

Viewing Multiple Interactive Plots Using plotly and trelliscopejs



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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

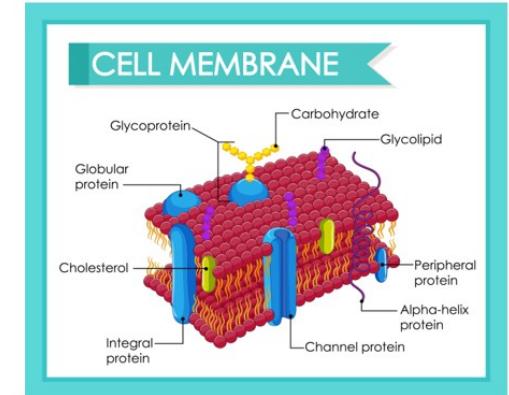
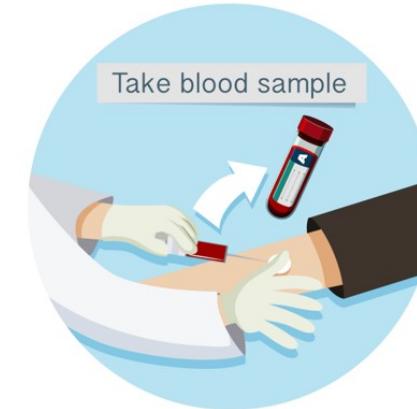
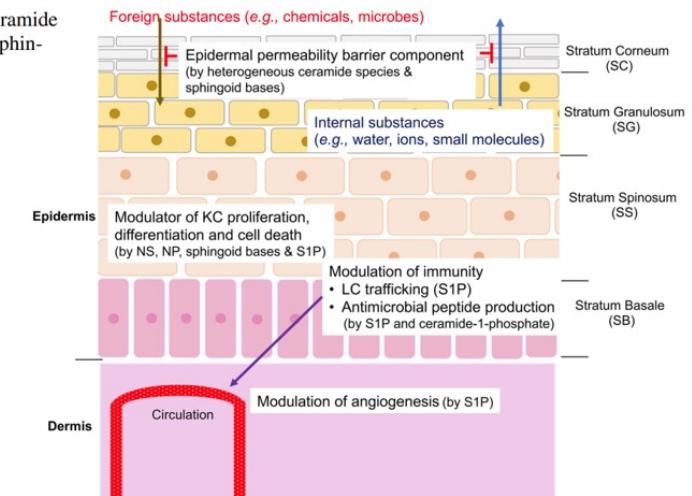


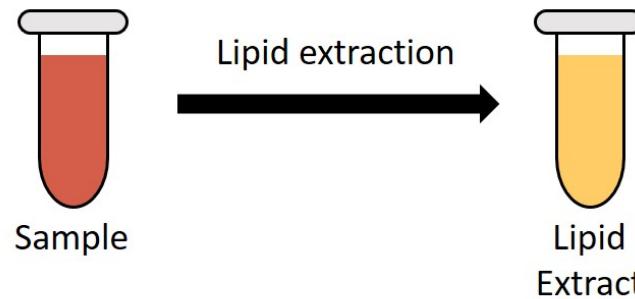
Fig. 7 Diverse roles of ceramide (*Cer*) and its metabolite sphingoid base in skin



Blood sample and cell membrane images 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

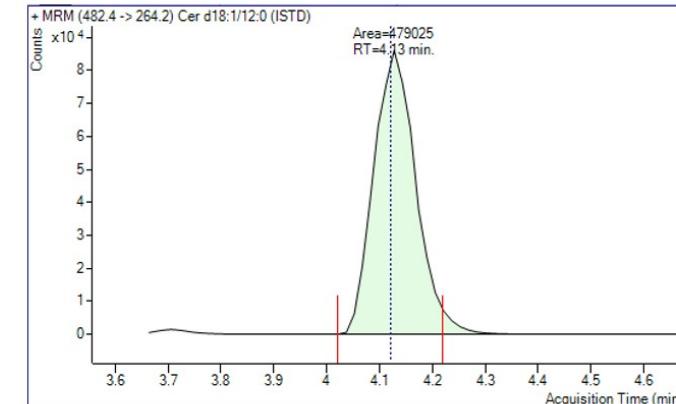


Liquid Chromatography/Mass Spectrometry

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

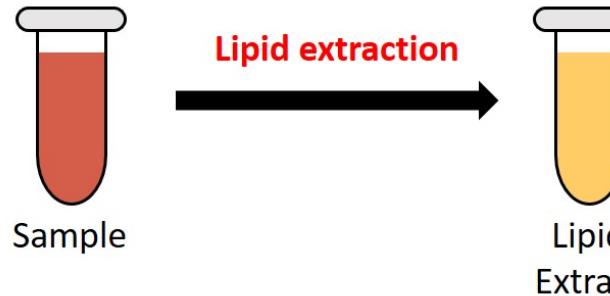
Peak Area Data

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

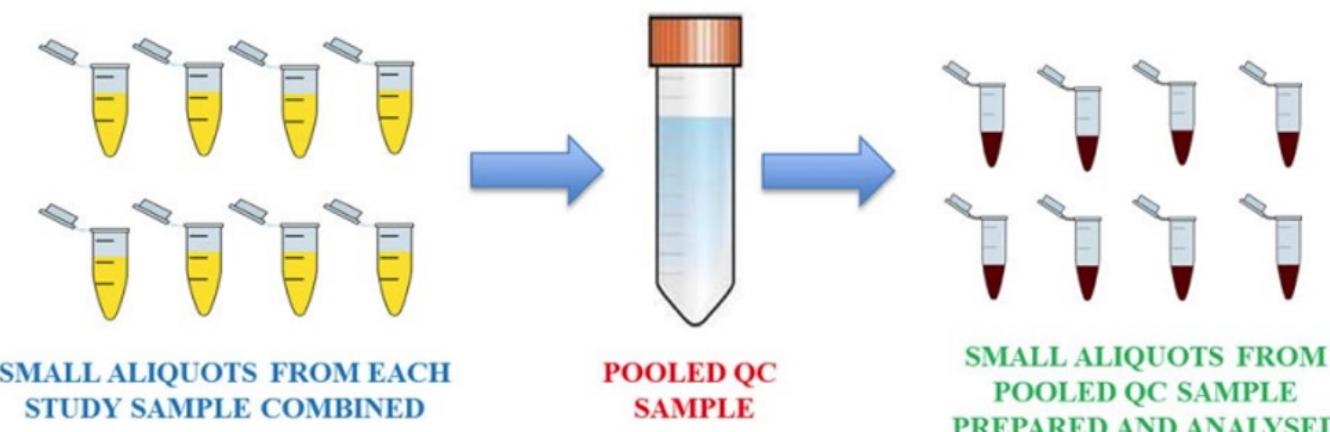


Liquid Chromatography/Mass Spectrometry

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.



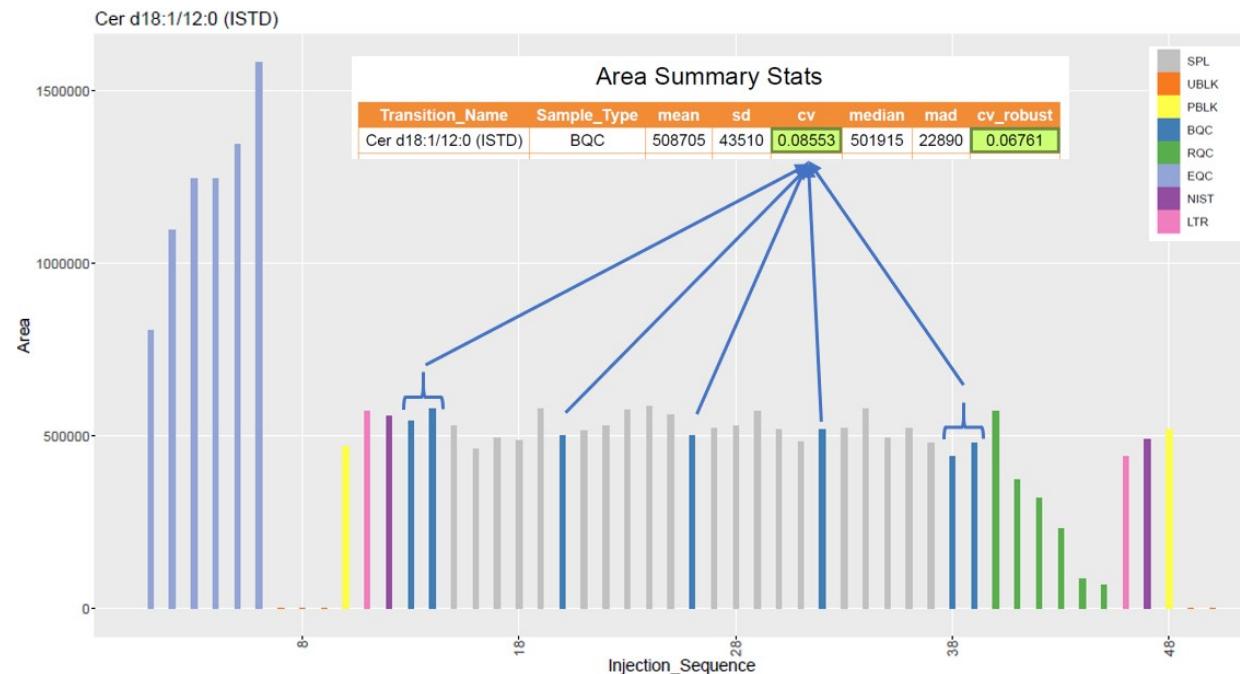
Injection_Sequence	QC_Sample_Type	Sample_Name
...
...
13	BQC	BQC 01
14	BQC	BQC 02
15	SPL	Sample 1
16	SPL	Sample 2
17	SPL	Sample 3
18	SPL	Sample 4
19	SPL	Sample 5
20	BQC	BQC 03
21	SPL	Sample 6
22	SPL	Sample 7
23	SPL	Sample 8
24	SPL	Sample 9
25	SPL	Sample 10
26	BQC	BQC 04
...
...

Quality Control Plot

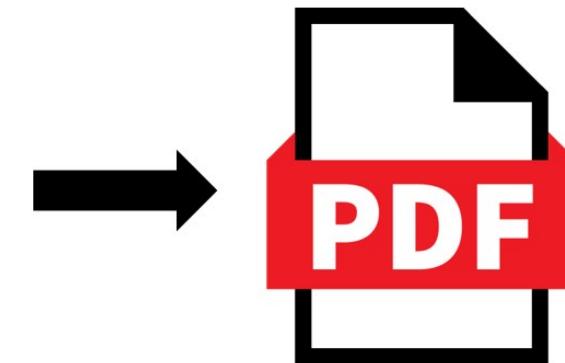
An injection sequence bar chart with some statistical summary is created for each transition.

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)



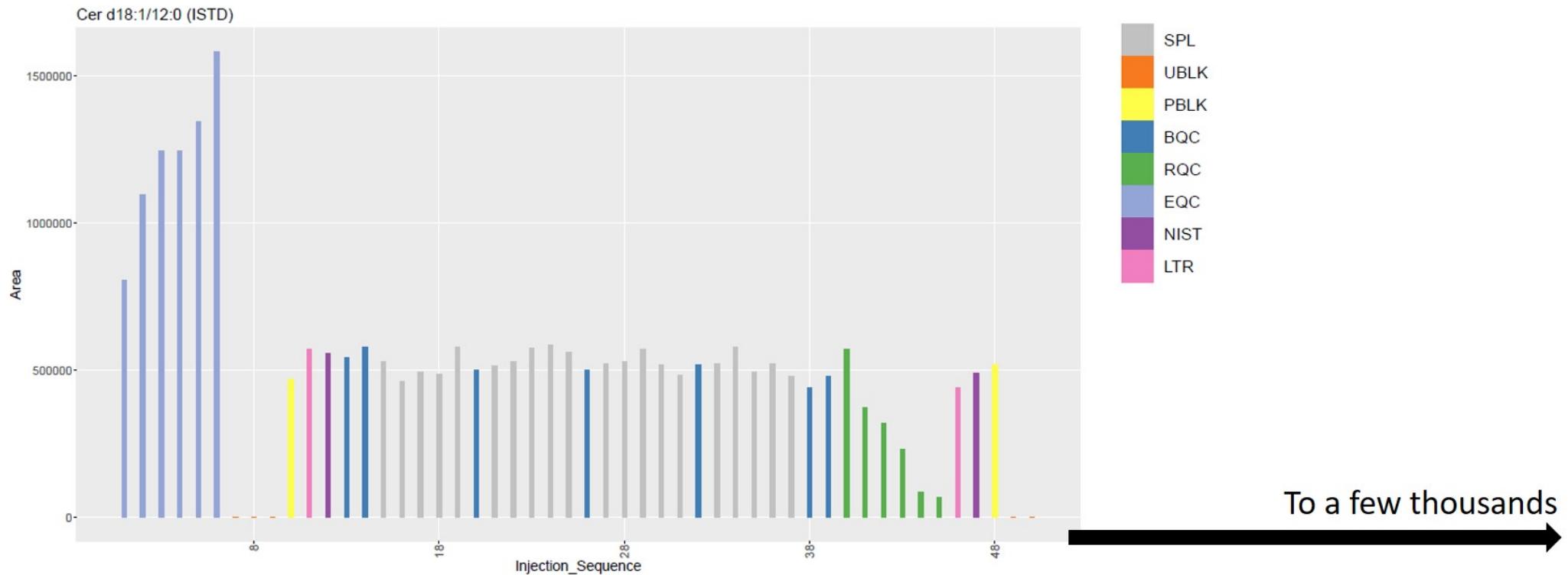
Injection Sequence Plot for Cer d18:1/12:0 (ISTD)



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.

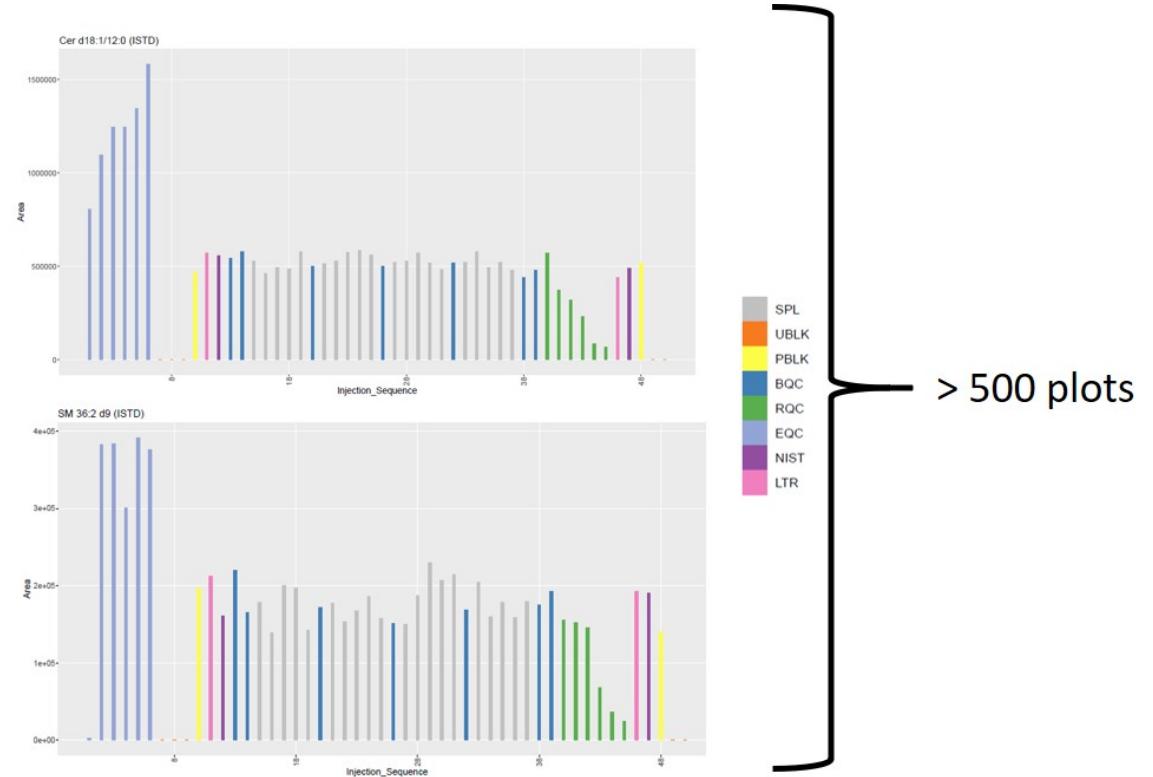


Motivation for using `plotly` and `trelliscopejs`

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
...
...

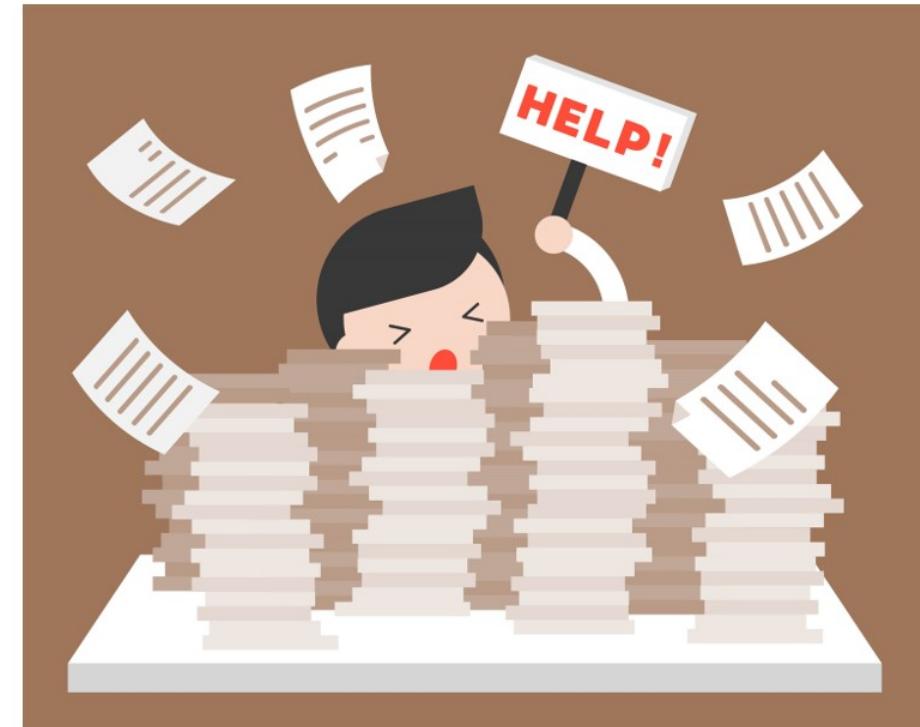
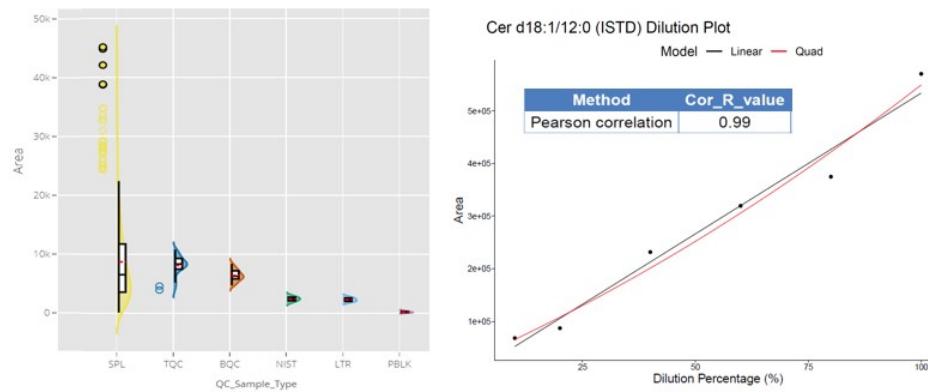
> 500 transition list



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 remain 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.



Data (D:) > Trelliscopejs_In_Quarto_Example > Dilution_Plot_Folder			
Name	Date modified	Type	Size
appfiles	1/8/2022 7:27 PM	File folder	
lib	2/8/2022 5:01 PM	File folder	
index.html	2/8/2022 5:01 PM	Chrome HTML Do...	1 KB



Dilution_Plot_Folder.zip 3/8/2022 5:48 PM Compressed (zipp...) 3,405 KB

`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, 2022-08-02 17:18

Injection_Sequence_Plot

750 panels, 2022-08-02 17:28

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/e336bd3a52f04c2de1f>—(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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Quarto Report Example With Plotly and Trelliscopejs

AUTHOR

Jeremy Selva    

[Code](#) ▾

Show All Code

Hide All Code

[View Source](#)

Introduction

Here is a report showing how to create injection sequence plot and dilution plot using [plotly](#) for each transition.



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

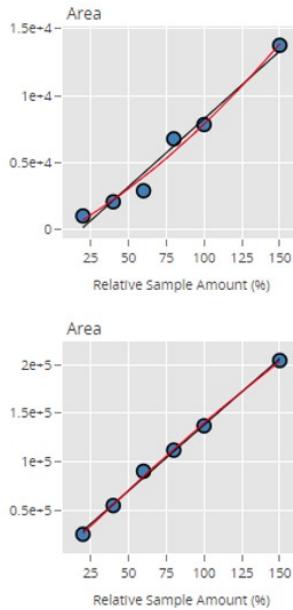
R 4.2.1 · D:Trelliscopejs_In_Quarto_Example/ ↗
> dilution_plot_table\$dilution_panel[[1]]



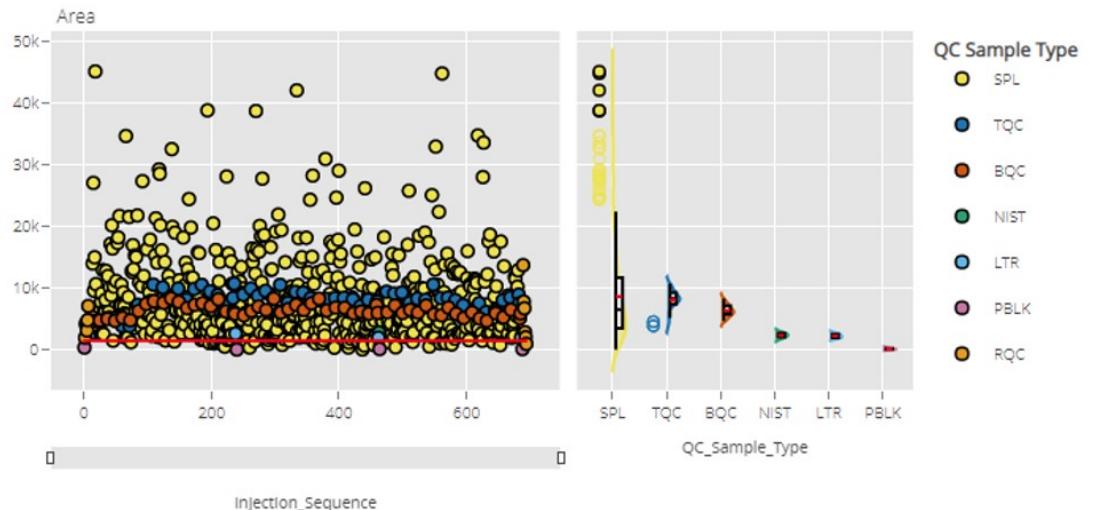
Patching `plotly` Plots

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.

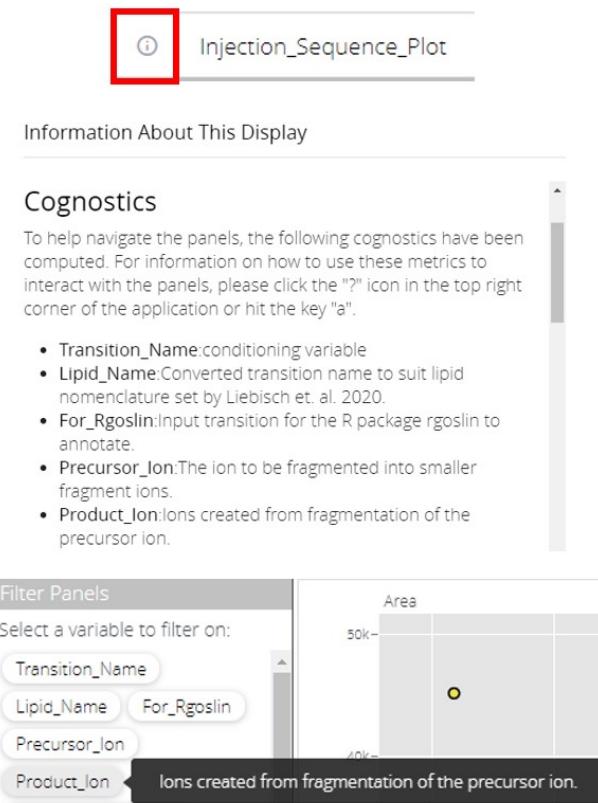


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- Cognostics Conversion Functions
- Cognostics Setup
- Cognostics Creation
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- References

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

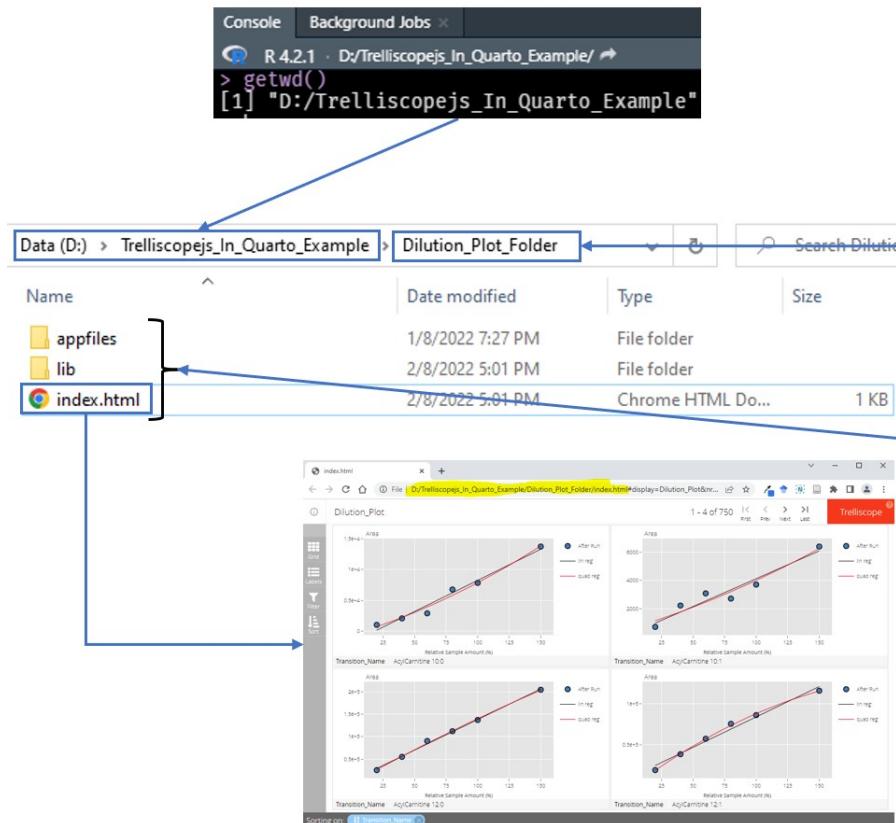
Cognostics Setup

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

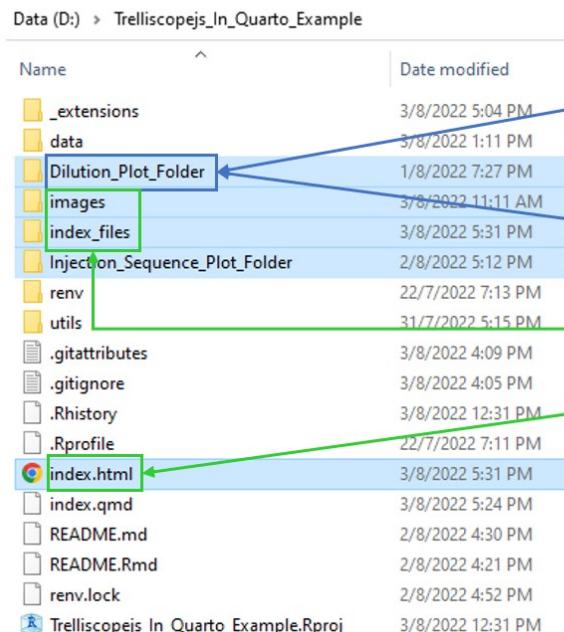
Dilution_Plot_Folder.zip 3/8/2022 5:48 PM

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



```
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
    )))

```

```
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



Results Distribution

Exported examples are found in the below GitHub page.

The screenshot shows a GitHub repository page for 'JauntyJJS / Trelliscopejs_In_Quarto_Example'. The repository is public and has 1 branch and 0 tags. The main commit is 'JauntyJJS add icons' with 19 commits. Below the commit list, three files are listed and highlighted with a red border: 'Dilution_Plot_Folder.zip', 'Injection_Sequence_Plot_Folder.zip', and 'Quarto_Example.zip'. The right sidebar provides an 'About' summary, links to 'Readme', and sections for 'Releases' and 'Packages'.

JauntyJJS / Trelliscopejs_In_Quarto_Example Public

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main 1 branch 0 tags Go to file Add file Code About

JauntyJJS add icons 93f28a2 1 hour ago 19 commits

Dilution_Plot_Folder add icons 1 hour ago

Injection_Sequence_Plot_Folder add icons 1 hour ago

_extensions add icons 1 hour ago

data Initial commit yesterday

images Add Dark Mode 6 hours ago

index_files add icons 1 hour ago

utils Add utils Folder yesterday

.gitattributes Use Git LFS to manage large zip files 3 hours ago

.gitignore Remove some qmd files 3 hours ago

Dilution_Plot_Folder.zip Use Git LFS to manage large zip files 3 hours ago

Injection_Sequence_Plot_Folder.zip Use Git LFS to manage large zip files 3 hours ago

Quarto_Example.zip Use Git LFS to manage large zip files 3 hours ago

About

Source code for a Quarto report using Plotly and Trelliscopejs

jauntyjjs.github.io/trelliscopejs_in_quarto...

Readme

0 stars

1 watching

0 forks

Releases

No releases published Create a new release

Packages

No packages published Publish your first package

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