

Building Shiny Apps

Challenges and Responsibilities

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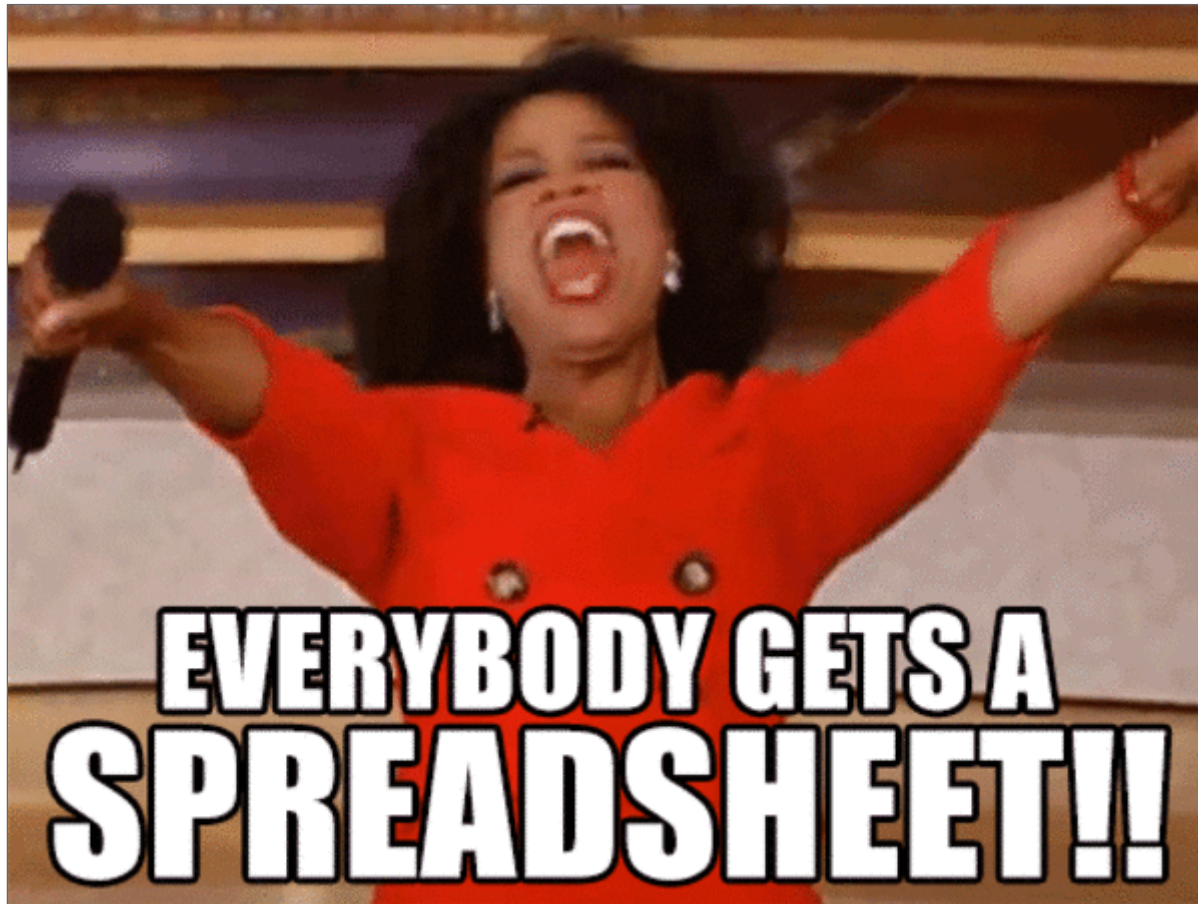
Saturday, January 27, 2018, Data/R Day Texas

Slides available at **<http://bit.ly/shiny-ddtx>**

Why Shiny?

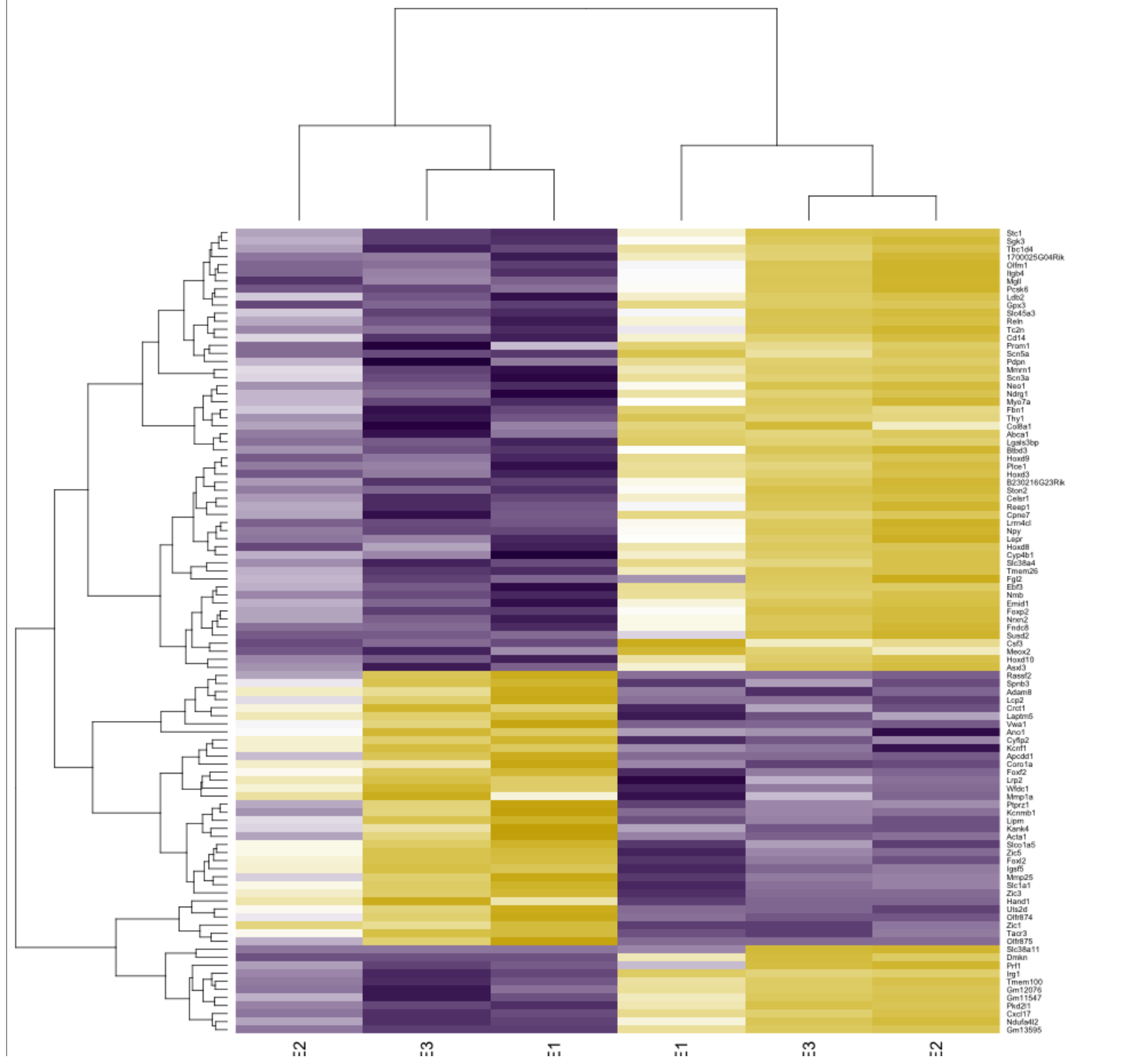
Motivation

Spreadsheets =(



Motivation

“Can you make me this plot? Ok now this plot? Wait one more plot...”



BE

BE

BE

HE

HE

HE

Queried Genes with FDR ≤ 0.01 (top 100 genes)
from LRT test for difference across groups: BE vs. HE

Plot Monkey?

Enter Shiny



Shiny

.com

My history

- Started with **Tableau**
 - Tableau + R + Bioconductor = :-| (in 2013)
 - (Now you can **host a shiny app in Tableau??**)
- Realization: **Shiny** can do this!
- Made one site with **one data set**
- Created general site for **input data set**

Motivation For All

Distribute your hard work!

Collaborator:

“How can I share my data?”

START: Shiny Transcriptome Analysis Resource Tool - Hypertension

Getting StartedDataGroup PlotsAnalysis PlotsGene Expression BoxplotsHeatmapsInstructionsNewsTerms & Conditions

Getting Started with START

[Features](#)
[More Help](#)

START App for Hypertension

This is an instance of the **START app** containing hypertension data described in the following manuscript by Nelson et al:

Nelson JW, Ferdaus MZ, McCormick JA, Minnier J, Kaul S, Ellison DH, Barnes AP. (2017) Endothelial Transcriptomics Reveals Activation of Fibrosis-Related Pathways in Hypertension. *Physiological genomics*. *physiolgenomics-00111*. pubmed PMID 29212850; doi 10.1152/physiolgenomics.00111.2017

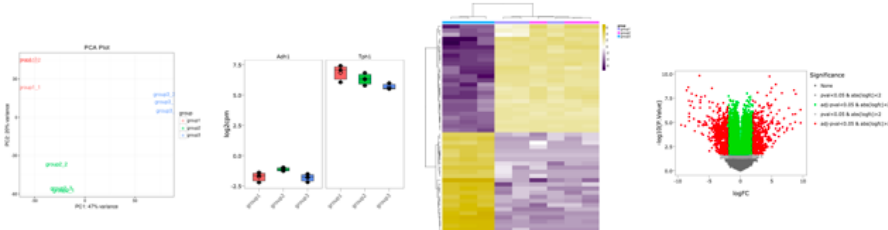
This app is hosted on Shinyapps.io here: https://kcvi.shinyapps.io/START_HT/

Information about the START App

The original version of START allows users to upload their own RNA-seq or transcriptomic data and visualize it interactively. You can find that app here: <https://kcvi.shinyapps.io/START/>

The START app allows users to visualize RNA-seq data starting with count data.

Features



[https://kcvi.shinyapps.io/START HT/](https://kcvi.shinyapps.io/START_HT/)

Developer/Statistician/Data Scientist:
“How can I get people to use my new method/package?”

The screenshot shows a web browser window with the address bar displaying 'qvalue.princeton.edu'. The page title is 'q-value estimation for FDR control'. The interface is divided into two main sections: a left sidebar for input and a right main panel for instructions and output.

Left Sidebar:

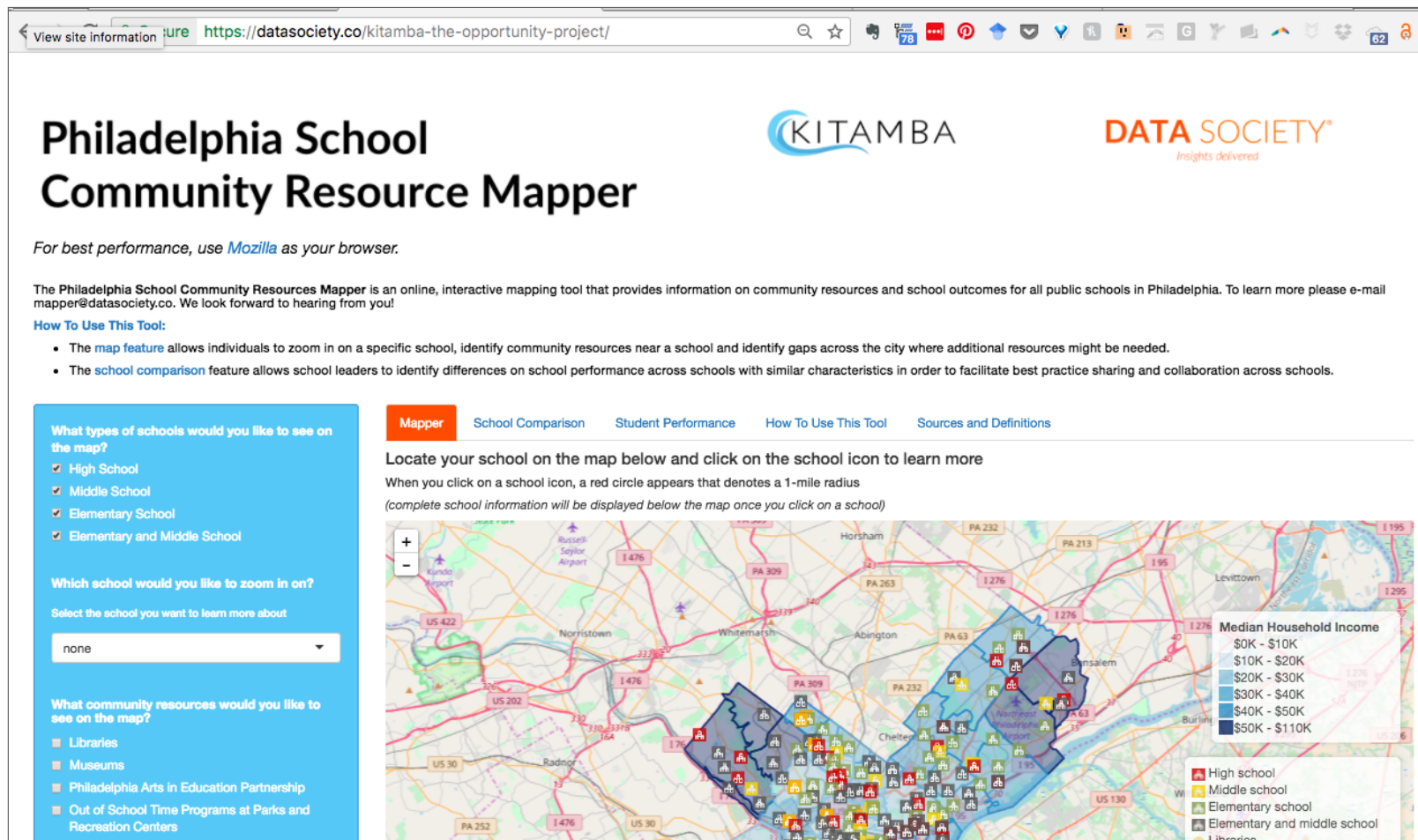
- Choose file containing p-values: A button labeled 'Choose File' and the text 'No file chosen'.
- Header: A checked checkbox.
- Separator: Radio buttons for 'Comma' (selected), 'Semicolon', 'Tab', 'Space', and 'End-of-line'.
- π_0 estimate inputs: A dropdown menu showing 'smoother'.
- λ range: A horizontal slider with markers at 0 and 0.95.
- λ step size: A text input field.

Right Main Panel:

- Navigation tabs: 'About', 'Output' (selected), and 'Help'.
- Using the App**: A section with a paragraph explaining the Shiny implementation and a list of four steps for using the application.
 1. Write your list of p-values to a text file that is tab, space, semicolon, comma delimited or has one p-value per line.
 2. Start by uploading your file using the 'Choose File' button located on the side panel.
 3. It is then possible to modify the settings that are used to estimate q-values with the various options on the side panel. See the 'Help' tab in the application or see the [user manual](#) for explanations of these options.
 4. To view useful visualizations of the results refer to the 'Figures' tab for plots produced by qvalue package. When you are finished with your analysis, you may click the 'Download Output' button to save your results.
- References**: A section with a single reference: 'Estimation Methods from Storey, J.D. (2002) A direct approach to false discovery rates, Journal of the Royal Statistical Society B'.

<http://qvalue.princeton.edu/>

Developer/Statistician/Data Scientist: Look at this analysis I did!



<https://gallery.shinyapps.io/TSupplyDemand/>

Everyone: Teach Some things! (learnr)

Continuous Data

Ted Laderas and Jessica Minnier
11/06/2017

Learning Objectives for this Session

- EDA with continuous variables
- How do we assess associations between two continuous variables?
- What is a factor that may be associated with BMI?
- Missingness and suspicious data elements
- T Test
- Explore other factors
- Advanced Topic: Linear Models - multiple predictors/associations

EDA with continuous variables

We saw bar plots and proportional plots used to visualize binary and categorical variables in the previous section. What are some good ways of visualizing continuous (quantitative) data?

Let's use the NHANES (National Health and Nutrition Examination Survey) data set to visualize the variable **BMI** as a continuous variable.

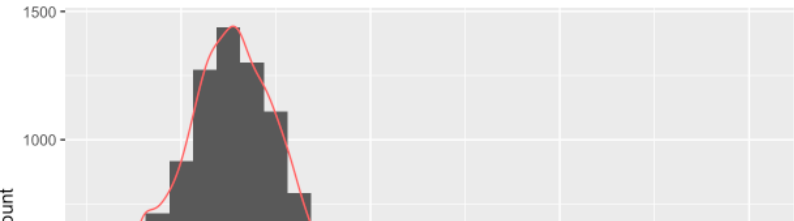
(Note: info about the NHANES data in the **NHANES** R package can be found [here](#) with the disclaimer that NHANES are survey data so to do proper analyses we should use sampling weights. For illustration of more straightforward analyses we will ignore this detail.)

✓ Histogram and density plots

A common visualization of the distribution of a continuous variable is a histogram (or the smoothed version—the density plot):

```
NHANES %>% ggplot(aes(x = BMI)) + geom_histogram(binwidth = 2.5) + geom_density(aes(y = 2.5 *  
  ..count.., color = "red")) + ggtitle("Histogram and Density of NHANES BMI") +  
  guides(color = FALSE)
```

Histogram and Density of NHANES BMI



The plot shows a histogram of BMI values with a red density curve overlaid. The x-axis represents BMI, and the y-axis represents the count, ranging from 0 to 1500. The distribution is unimodal and slightly right-skewed, peaking around a BMI of 25.

https://minnier.shinyapps.io/ODSI_continuousData/

Shiny basics

```
# what you see, client side  
ui <- fluidPage(  
  
)
```

```
# computations here!  
server <- function(input, output) {  
  
}
```

```
# run the app!  
shinyApp(ui = ui, server = server)
```

Shiny basics

```
# what you see, client side
ui <- fluidPage(
  # Title, panels
  plotOutput("myplot"), #from output$myplot
  selectInput("foo",choices=allthechoices)
)
```

```
# computations here!
server <- function(input, output) {

}

}
```

```
# run the app!
shinyApp(ui = ui, server = server)
```

Shiny basics

```
# what you see, client side
ui <- fluidPage(
  # Title, panels
  plotOutput("myplot"), #from output$myplot
  selectInput("foo",choices=allthechoices)
)
```

```
# computations here!
server <- function(input, output) {
  # reactive plots
  output$myplot <- renderPlot({ ggplot(yay) + geom_point() })
  # use input$foo here, maybe observe changes in UI
  observe({ dostuff(input$foo) })
}
```

```
# run the app!
shinyApp(ui = ui, server = server)
```

An example: START

Shiny Transcriptome Analysis Resource Tool

Github: <https://github.com/jminnnn/STARTapp>

DATA = RNA-seq gene expression

Home Layout Tables Charts SmartArt Formulas Data 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1	Genid	MGID	MGSymbol	Chr	Start	End	Strand	Length	youngBP12	youngBP12	youngBP12	youngBP12	oldBP12.1	oldBP12.2	oldBP12.3	oldBP12.4	oldBP12.5	oldBP12.6	oldBP12.7	oldBP12.8	oldBP12.9	oldBP12.10	oldBP12.11	oldBP12.12	oldBP12.13	oldBP12.14	oldBP12.15	oldBP12.16	oldBP12.17	oldBP12.18	oldBP12.19	oldBP12.20	oldBP12.21	oldBP12.22	oldBP12.23	oldBP12.24	oldBP12.25	oldBP12.26	oldBP12.27	oldBP12.28	oldBP12.29	oldBP12.30	oldBP12.31	oldBP12.32	oldBP12.33	oldBP12.34	oldBP12.35	oldBP12.36	oldBP12.37	oldBP12.38	oldBP12.39	oldBP12.40	oldBP12.41	oldBP12.42	oldBP12.43	oldBP12.44	oldBP12.45	oldBP12.46	oldBP12.47	oldBP12.48	oldBP12.49	oldBP12.50	oldBP12.51	oldBP12.52	oldBP12.53	oldBP12.54	oldBP12.55	oldBP12.56	oldBP12.57	oldBP12.58	oldBP12.59	oldBP12.60	oldBP12.61	oldBP12.62	oldBP12.63	oldBP12.64	oldBP12.65	oldBP12.66	oldBP12.67	oldBP12.68	oldBP12.69	oldBP12.70	oldBP12.71	oldBP12.72	oldBP12.73	oldBP12.74	oldBP12.75	oldBP12.76	oldBP12.77	oldBP12.78	oldBP12.79	oldBP12.80	oldBP12.81	oldBP12.82	oldBP12.83	oldBP12.84	oldBP12.85	oldBP12.86	oldBP12.87	oldBP12.88	oldBP12.89	oldBP12.90	oldBP12.91	oldBP12.92	oldBP12.93	oldBP12.94	oldBP12.95	oldBP12.96	oldBP12.97	oldBP12.98	oldBP12.99	oldBP12.100	oldBP12.101	oldBP12.102	oldBP12.103	oldBP12.104	oldBP12.105	oldBP12.106	oldBP12.107	oldBP12.108	oldBP12.109	oldBP12.110	oldBP12.111	oldBP12.112	oldBP12.113	oldBP12.114	oldBP12.115	oldBP12.116	oldBP12.117	oldBP12.118	oldBP12.119	oldBP12.120	oldBP12.121	oldBP12.122	oldBP12.123	oldBP12.124	oldBP12.125	oldBP12.126	oldBP12.127	oldBP12.128	oldBP12.129	oldBP12.130	oldBP12.131	oldBP12.132	oldBP12.133	oldBP12.134	oldBP12.135	oldBP12.136	oldBP12.137	oldBP12.138	oldBP12.139	oldBP12.140	oldBP12.141	oldBP12.142	oldBP12.143	oldBP12.144	oldBP12.145	oldBP12.146	oldBP12.147	oldBP12.148	oldBP12.149	oldBP12.150	oldBP12.151	oldBP12.152	oldBP12.153	oldBP12.154	oldBP12.155	oldBP12.156	oldBP12.157	oldBP12.158	oldBP12.159	oldBP12.160	oldBP12.161	oldBP12.162	oldBP12.163	oldBP12.164	oldBP12.165	oldBP12.166	oldBP12.167	oldBP12.168	oldBP12.169	oldBP12.170	oldBP12.171	oldBP12.172	oldBP12.173	oldBP12.174	oldBP12.175	oldBP12.176	oldBP12.177	oldBP12.178	oldBP12.179	oldBP12.180	oldBP12.181	oldBP12.182	oldBP12.183	oldBP12.184	oldBP12.185	oldBP12.186	oldBP12.187	oldBP12.188	oldBP12.189	oldBP12.190	oldBP12.191	oldBP12.192	oldBP12.193	oldBP12.194	oldBP12.195	oldBP12.196	oldBP12.197	oldBP12.198	oldBP12.199	oldBP12.200	oldBP12.201	oldBP12.202	oldBP12.203	oldBP12.204	oldBP12.205	oldBP12.206	oldBP12.207	oldBP12.208	oldBP12.209	oldBP12.210	oldBP12.211	oldBP12.212	oldBP12.213	oldBP12.214	oldBP12.215	oldBP12.216	oldBP12.217	oldBP12.218	oldBP12.219	oldBP12.220	oldBP12.221	oldBP12.222	oldBP12.223	oldBP12.224	oldBP12.225	oldBP12.226	oldBP12.227	oldBP12.228	oldBP12.229	oldBP12.230	oldBP12.231	oldBP12.232	oldBP12.233	oldBP12.234	oldBP12.235	oldBP12.236	oldBP12.237	oldBP12.238	oldBP12.239	oldBP12.240	oldBP12.241	oldBP12.242	oldBP12.243	oldBP12.244	oldBP12.245	oldBP12.246	oldBP12.247	oldBP12.248	oldBP12.249	oldBP12.250	oldBP12.251	oldBP12.252	oldBP12.253	oldBP12.254	oldBP12.255	oldBP12.256	oldBP12.257	oldBP12.258	oldBP12.259	oldBP12.260	oldBP12.261	oldBP12.262	oldBP12.263	oldBP12.264	oldBP12.265	oldBP12.266	oldBP12.267	oldBP12.268	oldBP12.269	oldBP12.270	oldBP12.271	oldBP12.272	oldBP12.273	oldBP12.274	oldBP12.275	oldBP12.276	oldBP12.277	oldBP12.278	oldBP12.279	oldBP12.280	oldBP12.281	oldBP12.282	oldBP12.283	oldBP12.284	oldBP12.285	oldBP12.286	oldBP12.287	oldBP12.288	oldBP12.289	oldBP12.290	oldBP12.291	oldBP12.292	oldBP12.293	oldBP12.294	oldBP12.295	oldBP12.296	oldBP12.297	oldBP12.298	oldBP12.299	oldBP12.300	oldBP12.301	oldBP12.302	oldBP12.303	oldBP12.304	oldBP12.305	oldBP12.306	oldBP12.307	oldBP12.308	oldBP12.309	oldBP12.310	oldBP12.311	oldBP12.312	oldBP12.313	oldBP12.314	oldBP12.315	oldBP12.316	oldBP12.317	oldBP12.318	oldBP12.319	oldBP12.320	oldBP12.321																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		

Very quick tour

START: Shiny Transcriptome Analysis Resource Tool

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[Group Plots](#)
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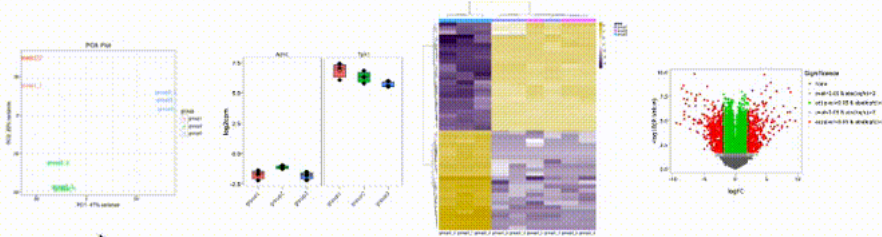
Getting Started with START

[Features](#)
[Data Formats](#)
[Save Data for Future Upload](#)
[More Help](#)

The START app allows users to visualize RNA-seq data starting with count data.

- Explore the app's features with the example data set pre-loaded by clicking on the tabs above.
- Upload your data in the "Input Data" tab.

Features



Visualize your data:

- clustering (PCA plots, heatmaps)
- group comparisons (scatterplots, volcano plots)
- gene-level boxplots of expression values

Data Format

- Must be a .CSV *comma-separated-value* file (you may export from Excel).
- File must have a header row.
- First/Left-hand column(s) must be gene identifiers.
- Format expression column names as `GROUPNAME_REPLICATE#`, e.g. `Treat_1`, `Treat_2`, `Treat_3`, `Control_1`, `Control_2`, `High_1`, `High_2`

Count or Expression Data

- Each row denotes a gene, each column denotes a sample.

gene.id	gene.name	group1_1	group1_2	group1_3	group2_1	group2_2	group2_3
1	ENSMUSG00000037171 Nodal	18584	7124	6359	32514	9365	9800
2	ENSMUSG00000032318 Isl2	0	0	0	0	0	0
3	ENSMUSG000000065866 U1	539	280	165	3467	498	448
4	ENSMUSG00000018507 Trpv2	111	50406	162	212083	79707	49974
5	ENSMUSG00000055971 Olfr378	66	36	29	317	70	52
6	ENSMUSG00000058297 Spock2	7	5	1	8	3	6

Analyzed Data

- Each row denotes a gene, each column denotes a sample.
- Additional columns provide Fold Changes and P-values

gene.id	gene.name	g1_1	g1_2	g2_1	g2_2	g3_1	g3_2	logFC_g1g2	logFC_g1g3	padj_g1g2	padj_g1g3
1	ENSMUSG00000000000 Nodal	7.357	7.414	7.737	7.629	7.487	7.624	-0.367	-0.083	0.469	0.628
2	ENSMUSG00000000000 Isl2	-7.782	-7.782	-7.782	-7.782	-2.400	-2.208	0.242	-4.240	0.922	0.013
3	ENSMUSG00000000000 U1	2.251	2.746	4.508	3.397	2.513	4.006	-1.409	-0.900	0.411	0.122

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Very quick tour

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Analyzed Data

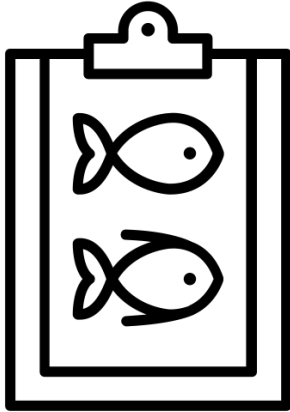
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4	ENSMUSG000000 U1	2.251	2.746	4.508	3.397	2.513	4.006	-1.409	-0.900	0.411	0.122

Who is your audience?

Example: START app

- likely biologists
- some not used to coding or large data sets



Created by Made
from Noun Project

Challenges: *User*

Data is larger than they are used to + Cannot query or share results easily

Interactive search boxes/filtering + Reactive visualization

RNA-Seq Gene Name (Select 1 or more)

Select Group

- ☒ group1
- ☒ group2
- ☒ group3

Select Gene Identifier Label

- ☒ unique_id
- ☐ Geneid
- ☐ MGIsymbol

Y axis:

- ☒ log2cpm_voom
- ☐ log2cpm
- ☐ count

[DotPlot](#)[Info](#)[Data Output](#)

Please select a gene.

Challenges, Input/Output Data

- Input data ~ multiple formats: **Special input formats**
- Interface with other software? **Export special formats**

First column # with gene IDs

Geneid

Last column # with gene IDs

MGIsymbol

First column # with expression values

BPH2J_1

Last column # with expression values

BPN3J_3

First column # with fold changes

Geneid

BPH2J_2

BPH2J_3

BPN3J_1

BPN3J_2

BPN3J_3

logFC.BPN3J.BPH2J

PValue.BPN3J.BPH2J

FDR.BPN3J.BPH2J

First column # with p-values

Geneid

Last column # with p-values

Geneid

Challenges, Input/Output Data

- Input data ~ multiple formats: **Special input formats**

Secure | <https://biit.cs.ut.ee/clustvis/>

ClustVis: a web tool for visualizing clustering of multivariate data (BETA)

Introduction | Data import | Data pre-processing | PCA | Heatmap | Export | Help | News

Enter data
Choose data input type:

- ☒ Load sample data
- ☐ Upload file
- ☐ Paste data
- ☐ Import public dataset from ArrayExpress
- ☐ Load saved settings
- ☐ Import prepared gene expression matrix

Choose dataset:

- ☒ NKI breast cancer dataset (PAM50 genes)
- ☐ Wisconsin Diagnostic Breast Cancer
- ☐ Iris flowers
- ☒ detect delimiter
- ☒ detect column and row annotations

Data matrix reshape:

- ☐ filter columns
- ☐ filter rows
- ☐ transpose matrix

Column annotations (7 rows, 337 columns):

	NKI_4	NKI_6	NKI_7	NKI_8	NKI_9	NKI_11	NKI_12	NKI_13	NKI_14	NKI_17	NKI_23	NKI_24	NK
ER status	1	1	0	0	1	1	0	1	1	1	1	0	1
Histological grade	3	2	1	3	3	3	3	3	1	2	2	3	3
BRCA mutation	0	0	0	0	0	0	0	0	0	0	0	0	0
Metastasis	0	0	0	0	0	0	0	0	0	0	0	0	0
Lymph node status	0	0	0	0	0	0	0	0	0	0	0	0	0
Treatment	0	0	0	0	0	0	0	0	0	0	0	0	0
Study	NKI	NKI	NKI	NKI	NKI	NKI	NKI	NKI	NKI	NKI	NKI	NKI	NK

Numeric data (56 rows, 337 columns):

	NKI_4	NKI_6	NKI_7	NKI_8	NKI_9	NKI_11	NKI_12	NKI_13	NKI_14	NKI_17	NKI_23	NKI_24
SFRP1 (NM_003012)	-0.31	-0.11	-0.03	0.26	-0.10	-0.21	0.33	-0.23	-0.12	0.05	0.57	0.50
TMEM45B (Contig50838_RC)	-0.99	-0.40	0.65	-0.23	0.34	0.70	-1.05	-0.42	-0.02	0.27	0.02	-1.07
PGR (NM_000926)	0.72	0.05	0.18	-0.40	0.10	-0.18	-0.43	-0.09	0.10	0.17	-0.44	-0.93

<https://biit.cs.ut.ee/clustvis/>

Challenges, Input/Output Data

- Input data ~ multiple formats: **Special input formats**

	B	C	D	E	F	G	H	I
1	Subtype	Expression	NKI_4	NKI_6	NKI_7	NKI_8	NKI_9	
2	ER status		1	1	0	0	1	
3	Histological grade		3	2	1	3	3	
4	BRCA mutation		0	0	0	0	0	
5	SFRP1 (NM_003012)	HER2-enriched	down	-0.306	-0.114	-0.026	0.263	-0.095
6	TMEM45B (Contig50838_RC)	basal-like	down	-0.994	-0.398	0.649	-0.231	0.341
7	PGR (NM_000926)	luminal B	no difference	0.724	0.054	0.183	-0.399	0.1
8	MDM2 (NM_002392)	luminal B	no difference	-0.086	0.195	-0.191	0.132	0.272
9	MKI67 (NM_002417)	luminal B	down	-0.027	0.016	-0.034	0.074	-0.139
10	MYBL2 (NM_002466)	luminal A	down	0.103	-0.103	-0.044	0.365	-0.057
11	CDH3 (NM_001793)	luminal B	down	-0.396	-0.77	-0.077	-0.165	-0.518
12	PTTG1 (NM_021000)	luminal A	down	0.123	-0.083	-0.279	0.127	-0.092
13	BAG1 (NM_004323)	HER2-enriched	no difference	-0.134	0.178	0.061	-0.238	-0.013
14	EXO1 (NM_003686)	luminal A	down	-0.101	-0.248	-0.17	0.403	-0.208
15								
16								

<https://biit.cs.ut.ee/clustvis/>

Challenges, Analysis

Many possible ways to analyze data:

- Restrict analyses performed
- Allow for uploading of analysis results

Download Instructions (pdf)

Use example file or upload your own data

- ☒ Upload Data
- ☐ START RData file
- ☐ Example Data

Input Data Type:

- ☐ Expression data: Gene Counts or log-expression (log2cpms)
- ☒ Analyzed data: Expression Values, p-values, fold changes

Download Example Analysis Results File

	gene_id	gene_name	g1_1	g1_2	g2_1	g2_2	g3_1	g3_2	logFC_g1g2	logFC_g1g3	padj_g1g2	padj_g1g3
1												
2	ENSMUSG00000000000	Nodal	7.357	7.414	7.737	7.629	7.447	7.624	-0.357	-0.083	0.469	0.628
3	ENSMUSG00000000000	Id2	-7.782	-7.782	-7.782	-7.782	-2.420	-2.208	0.242	-4.240	0.922	0.013
4	ENSMUSG00000000000	U1	2.251	2.746	4.508	3.397	2.513	4.006	-1.409	-0.900	0.411	0.122
5	ENSMUSG00000000000	Trpv2	-0.024	10.237	10.443	10.719	0.951	1.525	-6.355	2.731	0.444	0.317

- File must have a header row.
- Format expression column names as GROUPNAME_REPLICATE#: Group1_1, Group1_2, Group2_1, Group2_2...
- Number & order of fold changes must MATCH p-value number & order.

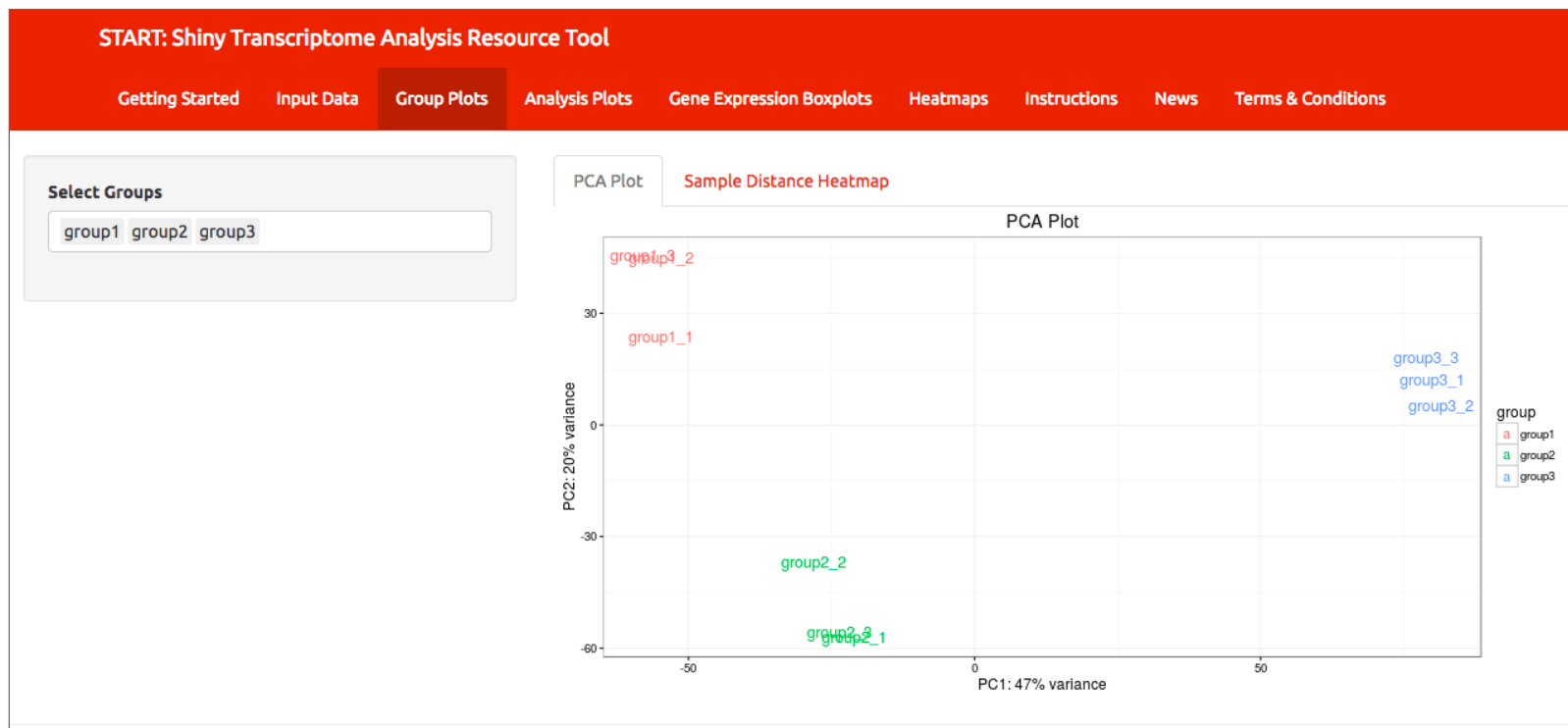
Choose File Containing Data (.CSV)

Choose File No file chosen

Challenges, Analysis

QA/QC

Present QA plots up front



Challenges, Analysis

QA/QC

Present QA plots up front

<https://github.com/joey711/shiny-phyloseq>

Dataset Upload and Selection

Select Dataset

closed_1457_uparse ▼

Upload [Biom-Format](#) File

Browse...

No file selected

Upload [.RData](#) File

Browse...

No file selected

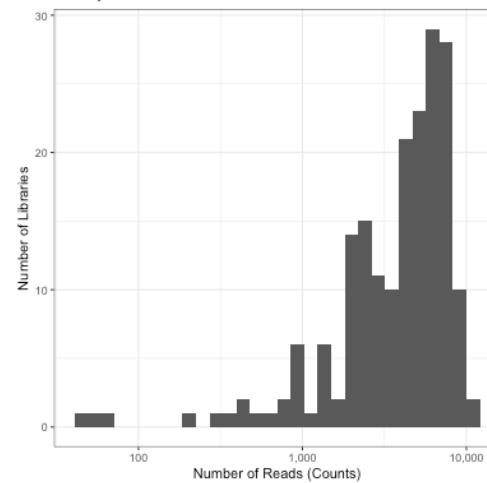
Upload [Tree](#) File

Browse...

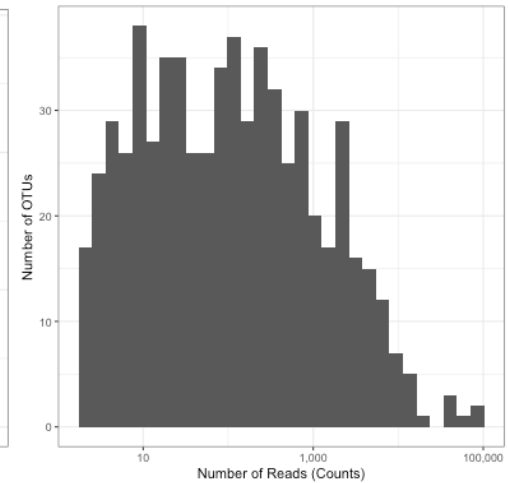
No file selected

Histograms for Selected Data

Library Sizes



OTU Totals



Data Summary

phyloseq-class experiment-level object
otu_table() OTU Table: [634 taxa and 190 samples]
sample_data() Sample Data: [190 samples by 71 sample variables]
tax_table() Taxonomy Table: [634 taxa by 7 taxonomic ranks]
phy_tree() Phylogenetic Tree: [634 tips and 633 internal nodes]

Responsibilities, Food for thought:

- Is resulting analysis **correct**?
- Are we encouraging “**data fishing**”?
- Misuse of **p-values**?
- Solutions? Use instructions and data inputs wisely.
- Other solutions? Avoid Hos, Bayesian posterior probabilities?

Landing page - Where am I?

- **Show** what the app is for/can do
- Point to **instructions** and **guidelines**

Bonus: **Jasmine Dumas** has a **shinyLP** package to help!

Application NavBar Title Home Page 1 Home Page 2 Home Page 3

Hi ShinyLP!

Call attention to important application features or provide guidance

Click Me

Directions

How to use the app

App Status

Include text with status, version and updates

Application Maintainers

Email Me: **Jasmine Dumas**

Security and License

Copyright 2016

Instructions, Please

- **So hard.**
- Not just a **vignette** of a package (users may not be coders)
- **Written** instructions vs. **video** demos
- **Gif** instructions

No one will use it if they don't know **how** to use it!

Instructions

Tauno Metsalu and Jaak Vilo: “Clustvis”

ClustVis: a web tool for visualizing clustering of multivariate data (BETA)

[Introduction](#)[Data import](#)[Data pre-processing](#)[PCA](#)[Heatmap](#)[Export](#)[Help](#)[News](#)

Help

- General
- Data import
- Public dataset from MEM
- List of datasets available
- List of pathways available
- Annotations based filtering
- Data pre-processing
- PCA and heatmap
- Interactivity of the plots
- Interpreting the output
- Mathematical basis
- ClustVis editions

General

You can move through the analysis steps by going to each of the tabs from left to right. All tabs work in a similar way: you can choose settings from the left panel, image or table on the right will automatically renew after that. Sometimes, it can take seconds to load. When moving from one tab to another, settings are saved automatically.

In general, different tabs provide the following options:

- Data import - choose input dataset, option to filter rows/columns based on annotations and transpose matrix
- Data pre-processing - option to aggregate columns with similar annotations, remove rows/columns with missing values, row centering and scaling, method for calculating principal components and imputing missing values
- PCA - options related to PCA plot
- Heatmap - options related to heatmap
- Export - create link with current settings, download intermediate results

The idle timeout (the time when browser session ends if user is inactive) is set to 30 minutes from server side but this can be overridden by browser configuration. To save uploaded data and selected settings, you can use a button on the 'Export' tab, a link is given to recover the settings later. This can also be used to send a link to a collaborator to show the same view. There is no planned expiration time for the links, users can delete the settings if they are concerned about the privacy. Though, when version of ClustVis changes, old saved settings may not be fully compatible with the new version if e.g. there are some new features.

Data import

We aimed for a simple input data format. The numeric data matrix is situated in the bottom right corner, dimensions presented in rows and points in columns. Row labels and annotations are left from the matrix, column labels and annotations are above the matrix. Annotation labels are in the first row and column, respectively. Format of the input file is shown on the image below. Annotations are optional, data sets without annotations can be uploaded as well (on the example image, omitting rows 2-4 and/or columns B and C). When taking data from spreadsheet program (e.g. MS Excel), you can copy-paste the data to 'Paste data' box or export the data as delimited text file (ending with .csv or .tab) and then upload this file to ClustVis. Uploading Excel native files directly (.xls or .xlsx) doesn't work.

Column annotation labels

Row annotation labels

Point labels (e.g. sample names)

Column annotations

Instructions

Tauno Metsalu and Jaak Vilo: “Clustvis”

Interactivity of the plots

Interpreting the output

Mathematical basis

ClustVis editions

centering and scaling, method for calculating principal components and imputing missing values

- PCA - options related to PCA plot
- Heatmap - options related to heatmap
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The idle timeout (the time when browser session ends if user is inactive) is set to 30 minutes from server side but this can be overridden by browser configuration. To save uploaded data and selected settings, you can use a button on the 'Export' tab, a link is given to recover the settings later. This can also be used to send a link to a collaborator to show the same view. There is no planned expiration time for the links, users can delete the settings if they are concerned about the privacy. Though, when version of ClustVis changes, old saved settings may not be fully compatible with the new version if e.g. there are some new features.

Data import

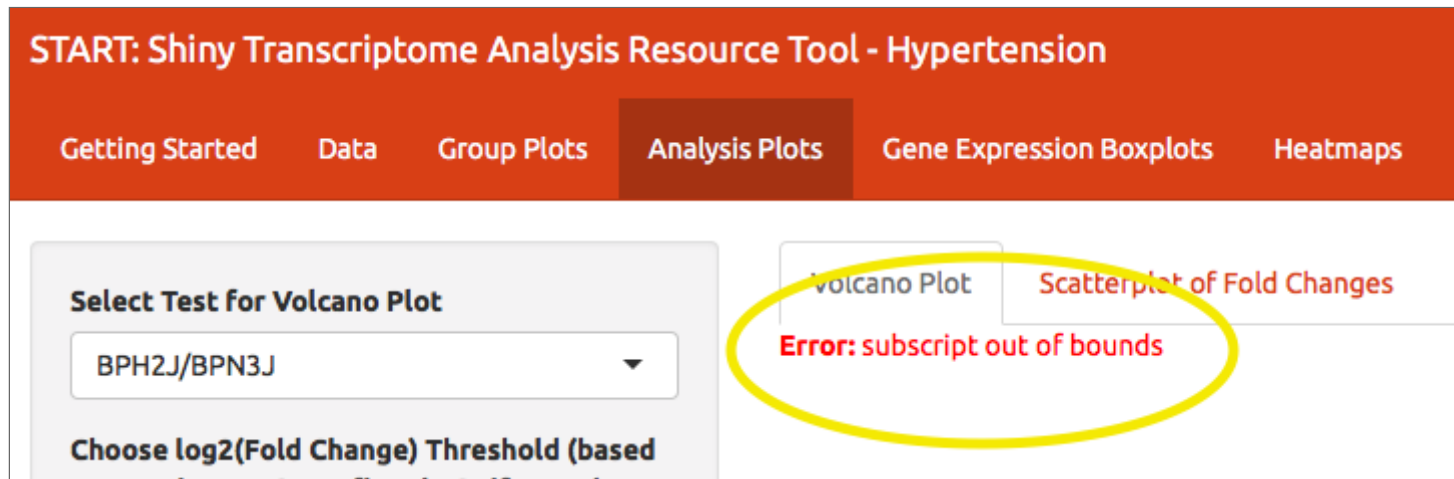
We aimed for a simple input data format. The numeric data matrix is situated in the bottom right corner, dimensions presented in rows and points in columns. Row labels and annotations are left from the matrix, column labels and annotations are above the matrix. Annotation labels are in the first row and column, respectively. Format of the input file is shown on the image below. Annotations are optional, data sets without annotations can be uploaded as well (on the example image, omitting rows 2-4 and/or columns B and C). When taking data from spreadsheet program (e.g. MS Excel), you can copy-paste the data to 'Paste data' box or export the data as delimited text file (ending with .csv or .tab) and then upload this file to ClustVis. Uploading Excel native files directly (.xls or .xlsx) doesn't work.

	B		C	D	E	F	G	H	I
1	Subtype		Expression	NK1_4	NK1_6	NK1_7	NK1_8	NK1_9	
2	ER status			1	1	0	0	1	
3	Histological grade			3	2	1	3	3	
4	BRCA mutation			0	0	0	0	0	
5	SFRP1 (NM_003012)	HER2-enriched	down	-0.306	-0.114	-0.026	0.263	-0.095	
6	TMEM45B (Contig50838_RC)	basal-like	down	-0.994	-0.398	0.649	-0.231	0.341	
7	PGR (NM_000926)	luminal B	no difference	0.724	0.054	0.183	-0.399	0.1	
8	MDM2 (NM_002392)	luminal B	no difference	-0.086	0.195	-0.191	0.132	0.272	

But Does It work?

Debugging Tips

Debugging is notoriously a pain here



The screenshot shows the interface of the "START: Shiny Transcriptome Analysis Resource Tool - Hypertension". The top navigation bar is orange and contains the following tabs: "Getting Started", "Data", "Group Plots", "Analysis Plots" (which is the active tab), "Gene Expression Boxplots", and "Heatmaps". Below the navigation bar, there are two main sections. The left section is titled "Select Test for Volcano Plot" and contains a dropdown menu with the text "BPH2J/BPN3J". Below this is a label "Choose log2(Fold Change) Threshold (based". The right section contains two buttons: "Volcano Plot" and "Scatterplot of Fold Changes". A yellow oval highlights the "Volcano Plot" button and the error message "Error: subscript out of bounds" displayed below it.

Thanks, stack trace:

```
Warning in origRenderFunc() :  
  Ignoring explicitly provided widget ID "db8a6bc6ca6e"; Shiny doesn't use them  
Warning in widgetFunc() :  
  renderDataTable ignores ... arguments when expr yields a datatable object; see ?renderDataTable  
Joining, by = "unique_id"  
Warning: Column `unique_id` joining character vector and factor, coercing into character vector  
Warning: Error in [: subscript out of bounds  
Stack trace (innermost first):  
 85: rna_scatterplot [fun-analysisres.R#334]  
 84: eval [server-analysisres.R#119]  
 83: eval  
 82: withProgress  
 81: "plotly"::"ggplotly" [server-analysisres.R#115]  
 80: func  
 79: origRenderFunc  
 78: output$scatterplot  
  1: shiny::runApp
```

Did you update a package?

Good luck with that.

Old fashioned methods work best

Breakpoints and tracing:

- `browser()` - I didn't say it was fun
- `print()` - every single function/observe statement gets a print

```
[1] "server-sampleplots-update-samples"
[1] "server-analysisres-update"
[1] "drawing volcano plot"
[1] "drawing scatterplot"
[1] "server-datafilter-update-filters"
[1] "server-sampleplots-update-samples"
[1] "server-datafilter-update-tests"
Warning in max(tmpfc, na.rm = T) :
  no non-missing arguments to max; returning -Inf
[1] "server-datafilter-update-expr"
Warning: Error in FUN: only defined on a data frame with
les
Stack trace (innermost first):
 61: FUN
 60: lapply
 59: Summary.data.frame
 58: observerFunc [server-filterdata.R#76]
  1: shiny::runApp
ERROR: [on_request_read] connection reset by peer
ERROR: [on_request_read] connection reset by peer
ERROR: [on_request_read] connection reset by peer
```

New methods are also nice

```
runApp(..., display.mode="showcase")
```

But, doesn't show why something broke.

START: Shiny Transcriptome Analysis Resource Tool

Getting StartedInput DataFilter DataGroup PlotsAnalysis PlotsGene Expression BoxplotsHeatmaps

InstructionsNewsTerms & Conditions

Select Value to Plot

☒ log2cpm_voom
☐ log2cpm
☐ count

Select Groups

group1 group2 group3

Select Samples

group1_1 group1_2
group1_3 group2_1
group2_2 group2_3
group3_1 group3_2
group3_3

Select Principal Components

1 2

PCA PlotSample Distance Heatmap

PCA Plot

group

group1
group2
group3

fun-analysisres.Rfun-analyzecomts.Rfun-dotplot.R

fun-groupplots.Rfun-heatmap.Rhelpers.R

save_example_data.Rserver-analysisres.Rserver-data.R

server-dotplot.Rserver-filterdata.Rserver-heatmap.R

server-inputdata.Rserver-samplegroupplots.Rserver.R

ui-tab-analysisres.Rui-tab-dotplot.Rui-tab-filterdata.R

ui-tab-heatmap.Rui-tab-help.Rui-tab-inputdata.R

ui-tab-landing.Rui-tab-news.Rui-tab-samplegroupplots.R

ui-tab-terms.Rui.Rwww

```
##  
##  
gene_heatmap <- function(data_long, valuenam, sampleid, annotation_row=NULL) {  
  data_long$value = data_long[, valuenam]  
  exprdat = data_long %>% select(unique_id, sampleid, value) %>% spread(sampleid, value)  
  exprdat = as.matrix(exprdat[, -1])  
  
  sampleDists <- dist(t(exprdat))  
  sampleDistMatrix <- as.matrix(sampleDists)  
  rownames(sampleDistMatrix) <- sampleid  
  if(!is.null(annotation_row)) rownames(annotation_row) <- sampleid  
  colnames(sampleDistMatrix) <- NULL  
  colors <- colorRampPalette( rev(brewer.pal(9, "Blues"))) (255)  
  heatmap::heatmap(sampleDistMatrix, clustering_distance_rows=sampleDists
```

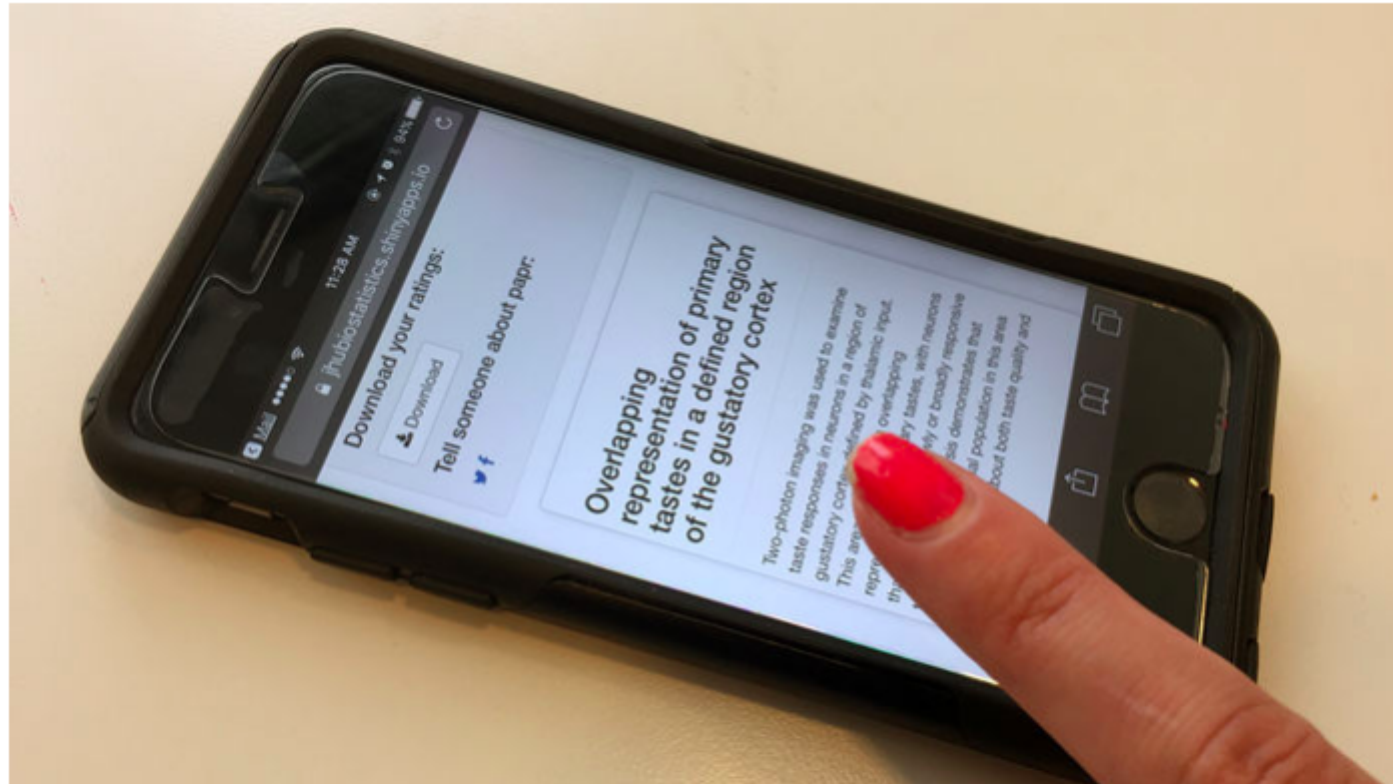
ShinyApp created by {Jessica Minnier + Jiri Sklenar + Jonathan Nelson} of
Knight Cardiovascular Institute, Oregon Health & Science University
Copyright (C) 2016, code licensed under GPLv3
Code available on Github: <https://github.com/jminnier/STARTapp>
Nelson JW, Sklenar J, Barnes AP, Minnier J. (2016) 'The START App: A Web-Based RNAseq Analysis and Visualization Resource.'

Random final tips:

- Test it first
 - Unit testing can save you so much headache
 - Run tests on example data
 - Create .Md file of test plots
- Security
 - Are users uploading sensitive data?
 - Security review of public apps vs commercial version
- Speed: **Why so slow?**
 - Rprofiler in Rstudio
 - Reduce start up time

Be Creative!

papr by Lucy D'Agostino McGowan, Nick Strayer, Jeff Leek



Papr lets you decide whether an abstract is "exciting," "boring," "probable," or "questionable."

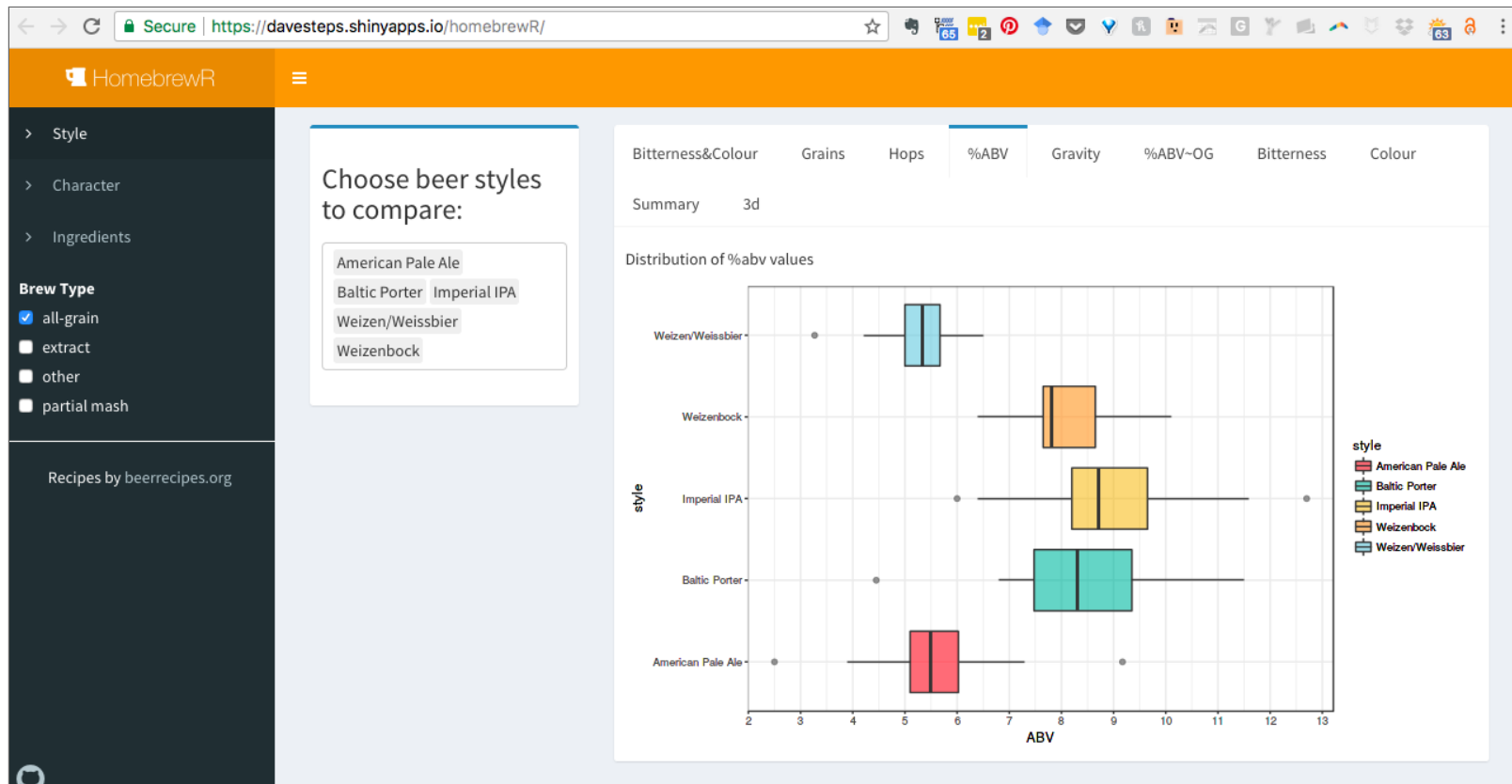
Science/AAAS

Great paper? Swipe right on the new 'Tinder for preprints' app

By **Dalmeet Singh Chawla** | Jun. 15, 2017, 5:00 PM

Have fun!

homebrewR by David Stephens



Thank you! Go forth and shiny!

Contact: @ **datapointier**

Github: **<https://github.com/jminnier/STARTapp>**

Slides available at **<http://bit.ly/shiny-ddtx>**

Code for slides available at

https://github.com/jminnier/presentation_austin_dataday201