

# Viewing Multiple Interactive Plots Using plotly and trelliscopejs



R/Medicine 2022

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# Introduction to Lipids

Lipids are organic compounds that are mostly insoluble in polar solvents like water.

Example of lipids are

- Cholesterol and Triglycerides in blood lipid panel test
- Phospholipids in cell membrane
- Ceramides in skin

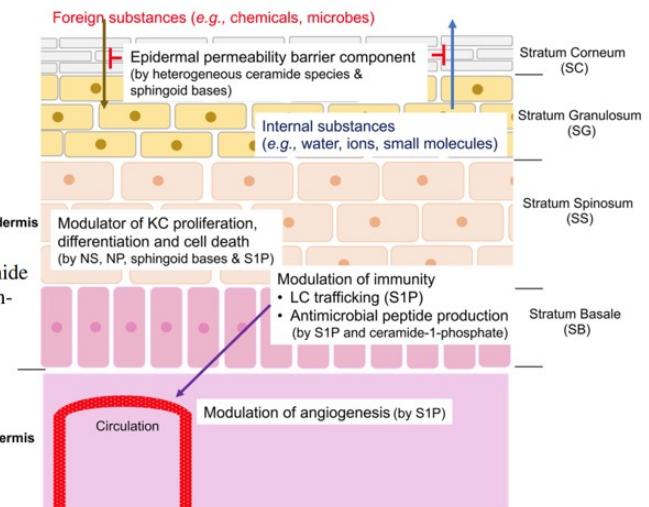
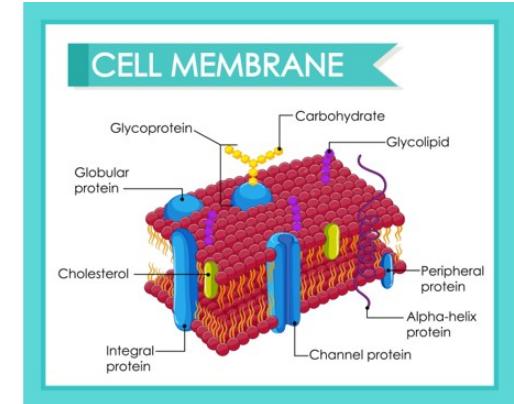
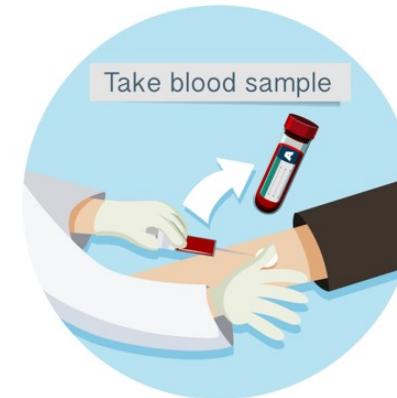
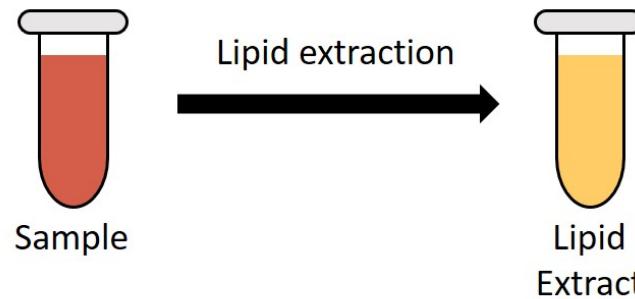


Fig. 7 Diverse roles of ceramide (Cer) and its metabolite sphingoid base in skin

Blood sample and cell membrane image from [brgfx](#)

Skin image from [Uchida and Park 2021](#)

# How Lipids are measured (Targeted Lipidomics)



Lipid measurement

Transition_Name	Precursor_Ion	Product_Ion
Cer d18:1/12:0 (ISTD)	482.4	264.4

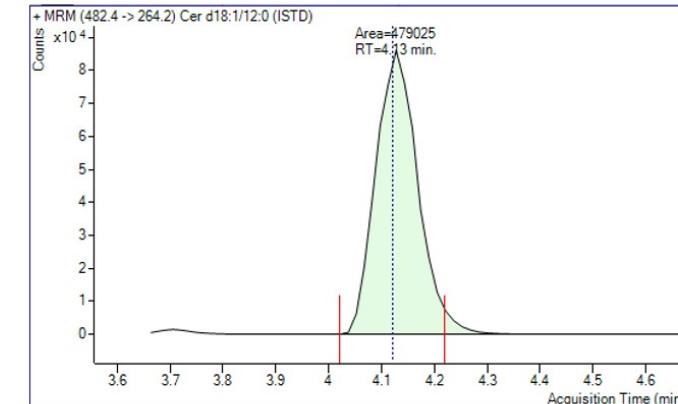


Liquid Chromatography/Mass Spectrometry

Sample_Name	Cer d18:1/12:0 (ISTD)
Sample 01	479025
Sample 02	570275
Sample 03	374854
Sample 04	319491
Sample 05	231691

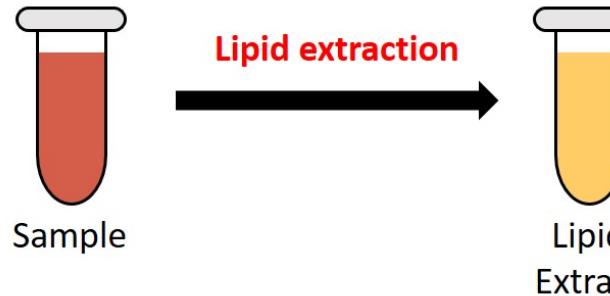
Peak Area Data

Peak integration



# Source of "Unwanted" Variation

- Lipid Extraction
  - Different pipettes used to do extraction.
- Lipid Measurement
  - Contaminant ions



Transition_Name	Precursor_Ion	Product_Ion
Cer d18:1/12:0 (ISTD)	482.4	264.4

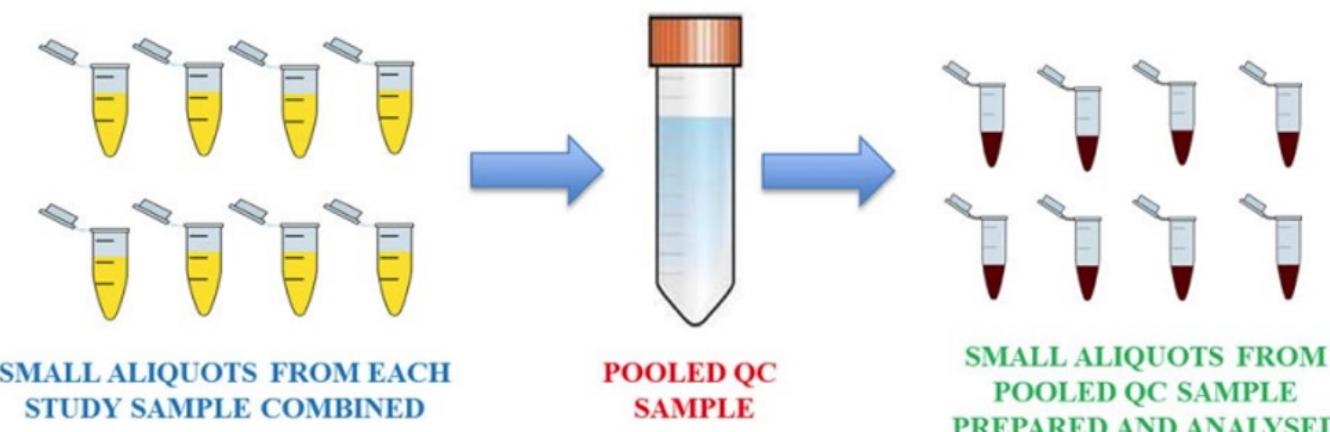


Liquid Chromatography/Mass Spectrometry

# Quality Control (QC) Samples

Quality control samples helps to check the severity of unwanted variation.

One example is the Batch Quality Control (BQC) to measure variation during lipid extraction and measurement.



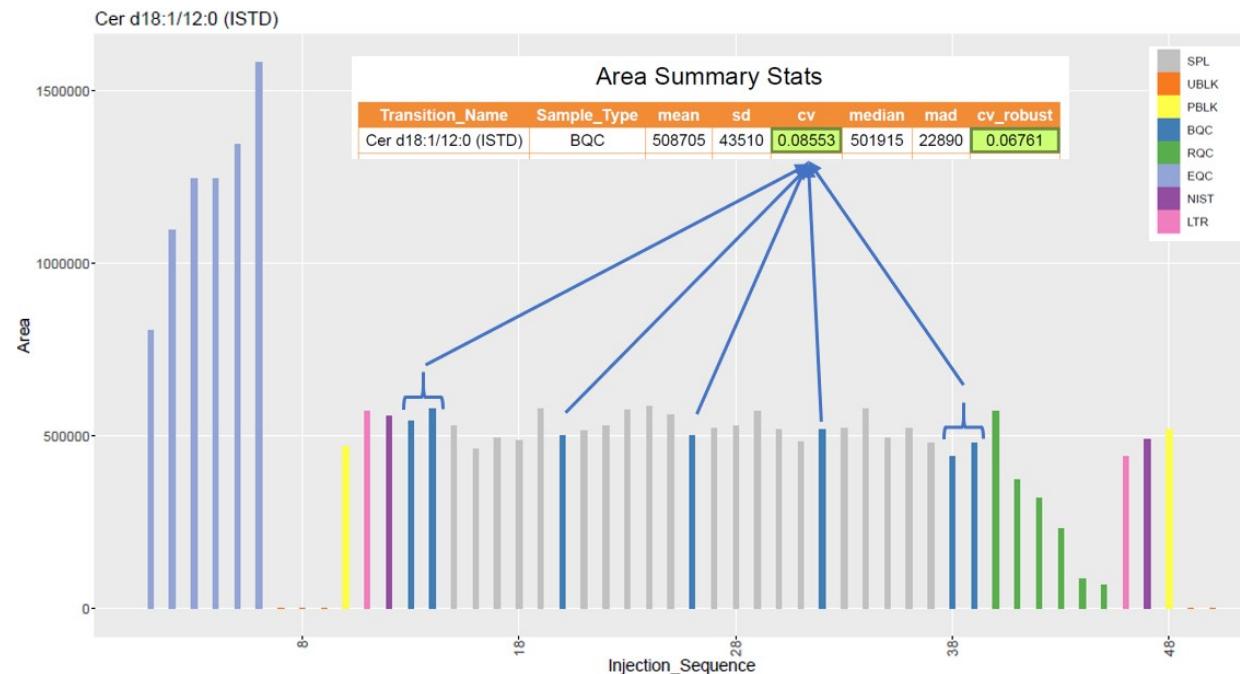
Injection_Sequence	QC_Sample_Type	Sample_Name
...	...	...
...	...	...
13	BQC	BQC 01
14	BQC	BQC 02
15	SPL	Sample 1
16	SPL	Sample 2
17	SPL	Sample 3
18	SPL	Sample 4
19	SPL	Sample 5
20	BQC	BQC 03
21	SPL	Sample 6
22	SPL	Sample 7
23	SPL	Sample 8
24	SPL	Sample 9
25	SPL	Sample 10
26	BQC	BQC 04
...	...	...
...	...	...

# Quality Control Plot

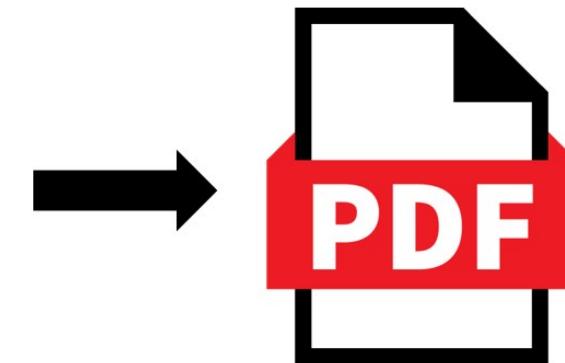
An injection sequence bar chart with some statistical summary is created for each transition.

Keep transitions whose BQC's coefficient of variation (CV) is low.

Report results as a pdf file of injection sequence bar charts. (One transition per page)



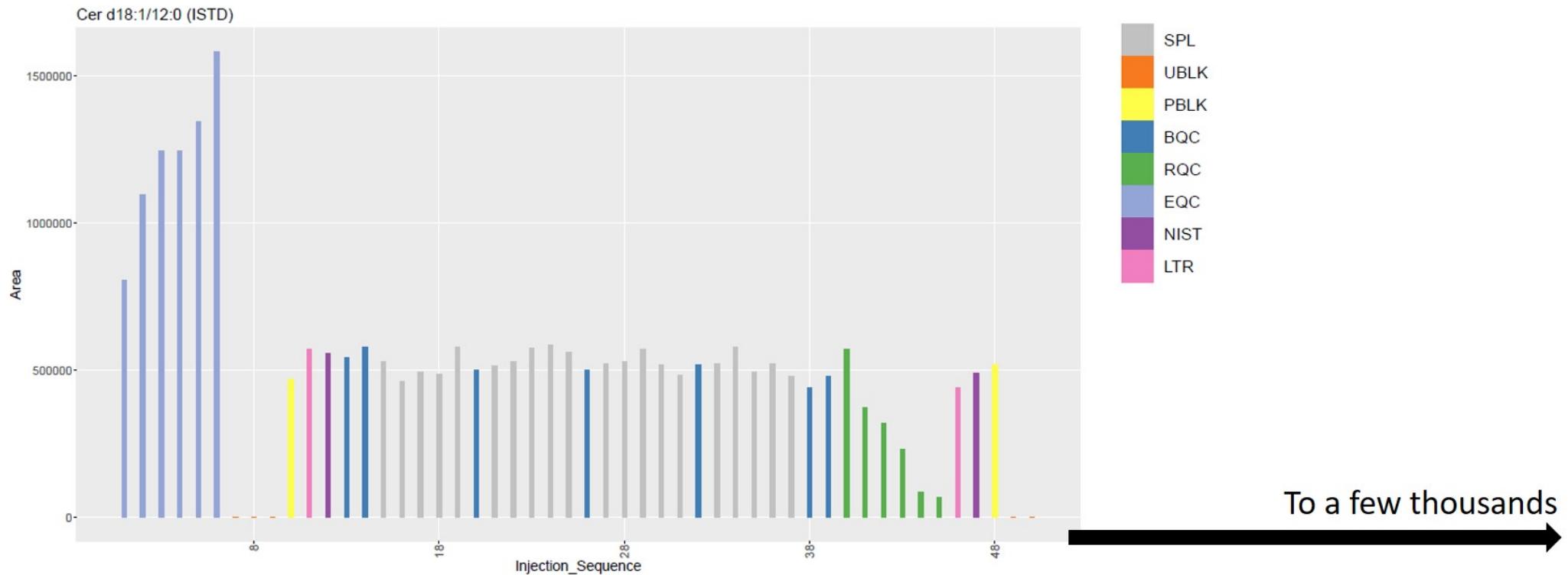
Injection Sequence Plot for Cer d18:1/12:0 (ISTD)



# Motivation for using `plotly` and `trelliscopejs`

Number of samples are getting larger (increase to few thousands).

Static bar charts and scatter plots will not work.

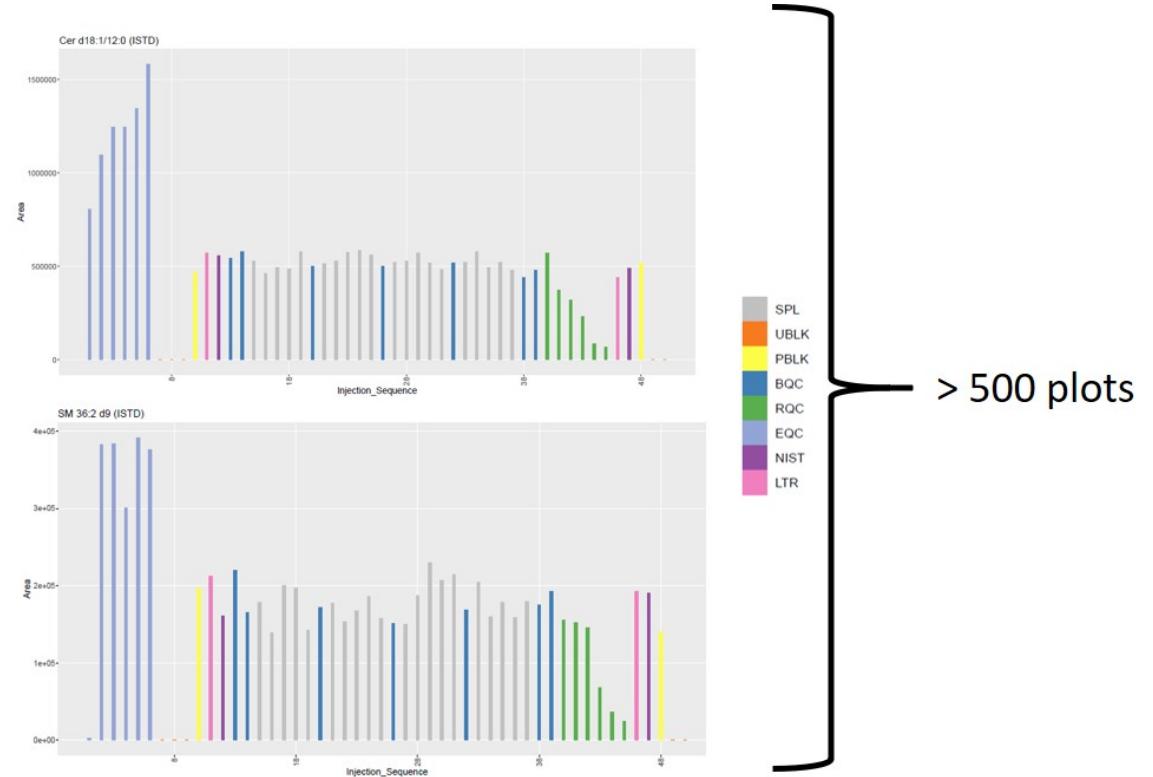


# Motivation for using `plotly` and `trelliscopejs`

Number of transitions have increased to **over 500**. This give a pdf file of **over 500 pages** full of plots.

Transition_Name	Precursor_Ion	Product_Ion
...	...	...
...	...	...
Cer d18:1/12:0 (ISTD)	482.4	264.4
LPC 18:1 d7 (ISTD)	529.7	184.1
SM 36:2 d9 (ISTD)	739.2	184.1
...	...	...
...	...	...

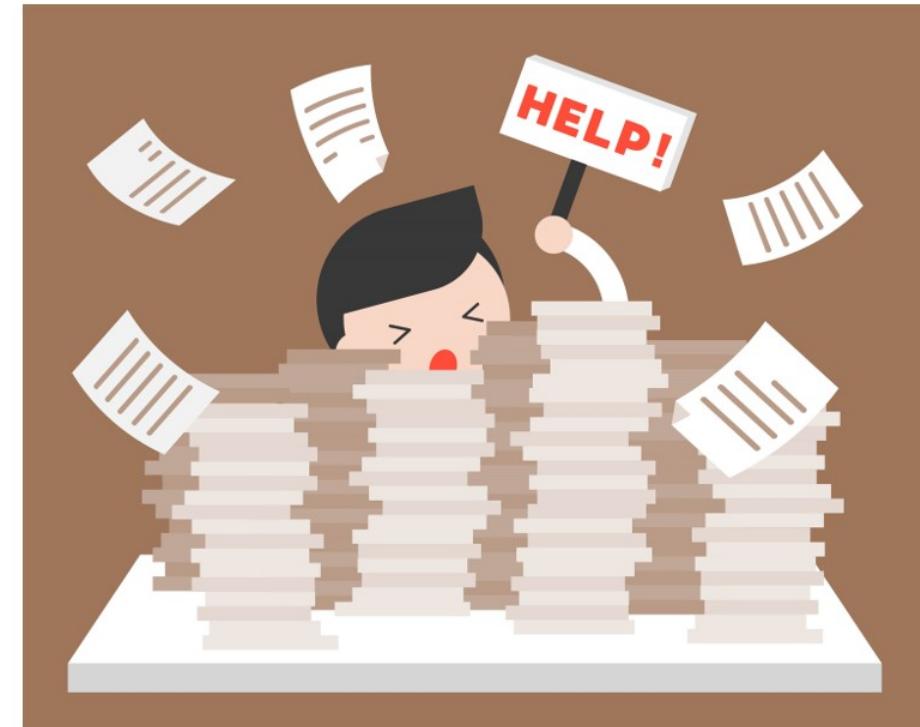
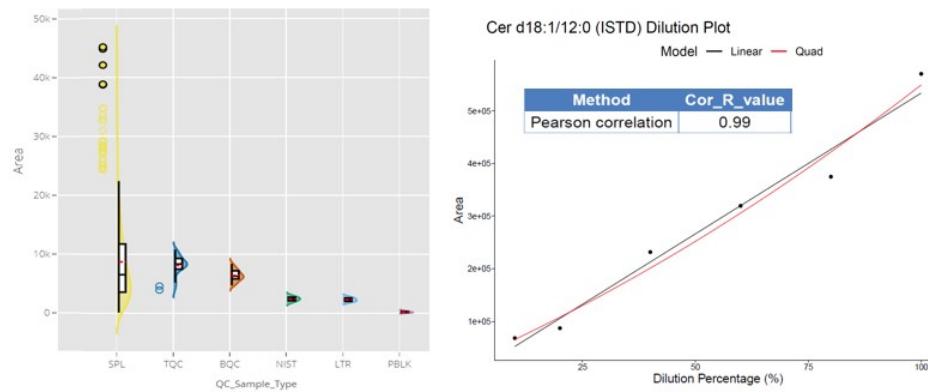
> 500 transition list



# Motivation for using `plotly` and `trelliscopejs`

Different QC sample types give rise to different types of plots, resulting in the creation of **multiple pdf files of over 500 pages**.

QC_Sample_Type	Name	Description
SPL	Study Sample	"Unknown" sample
BQC	Batch QC	Pooled samples to check variability during lipid extraction and measurement from instrument
TQC	Technical QC	Pooled lipid extracts to check variability during lipid measurement from instrument
RQC	Response QC	Dilution series to check for linear response/saturation (e.g. TQC)
LTR	Long Term Reference Plasma with ISTD	Long Term Reference Plasma with ISTD
NIST	NIST SRM1950 Reference Plasma with ISTD	NIST SRM1950 Reference Plasma with ISTD
PBLK	Processed Blank	Processed or Extracted solvent with ISTD



# Motivation for using `plotly` and `trelliscopejs`

Using `plotly` to create interactive plots is moving in the right direction.

However, distribution of such results to collaborators/managers remains a challenge.

Interactive plots cannot be stored in pdf files.

`Shiny` was considered but

- Lack expertises to maintain a secure web server to run `Shiny` applications.
- Cannot expect collaborators/managers to install/run R packages and code to rebuild the `Shiny` application just to view the results.



`plotly` logo from [Wikimedia](#)

`trelliscopejs` hex logo from the R package's [GitHub page](#)

## Select a Display to Open

no thumbnail

no thumbnail

**Dilution\_Plot**

750 panels, 2022-08-07 15:45

**Injection\_Sequence\_Plot**

750 panels, 2022-08-07 15:48

**CLOSE**

# Quarto Example

Thanks to open science, I am able to create a walk through example using Quarto  .

Article | Open Access | Published: 10 January 2022

## Lipidomic profiling of human serum enables detection of pancreatic cancer

Denise Wolrab, Robert Jirásko, ... Michal Holčapek  + Show authors

*Nature Communications* 13, Article number: 124 (2022) | [Cite this article](#)

9421 Accesses | 5 Citations | 41 Altmetric | [Metrics](#)

### Data availability

All data necessary to support the conclusions are available in the manuscript or supplementary information. Source data are provided with this paper. Raw data, instructions for software handling, and the software are deposited at figshare.com:  
<https://figshare.com/s/cc087785ca362af7118e>—(UHPSFC/MS; Phase I and Phase II).  
<https://figshare.com/s/e336bdf3a52f04c2def>—(Shotgun-MS (LR and HR); Phase II).  
<https://figshare.com/s/cb071be45cd91a7c90e2>—(MALDI-MS; Phase I).  
<https://figshare.com/s/1fd10f273b049b93fa24>—(RP-UHPLC/MS; Phase II). [Source data](#) are provided with this paper.

### Supplementary information

[Supplementary Information](#)

[Peer Review File](#)

[Description of Additional Supplementary Files](#)

[Supplementary Data 1-20](#)

[Reporting Summary](#)

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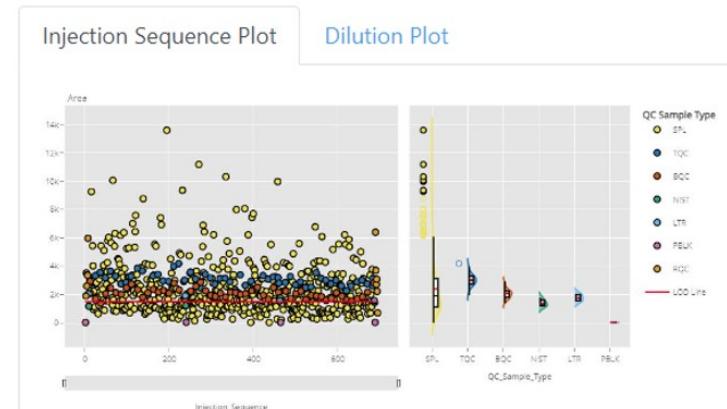
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## Quarto Report Example With Plotly and Trelliscopejs

Written by Jeremy Selva    

## Introduction

Here is a report showing how to create injection sequence plot and dilution plot using [plotly](#) for each Multiple Reaction Monitoring (MRM) transition in Mass Spectrometry.



# Column Of Plots

Use `dplyr::mutate` and `trelliscopejs::pmap_plot` to save `plotly` plots as a new column.

```
dilution_plot_table <- summary_data |>  
dplyr::mutate(  
  dilution_panel = trelliscopejs::pmap_plot(  
    list(dilution_data = .data[["dilution_data"]]),  
    plot_dil_curve_plotly,  
    dilution_title = "",  
    dilution_pal = dilution_pal,  
    sample_name_var = "Sample_Name",  
    dil_batch_var = "Dilution_Batch_Name",  
    conc_var = "Relative_Sample_Amount_[%]",  
    conc_var_units = "%",  
    conc_var_interval = 25,  
    signal_var = "Area",  
    x_axis_title = "Relative Sample Amount",  
    y_axis_title = "Area",  
    y_axis_rangemode = "normal",  
    lin_reg_name = "lin reg",  
    quad_reg_name = "quad reg",  
    show_legend = TRUE,  
    show_y_axis_title = TRUE,  
    annotation_var = c("Dilution_Batch_Name",  
                      "Injection_Sequence",  
                      "Acquisition_Time_Stamp",  
                      "Vial_Position")  
) |>  
dplyr::select(-c("dilution_data", "sample_data"))
```

Map over multiple inputs simultaneously and return a vector of plots

Source: R/tidy.R  
  
Map over multiple inputs simultaneously and return a vector of plots  
  
map2\_plot(.x, .y, .f, ...)  
pmap\_plot(.l, .f, ...)

R Trelliscopejs\_In\_Quarto\_Example - main - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

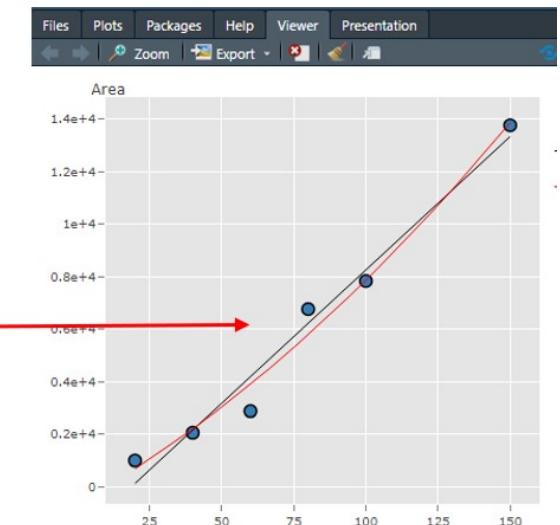
dilution\_plot\_table

Transition_Name	dilution_panel	Lipid_Name
1 AcylCarnitine 10:0	list(x = list(visdat = list(`77644c483021` = funct [...]	CAR 10:0
2 AcylCarnitine 10:1	list(x = list(visdat = list(`776423dd5818` = funct [...]	CAR 10:1
3 AcylCarnitine 12:0	list(x = list(visdat = list(`776449445435` = funct [...]	CAR 12:0
4 AcylCarnitine 12:1	list(x = list(visdat = list(`77647ac9148a` = funct [...]	CAR 12:1
5 AcylCarnitine 13:0	list(x = list(visdat = list(`77642fcbb0cb` = funct [...]	CAR 13:0
6 AcylCarnitine 14:0	list(x = list(visdat = list(`7764393e52d3` = funct [...]	CAR 14:0

Showing 1 to 6 of 750 entries, 44 total columns

Console Background Jobs

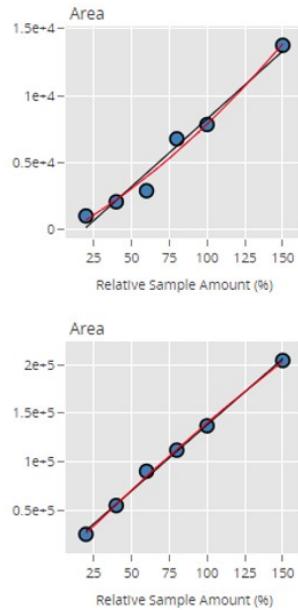
R 4.2.1 · D:Trelliscopejs\_In\_Quarto\_Example/ ↵  
> dilution\_plot\_table\$dilution\_panel[[1]]



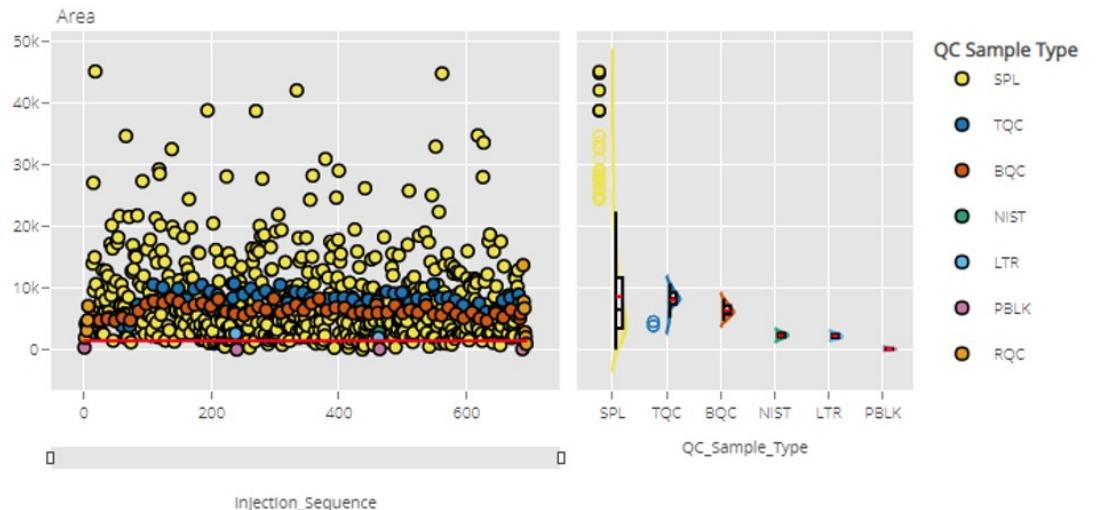
# Patching `plotly` Plots

Use `manipulateWidget::combineWidgets` and `plotly::subplot` to patch different `plotly` plots.

```
manipulateWidget::combineWidgets(ncol = 2,  
                                nrow = 2,  
                                dilution_plot_table$dilution_panel[[1]],  
                                dilution_plot_table$dilution_panel[[2]],  
                                dilution_plot_table$dilution_panel[[3]],  
                                dilution_plot_table$dilution_panel[[4]])
```

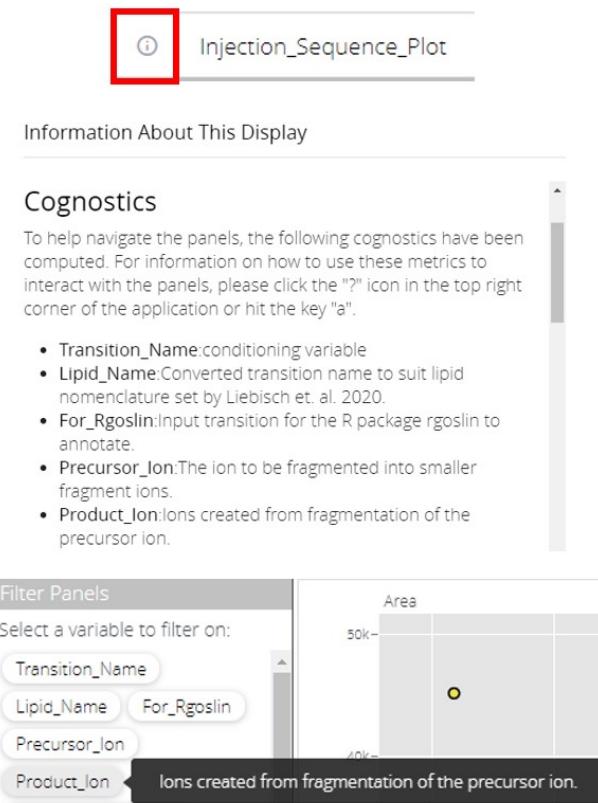


```
combined_plots <- plotly::subplot(scatterplot_panel,  
                                    raincloud_panel,  
                                    widths = c(0.6, 0.4),  
                                    margin = 0.01,  
                                    shareX = TRUE,  
                                    shareY = TRUE  
)
```



# trelliscopejs cognostics

Providing metadata information as `trelliscopejs` cognostics can help to improve the user experience.  
Refer to the Quarto   example on how to do it.



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- References

## Cognostics

To output these interactive plots as a trellis plot in html, we need to convert our current tibble and `dilution_plot_table` and `injection_sequence_table` into a cognostics dataframe.

The cognostics dataframe consist of three components

1. A group of columns known as conditioning variables. They will form the unique id of the trellis plot. As such, each row of these columns must be unique. In our example, the column used is `Transition_Name`.
2. One column that holds the images to display each plot in the trellis. This column is known as the panel variable. We just created this column using `trelliscopejs::pmap_plot` earlier.
3. The other columns will be grouped as general cognostics columns.

## Cognostics Conversion Functions

The relevant functions to convert all columns, except the panel variable, to cognostics objects are as follows.

### ► Code

## Cognostics Setup

The function `trelliscopejs::cog` is used to convert a column into cognostic object. The following meta information must be provided in order for the conversion to be successful.

# Results Distribution

To export a `trelliscopejs` object.

Step 1. Set working directory



Step 2. Call script in console

```
trelliscope_name <- "Dilution Plot"

dilution_trellis |>
  trelliscopejs::trelliscope(
    name = trelliscope_name,
    panel_col = "dilution_panel",
    path = "Dilution_Plot_Folder",
    state = list(sort = list(trelliscope
      nrow = 2,
      ncol = 2,
      height = 520,
      width = 1100,
      self_contained = FALSE,
      thumb = FALSE,
      auto_cog = FALSE
    )
  )
```

Step 3. Compress Folder

Dilution\_Plot\_Folder.zip

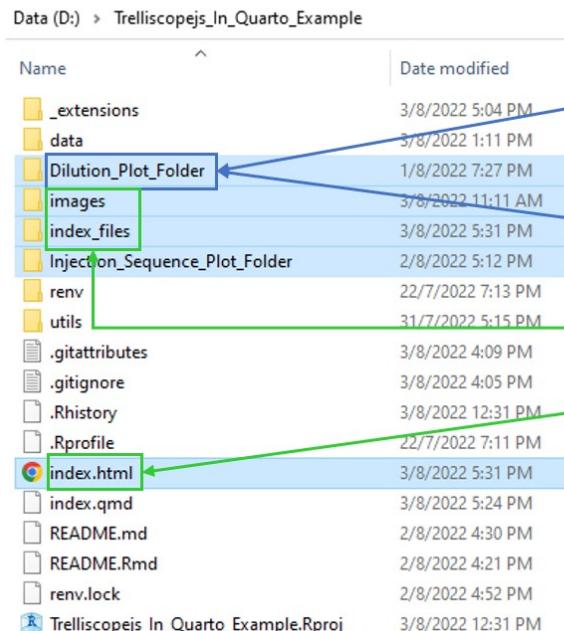
3/8/2022 5:48 PM

# Results Distribution

To export a Quarto document with `trelliscopejs` object.

Step 1. Set working directory

```
Console Background Jobs x
R 4.2.1 · D:/Trelliscopejs_In_Quarto_Example/ ↵
> getwd()
[1] "D:/Trelliscopejs_In_Quarto_Example"
```



Step 2. Render Quarto script



Source Code

```
tidyverse::quiet: TRUE
format:
html:
theme:
light: cerulean
dark: cyborg
toc: true
toc-depth: 3
toc-location: left
number-sections: false
code-fold: show
code-overflow: scroll
code-line-numbers: true
code-copy: hover
code-tools: true
self-contained: false
smooth-scroll: true
```

Step 3. Compress Highlighted Files/Folders

`Quarto_Example.zip` 3/8/2022 6:59 PM

# Results Distribution

Exported examples are found under the [Releases](#) section in the below GitHub page.

The screenshot shows a GitHub repository page for 'JauntyJJS / Trelliscopejs\_In\_Quarto\_Example'. The repository has 1 branch and 2 tags. The 'Code' tab is selected. On the right, there is an 'About' section describing the source code for a Quarto report using Plotly and Trelliscopejs. Below it is a 'Releases' section with 2 releases. The latest release is 'Version 1.0.1' (Latest), which was posted 4 minutes ago. This release contains 8 assets:

Asset	Size	Last Updated
data.zip	4.46 MB	2 minutes ago
Dilution_Plot_Folder.zip	3.33 MB	3 minutes ago
docs.zip	52.4 MB	3 minutes ago
index_files.zip	57.5 MB	3 minutes ago
Injection_Sequence_Plot_Folder.zip	50.7 MB	3 minutes ago
Quarto_Example.zip	57.5 MB	3 minutes ago
Source code (zip)		5 minutes ago
Source code (tar.gz)		5 minutes ago

Red boxes highlight the 'Releases' section, the 'Version 1.0.1' release, and the assets within it. Red arrows point from the highlighted sections on the left to their corresponding counterparts on the right.

# Enjoy The Conference

## Summary

- Quality control samples are useful to check for unwanted variation in a targeted lipidomics workflow.
- `plotly` and `trelliscopejs` can help to explore many interactive plots in an effective way.
- Hope that the Quarto  example and advice provided are useful.



Images by [Amonrat Rungreangfangsai](#)

Xaringan Slide Template by [Sharla Gelfand](#) 

<https://jauntyjjs.github.io/RMedicine2022>  PDF