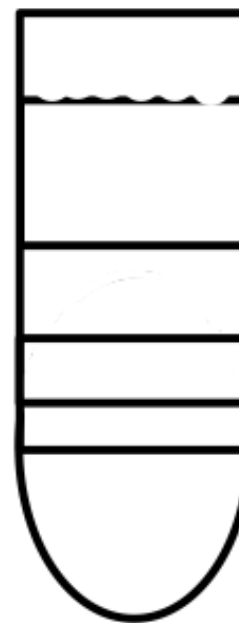# How to Lex

A Sample De-Multip*Lex*ing 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!
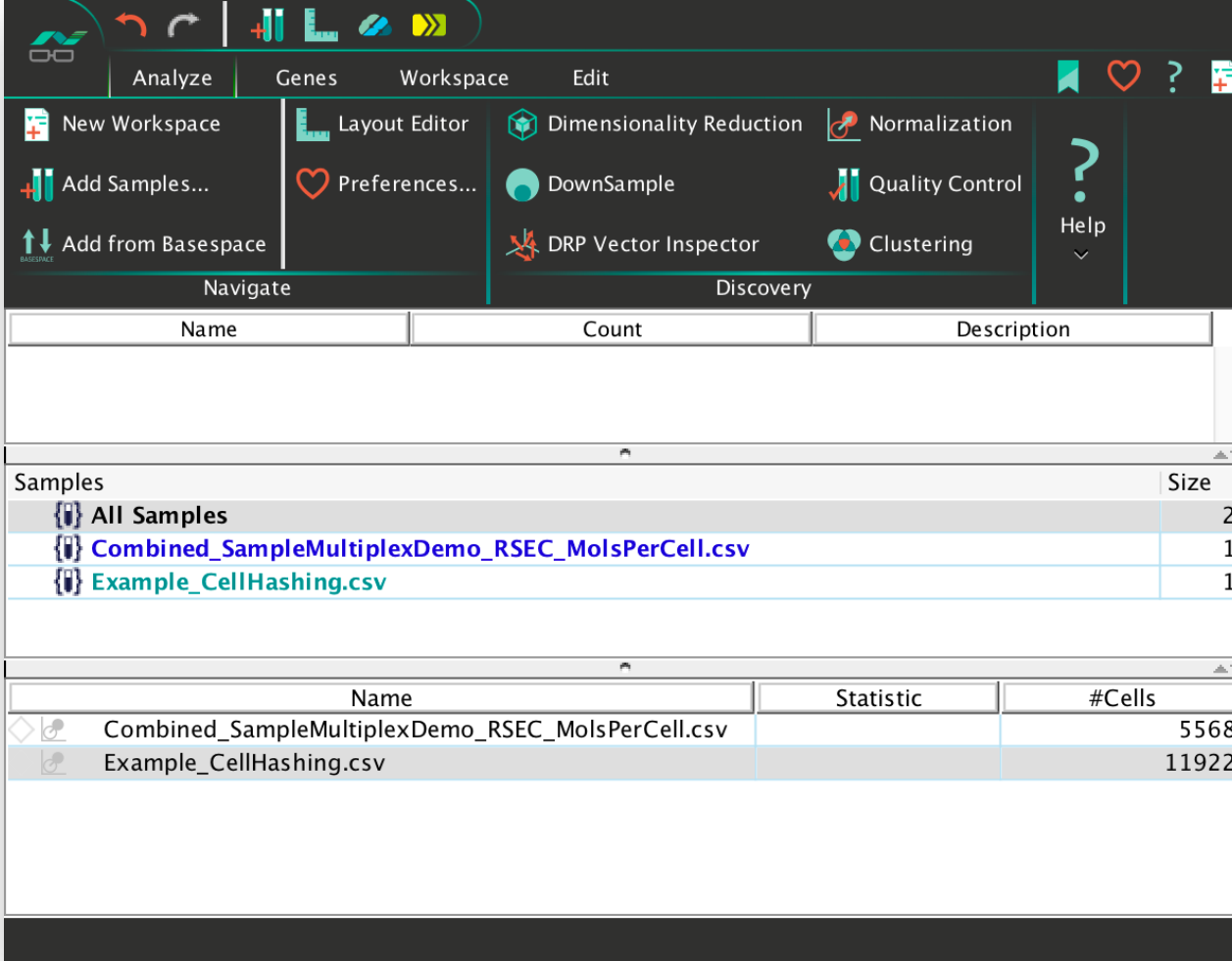
∗ Lex now also able to "de-concatenate" combined samples

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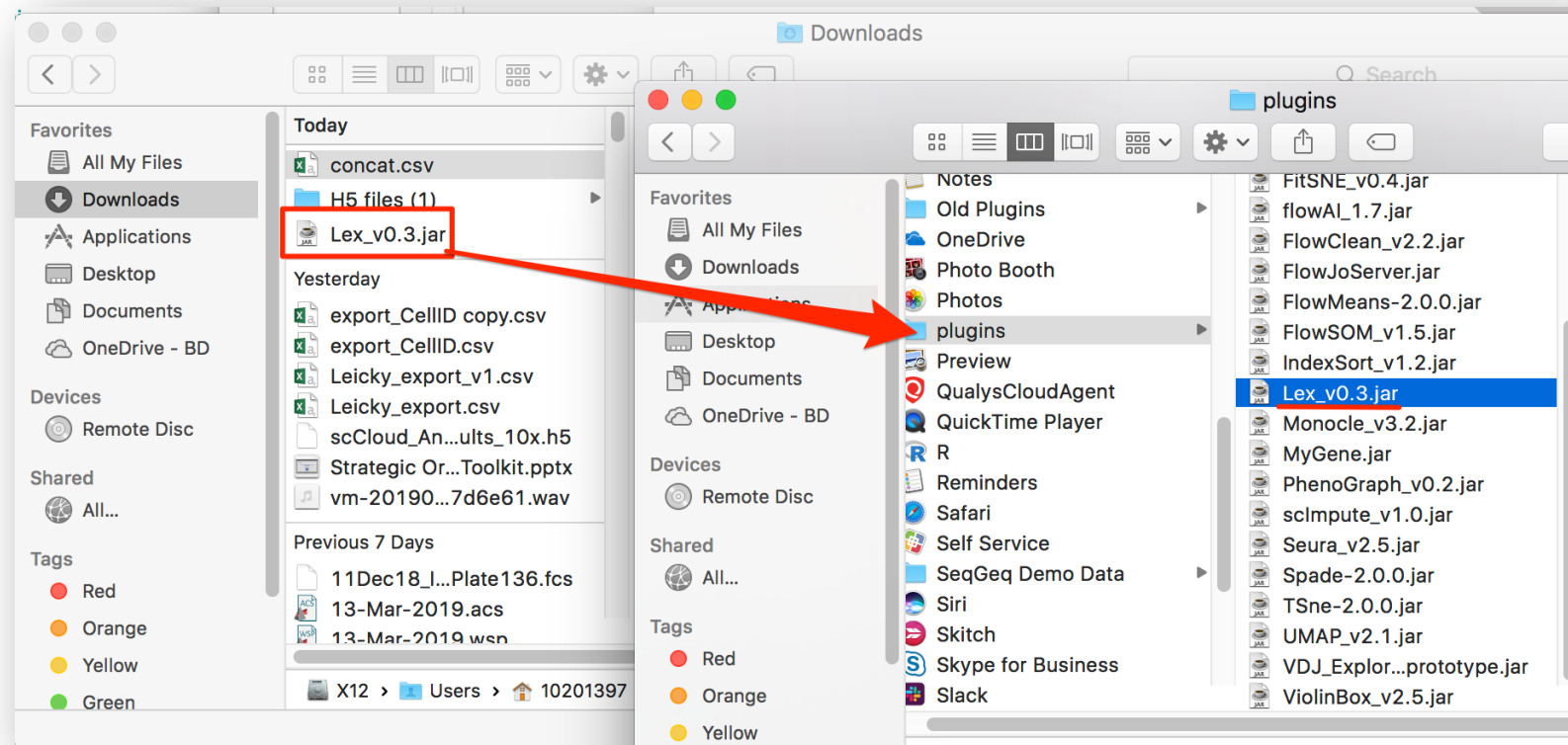
Step 1b – Restart SeqGeq

Step 2 - Load your data into SeqGeq just as you normally would and select the multiplexed data file
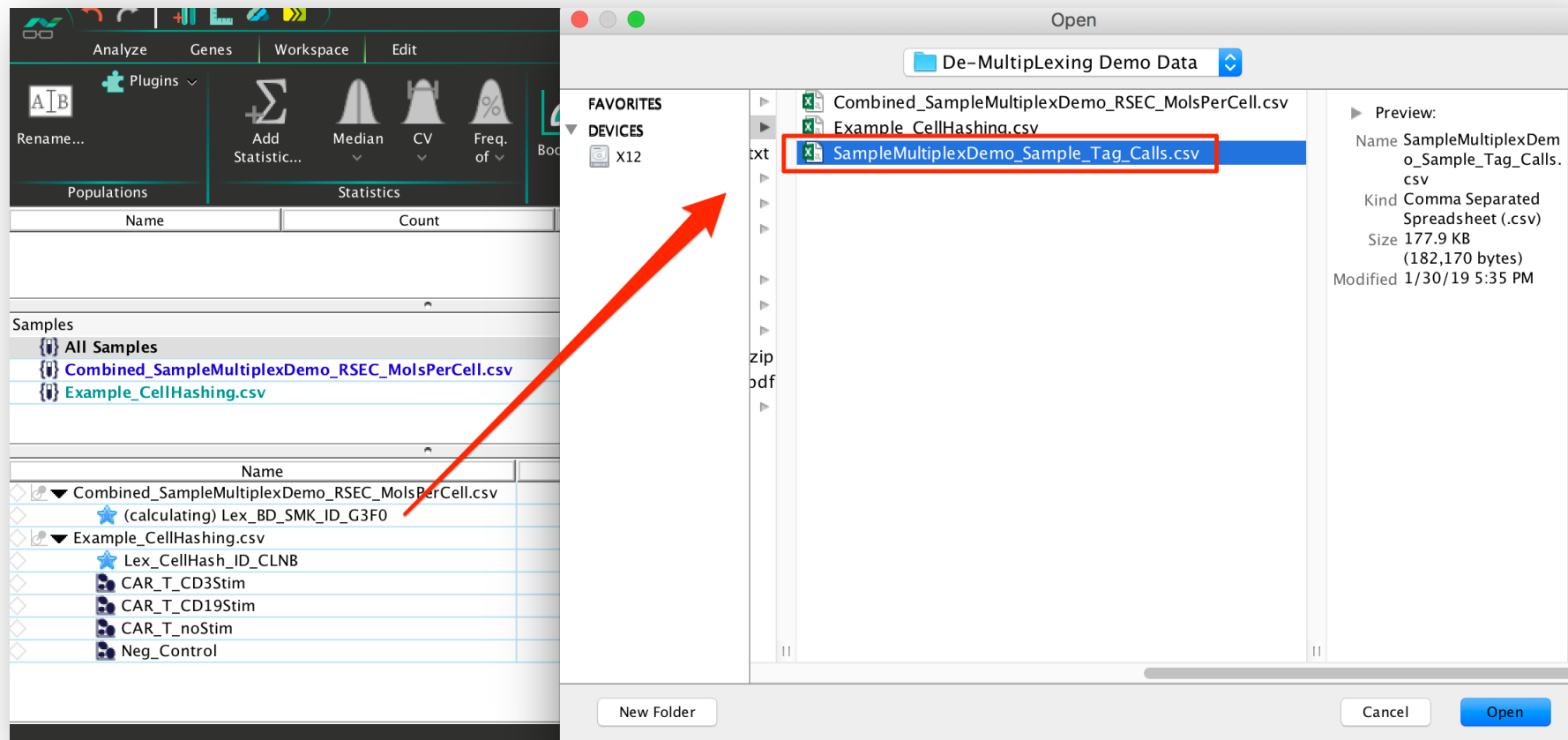
Step 3 - Visit the Plugins section of the SeqGeq workspace

Choose Either:
Lex_BDs_SMK, Lex_CellHash or
Lex_DeConcatenate. Based on the type of sample multiplexing performed

CellID and Sample Names from BD™s Sample Multiplexing Kit:

CellID with Cell Hashed Sample Name:

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

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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