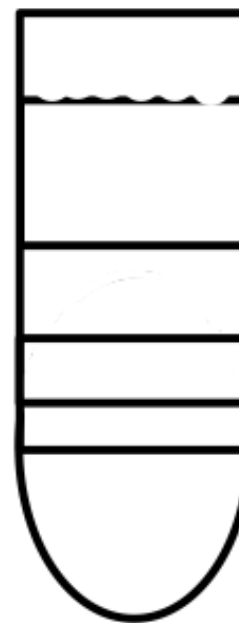




How to Lex

A Sample De-Multiplexing Plugin for SeqGeq



Why Would I Want This Tool?

So you've generated multiplexed sample data (many samples sequenced in a single tube simultaneously with sample oligo-tags).

Cool!

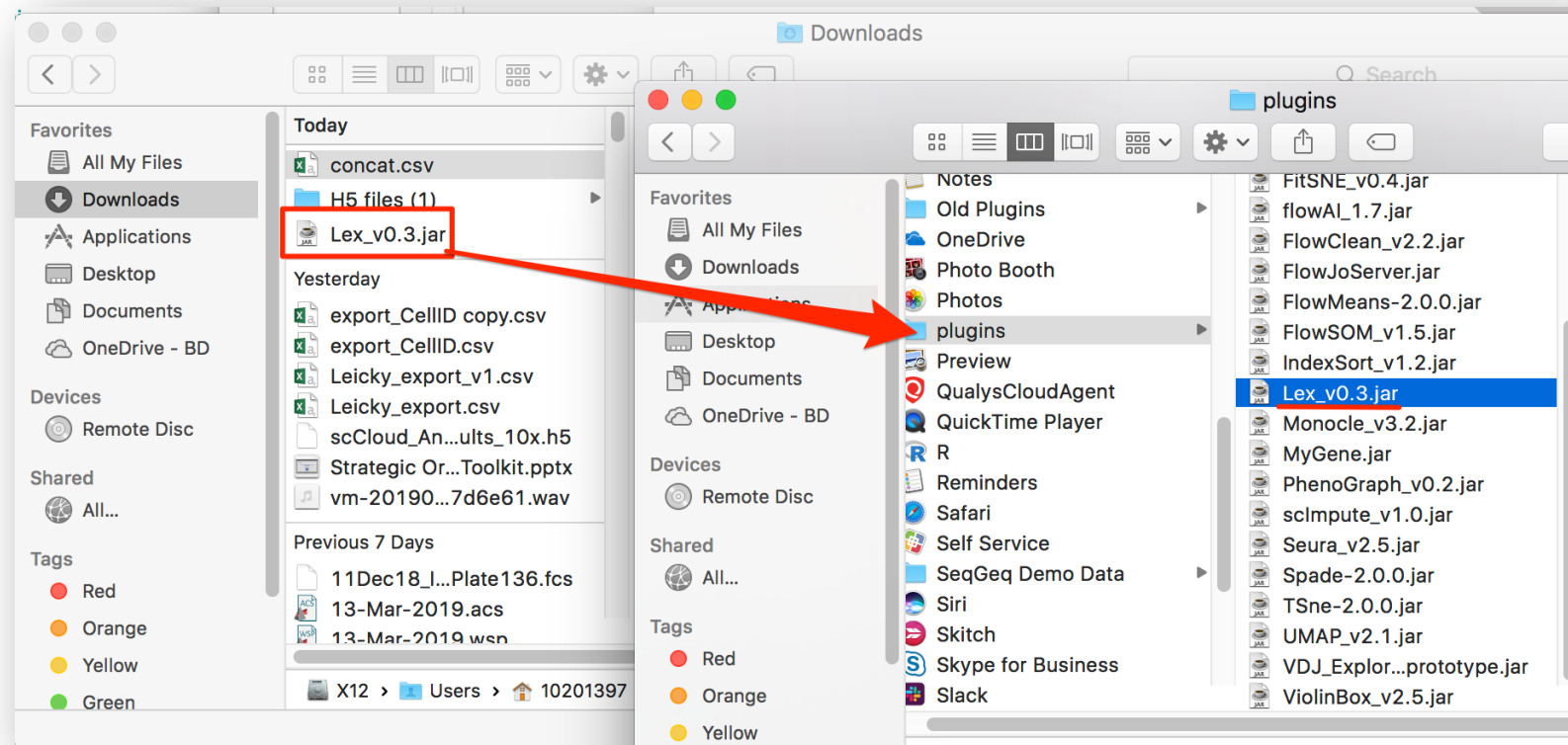
Now you just need to pull those samples apart within downstream analysis.

Whether your data is combined by using **Cell Hashing**, or **BD™'s Sample Multiplexing Kit**, or you've simply concatenated your samples together in SeqGeq - Lex is here to help!

* Lex now also able to "de-concatenate" combined samples



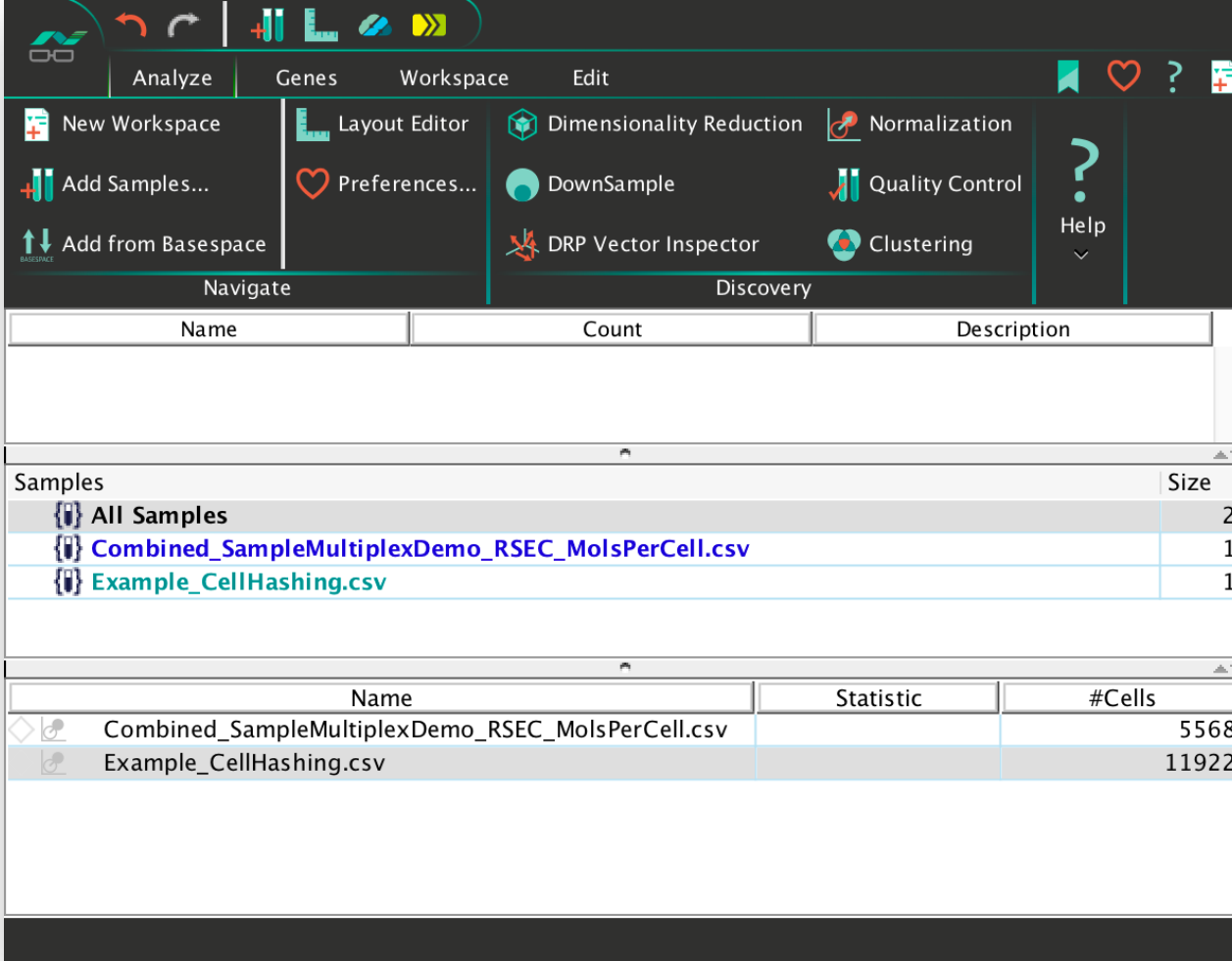
Step 1a - Install Lex within your plugins folder, simply by dragging and dropping the plugin JAR into that directory



Step 1b – Restart SeqGeq



Step 2 - Load your data into SeqGeq just as you normally would and select the multiplexed data file



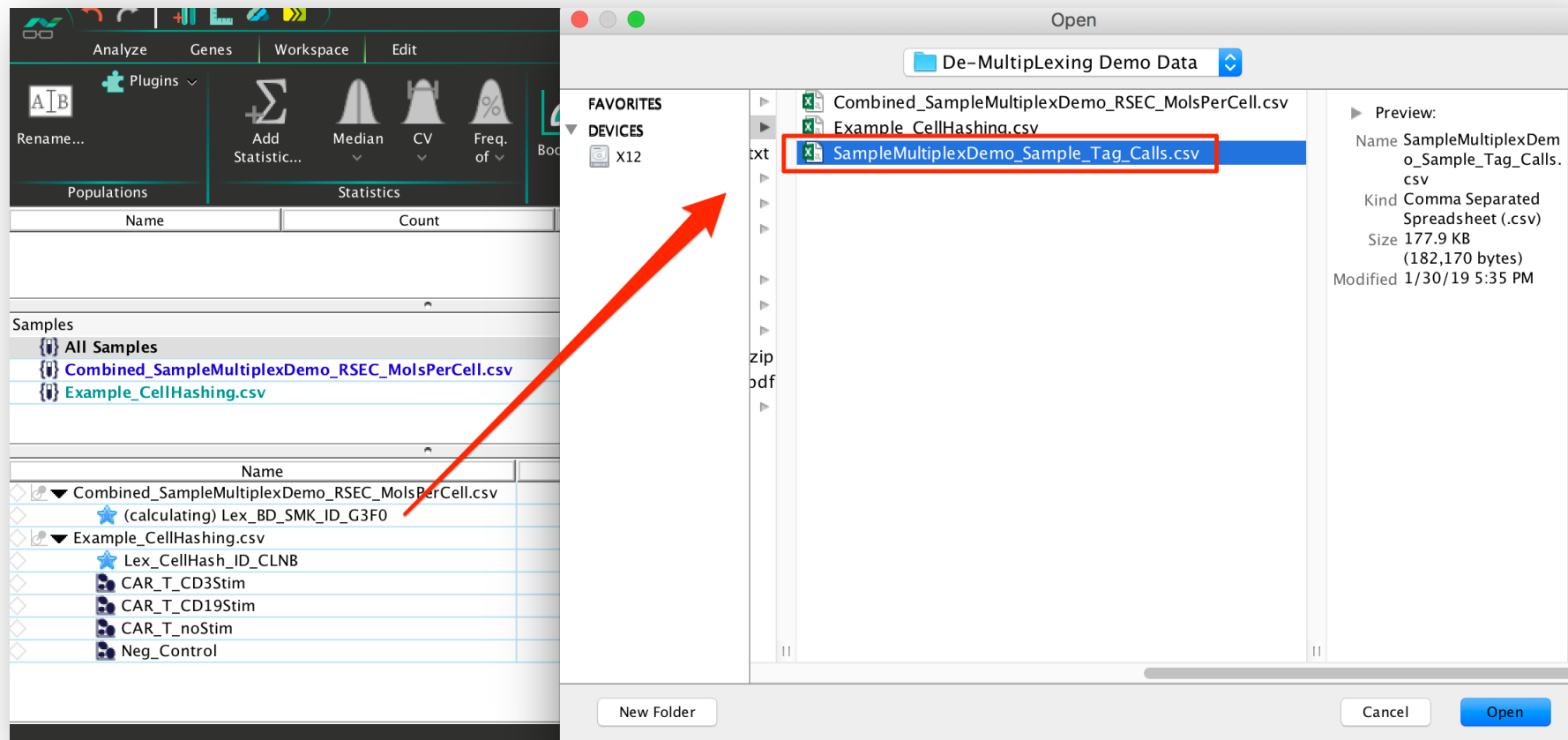
The screenshot displays the SeqGeq software interface. The top menu bar includes 'Analyze', 'Genes', 'Workspace', and 'Edit'. The 'Analyze' tab is active, showing a sidebar with options: 'New Workspace', 'Add Samples...', 'Add from Basespace', 'Layout Editor', 'Preferences...', 'Dimensionality Reduction', 'DownSample', 'DRP Vector Inspector', 'Normalization', 'Quality Control', 'Clustering', and 'Help'. The main panel shows a table of loaded samples.

Name	Count	Description
Samples		
All Samples	2	
Combined_SampleMultiplexDemo_RSEC_MolsPerCell.csv	1	
Example_CellHashing.csv	1	

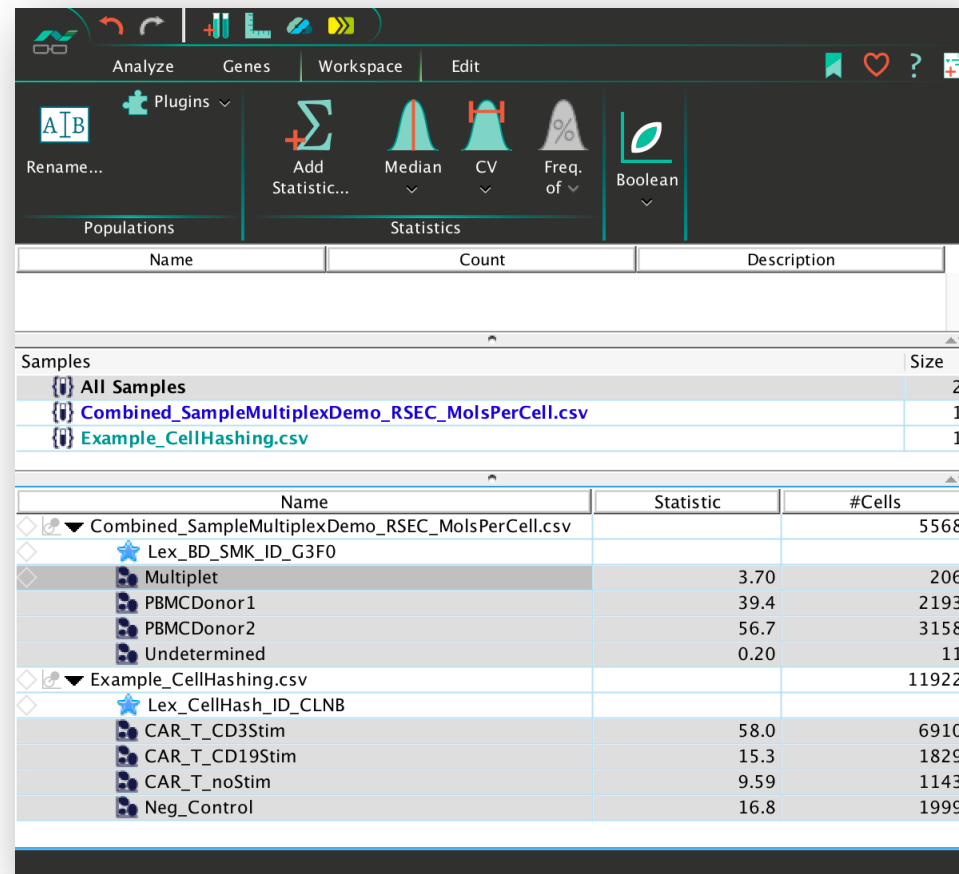
Name	Statistic	#Cells
Combined_SampleMultiplexDemo_RSEC_MolsPerCell.csv		5568
Example_CellHashing.csv		11922



If you're using BDs SMK you'll need to select the associated Sample Tag Calls CSV file



Once distinguished you can now analyze or otherwise treat “sample subpopulations” in the data matrix just like any other population within the SeqGeq workspace



The image shows the SeqGeq workspace interface. At the top, there are tabs for 'Analyze', 'Genes', 'Workspace', and 'Edit'. Below these are icons for 'Rename...', 'Add Statistic...', 'Median', 'CV', 'Freq. of', and 'Boolean'. The main area displays two tables: 'Samples' and a detailed view of the 'Combined_SampleMultiplexDemo_RSEC_MolsPerCell.csv' file.

Name	Count	Description
Samples		
All Samples	2	
Combined_SampleMultiplexDemo_RSEC_MolsPerCell.csv	1	
Example_CellHashing.csv	1	

Name	Statistic	#Cells
Combined_SampleMultiplexDemo_RSEC_MolsPerCell.csv		5568
Lex_BD_SMK_ID_G3F0		
Multiplet	3.70	206
PBMCDonor1	39.4	2193
PBMCDonor2	56.7	3158
Undetermined	0.20	11
Example_CellHashing.csv		11922
Lex_CellHash_ID_CLNB		
CAR_T_CD3Stim	58.0	6910
CAR_T_CD19Stim	15.3	1829
CAR_T_noStim	9.59	1143
Neg_Control	16.8	1999



A Note on DeConcatenating Samples

The DeConcatenation process *only works on concatenated samples*, for the time being.

As a result, if you want to concatenate and then deConcatenate subsets, you'll first need to export them as separate individual samples, then concatenate, in order to effectively use the Lex option to nicely re-annotate the combined populations automatically.



Resources

- Demo Videos of Lex in Action:

tinyurl.com/Lex-DeMultiplex

tinyurl.com/Lex-DeConcat

- Documentation:

docs.flowjo.com/seqgeq

- Support:

seqgeq@bd.com



Thank You!

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