item is removed from the list.

Once you remove the items,you can view the new list or save the list to your computer.

5. Click the **export link** at the bottom of the items list to open and view the new list or save the list on your computer. Click **Open** or **Save**.

Combining Existing Lists to Create a New List

You may create new lists from existing lists. To create a custom list from existing lists, follow these steps:

1. At the top of the Manage List page, click on the type of lists you would like to view (**PatientDID List** or **Gene List**).
2. Find the category for the new list, and click the box next to the category name. Click more than one box to select multiple categories.

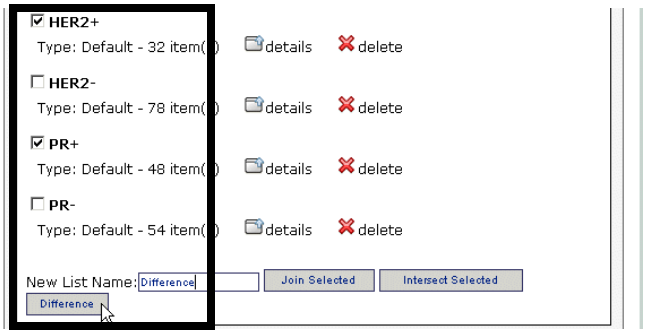


Figure 7.3 Combining existing lists

3. Enter a unique name for the new list you are creating, and then click the appropriate button:
   - **Join** combines two or more categories into a new list.
   - **Intersect** creates a new list from only the items that appear on more than one selected list category.
   - **Difference** creates up to two lists each comprising items that appeared in one of the selected lists. For example, if you select **HER2+** and **PR+**, the new lists are "HER2+ - PR+" comprising the items that appeared in the Astrocytoma list only and "PR+ - HER2+" comprising the items appearing in the GBM list only (*Figure 7.4*).

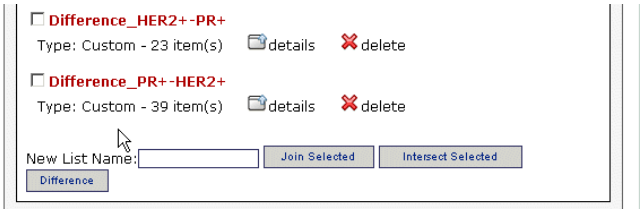


Figure 7.4 New Difference lists

The new list appears on the Manage Lists page and in the blue panel in red (*Figure 7.4*).

The new list appears in the blue panel in red.

Deleting an Entire List

To delete one or more lists from a list type, follow these steps:

1. At the top of the Manage List page, click on the type of lists you would like to view (**PatientDID List** or **Gene List**).
2. Find the list you want to delete, and click the box next to the list name. Click more than one box to select multiple lists for deletion.

Figure 7.5 Deleting an entire list

3. To delete the selected lists, click an **x delete** icon. The selected categories are removed.

Adding a New "Custom" List

You may add a new list type by *uploading* a list from your computer or *manually creating* a list. To add a new list, follow these steps:

1. At the top of the Manage List page, click **Add List**.

   The **Upload List or Manually type List** block appears.

2. To upload a list, follow these steps:

   1. Click **Upload List** at the top of the box.

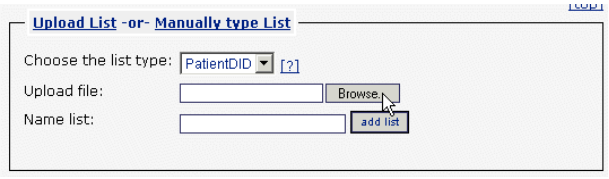


Figure 7.6 Uploading a list

   2. From the **Choose the list type** drop-down list box, select the list to be uploaded.
   3. Click the **Browse** button beside the **Upload file** box. Navigate to and select the file on your computer that you would like to upload.
   4. Enter a unique name for the list, and then click the **Add List** button. The new list appears on the blue panel in red.

3. To create and add a list manually, follow these steps:
    1. Click **Manually Type List** at the top of the box.

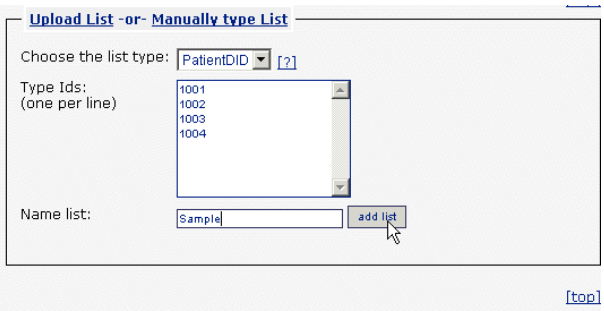


Figure 7.7 Manually typing a list

    2. From the **Choose the list type** drop-down list box, select the list to be uploaded.
    3. In the **Type Ids** box, enter items into the text block by typing them one to a line.
    4. Enter a unique name for the list, and then click the **Add List** button. The new list appears on the blue panel in red.
    5. To open and view the newly created list or save it to your computer, click on the list name in the blue panel. Click **Open** or **Save**.
6. To open and view the newly created list or save it to your computer, click on the list name in the blue panel. Click **Open** or **Save**.

GLOSSARY

Acronyms and other terms referred to in the chapters of this User's Guide are described in this glossary.

Term	*Definition*
NCIA	National Cancer Imaging Archive
Class Comparison	Differential gene expression across the tumor types will be evaluated by calculating the typical *t*-statistic for each reporter. Both parametric and non-parametric *p*-value will be computed.
False Discovery Rate (FDR)	The expected proportion of Type I errors among rejected hypotheses in simultaneous testing of multiple null hypotheses.
Family-wise Error Rate (FWER)	Denotes the probability of having at least one false significant test result within the set of tested hypotheses.
Gene List	A pre-defined or user-defined list in I-SPY comprising genes with a set of characteristics. Used to filter a query.
Hierarchical Clustering	Hierarchical cluster analysis is a statistical method for finding relatively homogeneous clusters of cases based on measured characteristics. It starts with each case in a separate cluster and then combines the clusters sequentially, reducing the number of clusters at each step until only one cluster is left.
High Order Analysis	After data preprocessing (filtering and normalization), further statistical analysis of gene expression data are performed, including class comparison, class discovery and class prediction.

Table 8.1 Glossary of I-SPY terms

Term	Definition
IHC (Immunohistochemistry)	Method of analyzing and identifying cell types based on the binding of antibodies to specific components of the cell. It is sometimes referred to as immunocytochemistry.
NCI	National Cancer Institute
NCICB	National Cancer Institute Center for Bioinformatics
PatientDID List	A pre-defined or user-defined list in I-SPY comprising patients with a set of characteristics. Used to filter a query.
Principal Component Analysis	PCA is commonly used in microarray research as a tool. It is designed to capture the variance in a dataset in terms of principle components. In effect, one is trying to reduce the dimensionality of the data to summarize the most important (i.e. defining) parts while simultaneously filtering out noise.
Wilcoxon Test	Nonparametric statistics for testing hypotheses about whether two samples differ.

Table 8.1 Glossary of I-SPY terms