



Introduction

The examples below illustrate the use of Jasper OLAP, an open source web-based OLAP (on-line analytical processing) system, to explore data generated by the Human Immune Monitoring Center (HIMC) and integrated into the Stanford Data Miner.

While your data may not match these examples, the instructions should give you a sense of how to:

- 1) Expand (drill down) and collapse data views
- 2) Change the active values in a dimension
- 3) Change dimensions on rows and columns

Feel free to explore. Your actions will not modify the underlying data.

1. Expanding and collapsing a data view

Upon login, select an **Analysis View** from the right-hand menu:

Analysis Views			
<input type="checkbox"/>	Davis Data, Assay Only	Assay results without person and sample metadata /PI_Data/Davis_Mark/Analysis/Basic	4/12/12 8:21 PM
<input type="checkbox"/>	Davis Data, Assay Plus Person	Assay results integrated with person and sample metadata /PI_Data/Davis_Mark/Analysis/Basic	4/13/12 5:56 PM

This will take you to the main OLAP interface:

Davis Data, Assay Only

Dimensions		Sample Type	
		+ All Sample Types	
Analyte Tree		Measures	
Assay		<input type="radio"/> Mean	<input type="radio"/> N
All Analytes	+ CyTOF	37.5	15,456
	+ HAI		
	+ Human Luminex 37 plex		
	+ Human Luminex 50 plex	1,024.4	18,121
	+ Human Luminex 51 plex	901.1	100,228
	+ Human Luminex MAG 39 plex		
	+ Human MSD 4 plex	740.0	6,112
	+ Human MSD 9 plex		
	+ Human MSD CRP		
	+ Lyoplate 1	41.4	23,570
	+ Mouse Luminex 26 plex	1,158.8	3,390
	+ Mouse Luminex IL-22		
	+ Phospho-flow cytokine stim	1,055.2	58,692

Filter: Unit Type=[Units].[All Units].[primary]

Expand the data by clicking on any of the + signs:

Davis data, assay only

Dimensions			Sample Type	
Analyte Tree	Assay Group	Panel	+ All Sample Types	
			Measures	
			○ Mean	○ N
- All Analytes			918.2	186,759
All Analytes	- Flow phenotype		41.4	23,570
	Flow phenotype	+ Activated T	40.2	3,451
		+ B cell	41.5	2,842
		+ CXCR3	49.0	3,248
		+ CXCR3 FMO	38.5	3,248
		+ NK-NKT	36.2	4,488
		+ T cell	44.4	3,654
		+ Treg	41.7	2,639
	+ Luminex/MSD		914.0	127,321
	+ Phospho flow		1,509.3	35,868

Filter: Unit Type=[Unit Type].[All Types].[primary]

(Collapse data by clicking on a - sign.)

2. Changing the selected values in a dimension

To modify the view, click on the cube icon in the tool bar:

The screenshot shows the 'Davis Data, Assay Only' interface. On the left is a vertical toolbar with various icons. A blue arrow points to the cube icon. The main area displays a dimension selection dialog with a list of dimensions under 'Filter'. Below the dialog is a data table showing the current view of the data.

Davis Data, Assay Only

Columns

- Sample Type
- Measures

Rows

Analyte Tree

Filter


- Aliquot
- Analyte Generic Name
- Analyte Panel
- Analyte Specific Name
- Assay
- Assay Group
- In Range
- Kit Batch
- Project
- Project Assay Report
- Stim
- Tissue
- Units (Unit Type=primary)
- Wells

OK Cancel

Dimensions		Sample Type	
		+ All Sample Types	
		Measures	
Analyte Tree	Assay	○ Mean	○ N
All Analytes	+ CyTOF	37.5	15,456
	+ Human Luminex 50 plex	1,024.4	18,121
	+ Human Luminex 51 plex	901.1	100,228
	+ Human MSD 4 plex	740.0	6,112
	+ Lyoplate 1	41.4	23,570
	+ Mouse Luminex 26 plex	1,158.8	3,390
	+ Phospho-flow cytokine stim	1,055.2	58,692

Filter: Unit Type=[Units].[All Units].[primary]

Click on Measures to modify the selection of dimension values. Deselect N (the number of data points) by clicking on the checkbox.



Davis Data, Assay Only

Measures ✕

Mean

N

Min

Max

Median

None Group OK Cancel

Dimensions + -		Sample Type	
		+ All Sample Types	
Analyte Tree		Measures	
Assay		○ Mean	○ N
All Analytes	+ CyTOF	37.5	15,456
	+ Human Luminex 50 plex	1,024.4	18,121
	+ Human Luminex 51 plex	901.1	100,228
	+ Human MSD 4 plex	740.0	6,112
	+ Lyoplate 1	41.4	23,570
	+ Mouse Luminex 26 plex	1,158.8	3,390
	+ Phospho-flow cytokine stim	1,055.2	58,692

Filter: Unit Type=[Units].[All Units].[primary]

Click **OK** twice to return to the active view:

Davis Data, Assay Only

Dimensions + -		Sample Type
		<input checked="" type="checkbox"/> All Sample Types
Analyte Tree		Measures
Assay		<input type="radio"/> Mean
All Analytes	<input checked="" type="checkbox"/> CyTOF	37.5
	<input checked="" type="checkbox"/> Human Luminex 50 plex	1,024.4
	<input checked="" type="checkbox"/> Human Luminex 51 plex	901.1
	<input checked="" type="checkbox"/> Human MSD 4 plex	740.0
	<input checked="" type="checkbox"/> Lyoplate 1	41.4
	<input checked="" type="checkbox"/> Mouse Luminex 26 plex	1,158.8
	<input checked="" type="checkbox"/> Phospho-flow cytokine stim	1,055.2

Filter: Unit Type=[Units].[All Units].[primary]

3. Changing the dimensions on rows and columns

When editing the view, dimensions can be moved to rows or columns by clicking on the little boxes next to them. When you hover over the icon, an explanation appears. To remove a dimension from the rows or columns, click on the filter icon. In this example, we've moved **Stim** to **Columns** and **Sample Type** to **Filters**.

The screenshot shows a dialog box titled "Davis Data, Assay Only" with a toolbar on the left and a main content area. The content area is organized into three sections:

- Columns:** Contains "Stim" and "Measures".
- Rows:** Contains "Analyte Tree".
- Filter:** Contains "Aliquot", "Analyte Generic Name", "Analyte Panel", "Analyte Specific Name", "Assay", "Assay Group", "In Range", "Kit Batch", "Project", "Project Assay Report", "Sample Type", "Tissue", "Units (Unit Type=primary)", and "Wells".

At the bottom of the dialog are "OK" and "Cancel" buttons.

In addition, we can select various levels of the Analyte Tree:

Davis Data, Assay Only

Analyte Tree
<input type="checkbox"/> - All Analytes
<input type="checkbox"/> +• CyTOF
<input type="checkbox"/> +• HAI
<input type="checkbox"/> +• Human Luminex 37 plex
<input type="checkbox"/> +• Human Luminex 50 plex
<input type="checkbox"/> +• Human Luminex 51 plex
<input type="checkbox"/> +• Human Luminex MAG 39 plex
<input type="checkbox"/> +• Human MSD 4 plex
<input type="checkbox"/> +• Human MSD 9 plex
<input type="checkbox"/> +• Human MSD CRP
<input type="checkbox"/> +• Lyoplate 1
<input type="checkbox"/> +• Mouse Luminex 26 plex
<input type="checkbox"/> +• Mouse Luminex IL-22
<input type="checkbox"/> -• Phospho-flow cytokine stim
<input type="checkbox"/> +• B cell
<input checked="" type="checkbox"/> +• CD4+
<input type="checkbox"/> +• CD4+CD45RA+
<input type="checkbox"/> +• CD4+CD45RA-
<input type="checkbox"/> +• CD8+
<input type="checkbox"/> +• CD8+CD45RA+
<input type="checkbox"/> +• CD8+CD45RA-
<input checked="" type="checkbox"/> +• Mono
<input type="button" value="None"/> <input type="button" value="Group"/> <input type="button" value="OK"/> <input type="button" value="Cancel"/>

Stanford Data Miner and Jasper OLAP Overview

After returning to the main view, and expanding the dimensions, we are able to compare the effects of various cytokine stimulations on CD4+ T cells and Monocytes:

Davis Data, Assay Only

Dimensions				Stim																			
				All Stims		All Stims						IFNa		IFNg		IL-10		IL-2		IL-21		IL-6	
				Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N		
Analyte Tree	Assay	Panel	Generic Name	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean	N				
All Analytes	Phospho-flow cytokine stim	<input type="checkbox"/> CD4+		1,131.4	7,716	863.3	1,083	348.3	1,083	1,948.8	1,083	1,624.5	612	2,656.7	1,083	765.0	1,077						
		<input checked="" type="checkbox"/> CD4+ pSTAT1		1,225.0	2,572	1,318.0	361	500.3	361	1,877.1	361	1,451.1	204	2,569.3	361	1,108.4	359						
		<input checked="" type="checkbox"/> CD4+ pSTAT3		1,065.7	2,572	471.8	361	199.9	361	2,165.0	361	1,539.6	204	2,834.4	361	655.6	359						
		<input checked="" type="checkbox"/> CD4+ pSTAT5		1,103.4	2,572	800.1	361	344.7	361	1,804.2	361	1,882.8	204	2,566.4	361	530.9	359						
		<input type="checkbox"/> Mono		1,554.0	7,698	1,226.8	1,080	1,285.0	1,080	4,679.2	1,080	2,384.8	612	735.0	1,080	801.3	1,074						
		<input checked="" type="checkbox"/> Mono pSTAT1		1,763.1	2,566	1,950.2	360	2,183.9	360	4,493.6	360	1,902.0	204	767.8	360	887.8	358						
		<input checked="" type="checkbox"/> Mono pSTAT3		1,411.1	2,566	852.0	360	623.2	360	5,244.3	360	1,825.7	204	811.6	360	729.9	358						
		<input checked="" type="checkbox"/> Mono pSTAT5		1,487.7	2,566	878.2	360	1,048.1	360	4,299.6	360	3,426.8	204	625.6	360	786.1	358						

Filter: Unit Type=[Units],[All Units],[primary]

4. Other notes and tips

There are 3 sample types defined in the data model. They are person, control, and standard. Use filters or the sample type dimension to inspect the appropriate data.

The various units (pg/ml, avg MFI, Freq of Parent) are classified by Unit Type as primary or standard. Use filters or the dimensions to pick the appropriate units.

Data in a view can be sorted by clicking on the small dot at the top of a column.