

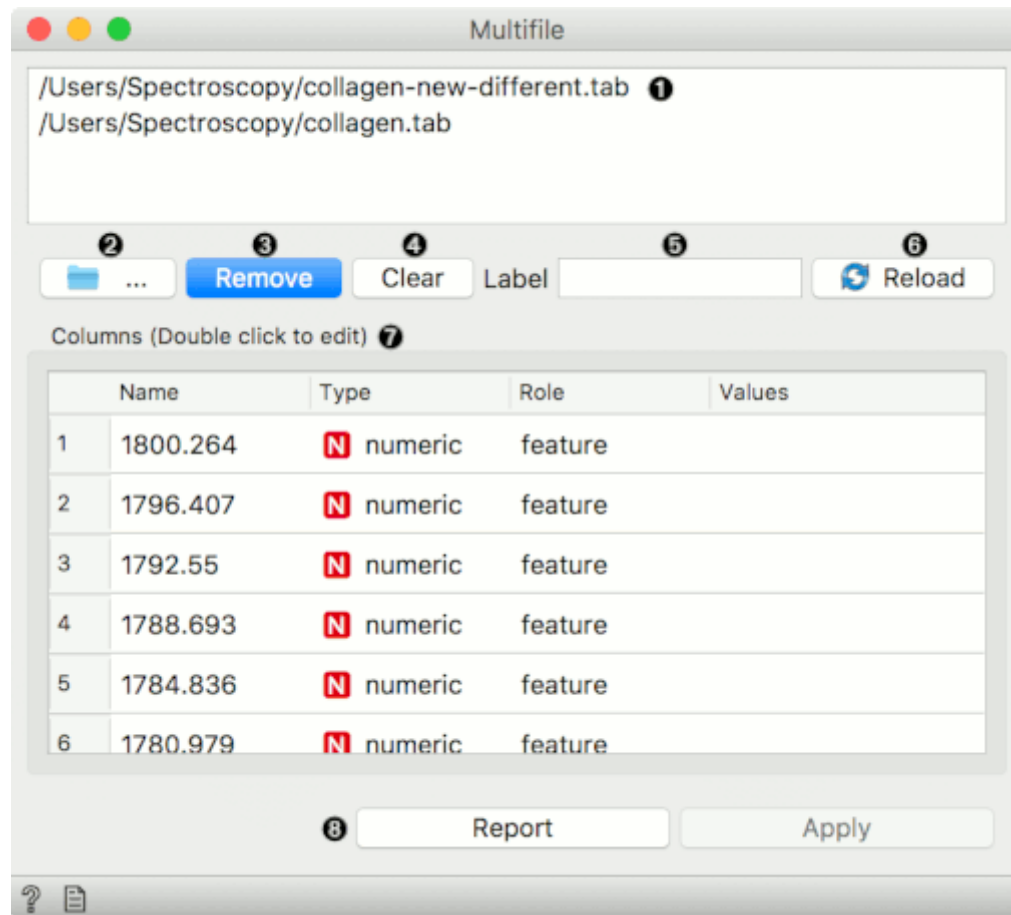
# Multifile

Read data from input files and send a data table to the output.

## Outputs

- Data: a data table of all the loaded files

The **Multifile** widget loads data from different sources and works like **Concatenate** widget for spectroscopy. The widget will output a union of attributes and features, with missing values for non-matching wavenumbers. To interpolate missing data, use the **Interpolate** widget.

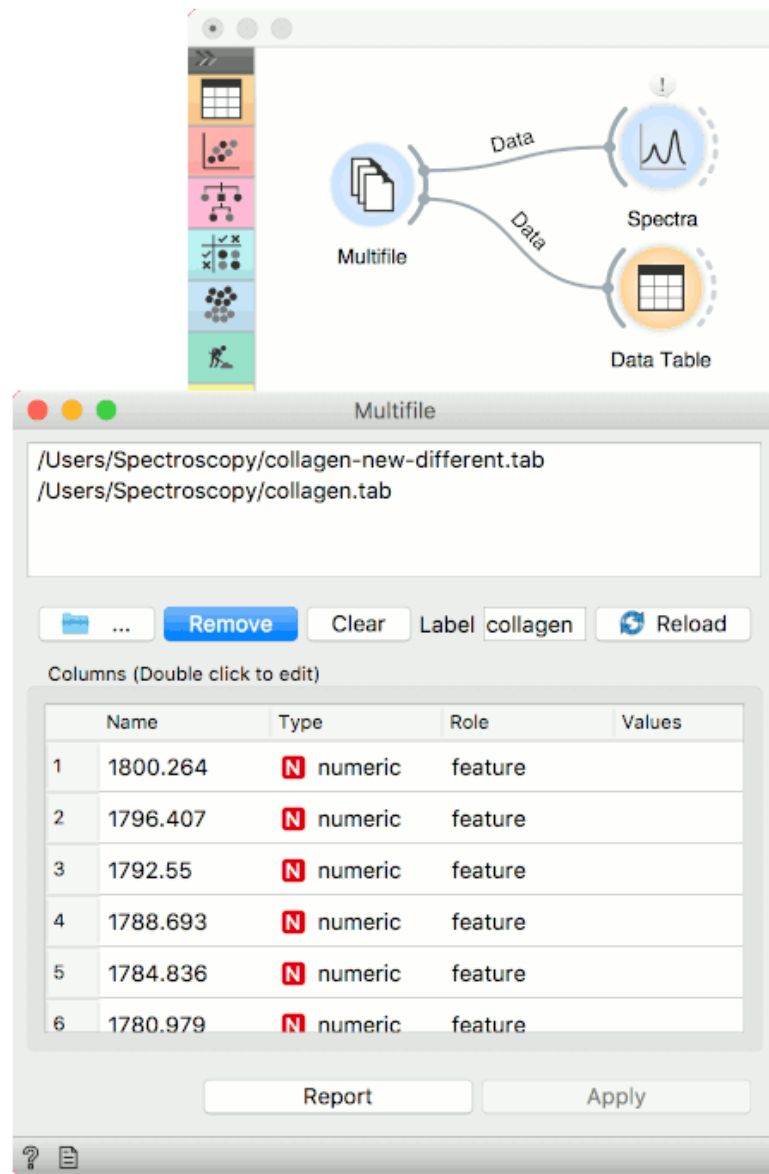


4. Clear all files.
5. Label the concatenated data.
6. Reload the files.
7. Domain editor. Features can be edited by double-clicking on them. The user can change the attribute names, select the type of variable per each attribute (*Continuous*, *Nominal*, *String*, *Datetime*), and choose how to further define the attributes (as *Features*, *Targets* or *Meta*). The user can also decide to ignore an attribute.
8. Add Multifile to the report. Apply to commit the changes.

## Example

Here is a simple example on how to use the **Multifile** widget. We have loaded two data set that were stored on our local machine. We used the folder icon to access the files and load them. Now our files are displayed in the top box. We have labelled the files *collagen*, make it clear what it is about.

We can observe the concatenated data in the **Spectra** widget or in a **Data Table**.



The image shows the Orange Data Mining workflow and the Multifile widget interface. The workflow consists of a Multifile widget connected to two Data widgets, which are then connected to Spectra and Data Table widgets. The Multifile widget interface shows the loaded files: /Users/Spectroscopy/collagen-new-different.tab and /Users/Spectroscopy/collagen.tab. The Label is set to collagen. The Columns table lists six numeric features: 1800.264, 1796.407, 1792.55, 1788.693, 1784.836, and 1780.979. The Report and Apply buttons are visible at the bottom.

**Multifile**

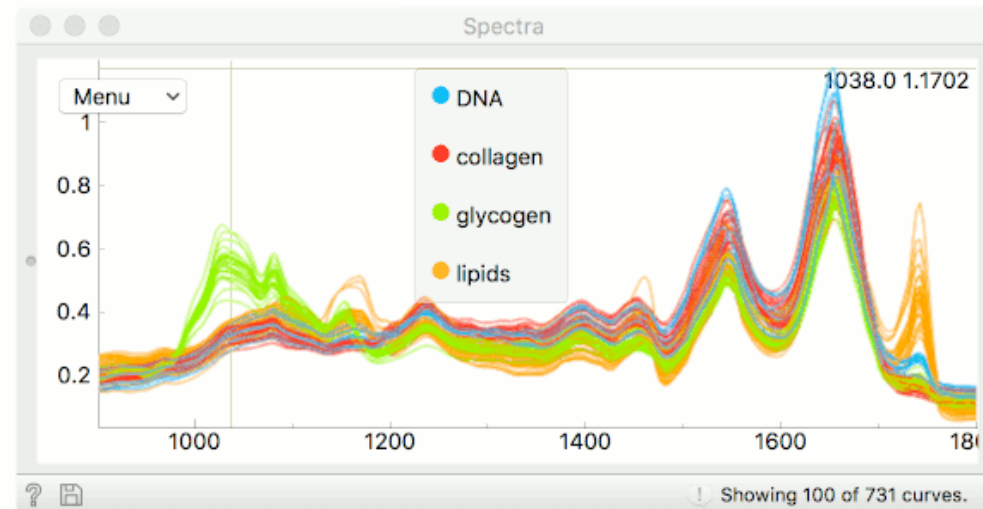
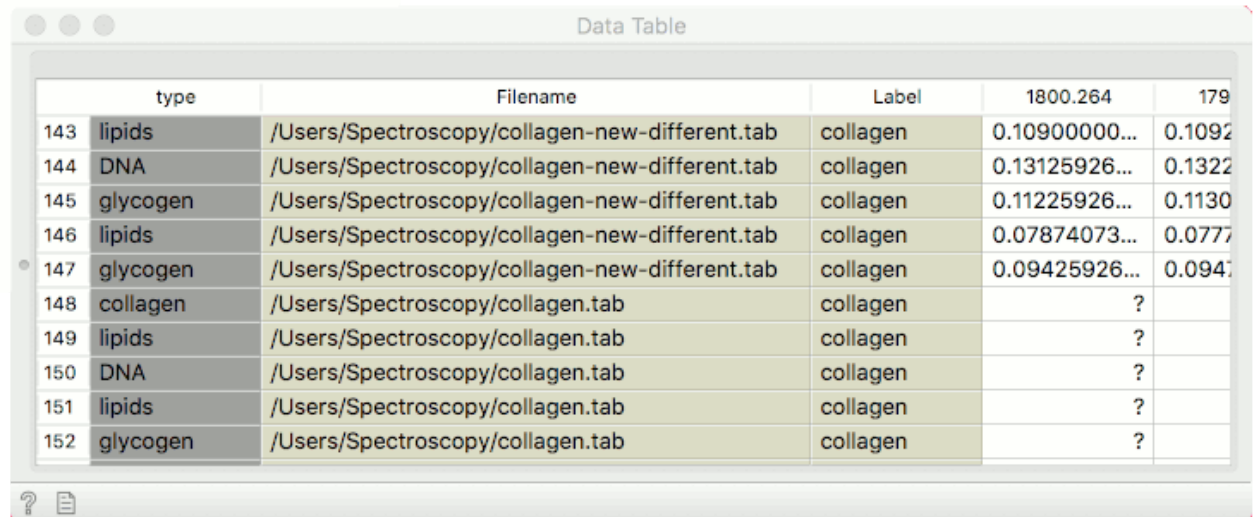
/Users/Spectroscopy/collagen-new-different.tab  
/Users/Spectroscopy/collagen.tab

Remove Clear Label collagen Reload

Columns (Double click to edit)

	Name	Type	Role	Values
1	1800.264	N numeric	feature	
2	1796.407	N numeric	feature	
3	1792.55	N numeric	feature	
4	1788.693	N numeric	feature	
5	1784.836	N numeric	feature	
6	1780.979	N numeric	feature	

Report Apply

The Data Table widget displays a list of samples with their type, filename, label, and feature values. The table has 6 columns: type, Filename, Label, 1800.264, and 179. The samples are listed in rows 143 to 152.

**Data Table**

	type	Filename	Label	1800.264	179
143	lipids	/Users/Spectroscopy/collagen-new-different.tab	collagen	0.10900000...	0.1092
144	DNA	/Users/Spectroscopy/collagen-new-different.tab	collagen	0.13125926...	0.1322
145	glycogen	/Users/Spectroscopy/collagen-new-different.tab	collagen	0.11225926...	0.1130
146	lipids	/Users/Spectroscopy/collagen-new-different.tab	collagen	0.07874073...	0.0777
147	glycogen	/Users/Spectroscopy/collagen-new-different.tab	collagen	0.09425926...	0.0942
148	collagen	/Users/Spectroscopy/collagen.tab	collagen	?	?
149	lipids	/Users/Spectroscopy/collagen.tab	collagen	?	?
150	DNA	/Users/Spectroscopy/collagen.tab	collagen	?	?
151	lipids	/Users/Spectroscopy/collagen.tab	collagen	?	?
152	glycogen	/Users/Spectroscopy/collagen.tab	collagen	?	?