

Shiny in Bioinformatics

RStudio, Inc.
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BioC Conference

Shiny Introduction

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R is great!

- Excellent for statistics
- Amazing at data visualization
- Vibrant and generous community

...but...

- A personal experience, not a shared one
- Sharing results generally means exporting to a static format
- Need to write code to manipulate visualizations and other output
- Modern visualization is animated and interactive - not obvious how to do this from R

Shiny is
R + interactivity + web
made easy

What is Shiny?



What is Shiny?

- Interactive web application around your R analyses
- Zero HTML/CSS/JavaScript knowledge required...
- ... but fully customizable and extensible with HTML/CSS/JavaScript

What is Shiny?

- Modern web UI with attractive defaults
- Designed to integrate with existing JavaScript libraries (including d3.js)
- Uses a “reactive” programming model which allows dramatically simpler code than traditional UI or web programming

What is Shiny?

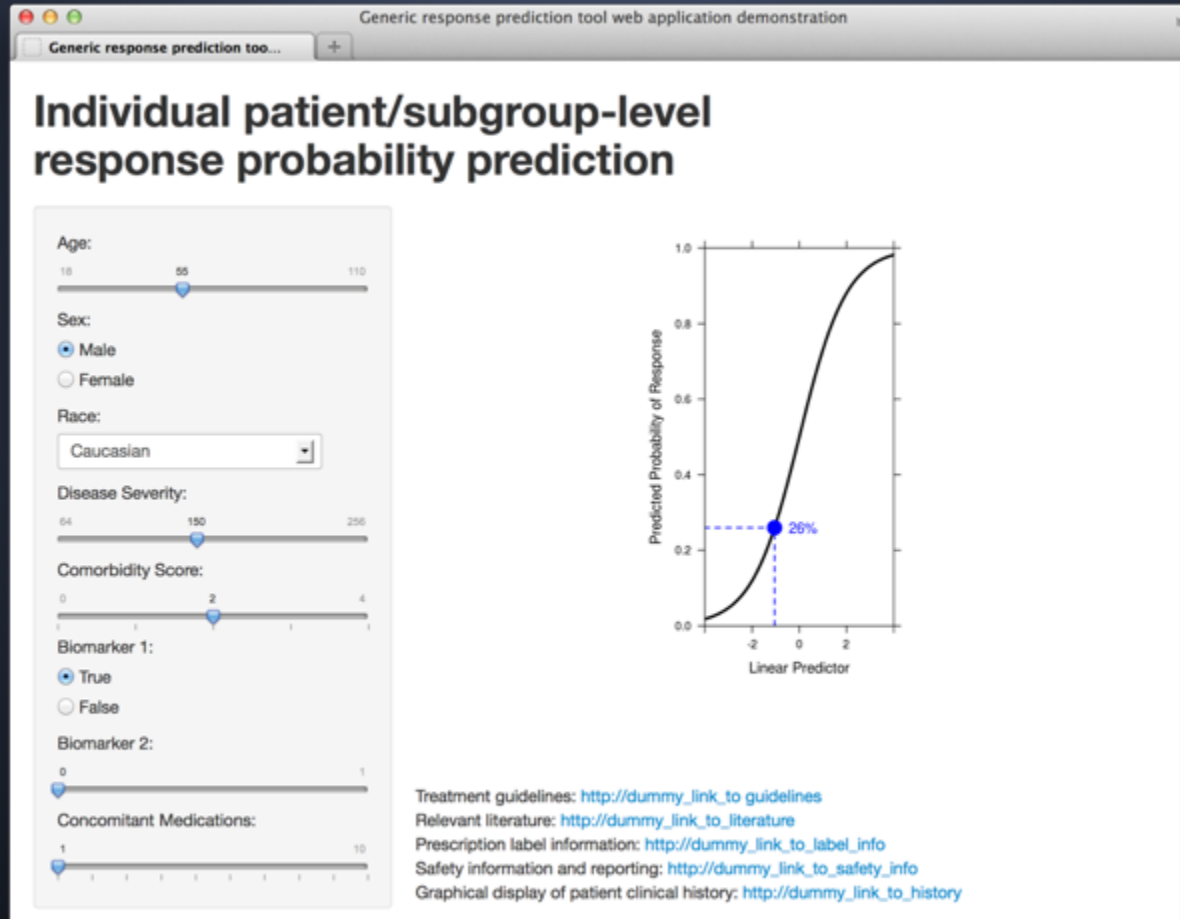
- Free and open source (GPLv3) R package
- Created and maintained by RStudio, Inc.
- First released in November 2012

Deploying Shiny Apps

- R package itself is not designed for deployment
- Shiny Server (AGPLv3)
 - <https://github.com/rstudio/shiny-server>
- Shiny Server “Pro” (Commercial)
 - Adds authentication, security, monitoring features to Shiny Server
 - Coming soon
- Shiny hosting on rstudio.com
 - Currently in free beta; sign up at <http://rstudio.com/shiny>

Shiny in Action

Visual Models



<http://spark.rstudio.com/genentech/generic-response-prediction-tool-web-application-demonstration-v2/>

Interactive Plotting

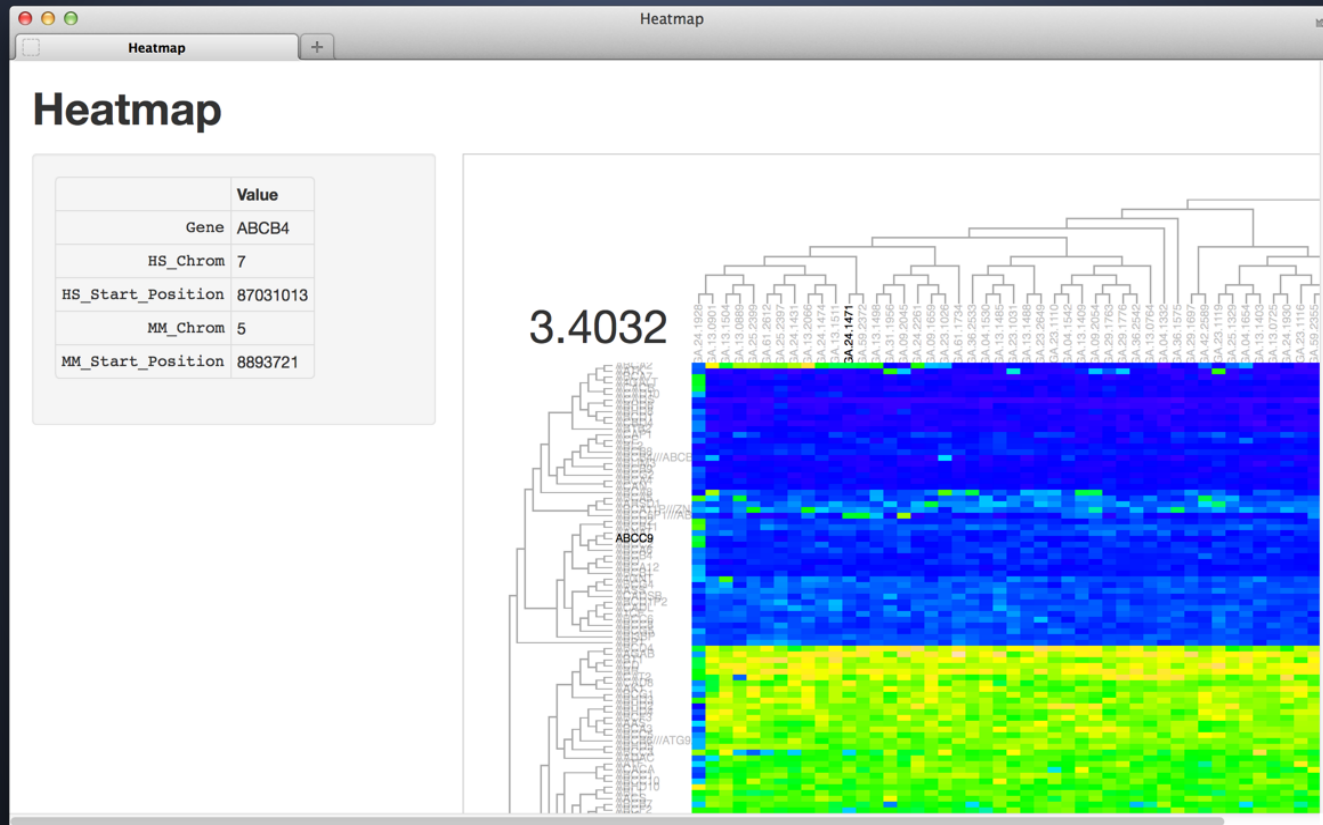
The screenshot shows a web browser window titled "Reconstruct Gene Networks". The page has a header with the same title. On the left side, there is a control panel with the following elements:

- An unchecked checkbox labeled "Use a file stored on my local machine."
- A "File URL:" label above a text input field containing the path `/sampleExp.csv`.
- A link that says "Download the sample dataset [here](#)".
- A label "One row represents a single:" above a dropdown menu currently set to "Sample".
- A label "Method to use to reconstruct the network:" above a dropdown menu currently set to "GeneNet".
- A label "Connection threshold:" above a horizontal slider. The slider has a blue handle at the 0.15 mark, with 0 on the left and 1 on the right.
- Text below the slider: "Use the slider to set the number of connections which will be displayed in the graph. Higher, more stringent thresholds will include fewer connections, while lower thresholds will display more connections".
- A link at the bottom: "All source available on [Github](#)".

On the right side of the page, there is a network graph visualization. It consists of approximately 20 black circular nodes connected by thin black lines. The nodes are arranged in a somewhat circular pattern on the left and right, with a few isolated nodes at the bottom. The connections form a complex web of relationships between the nodes.

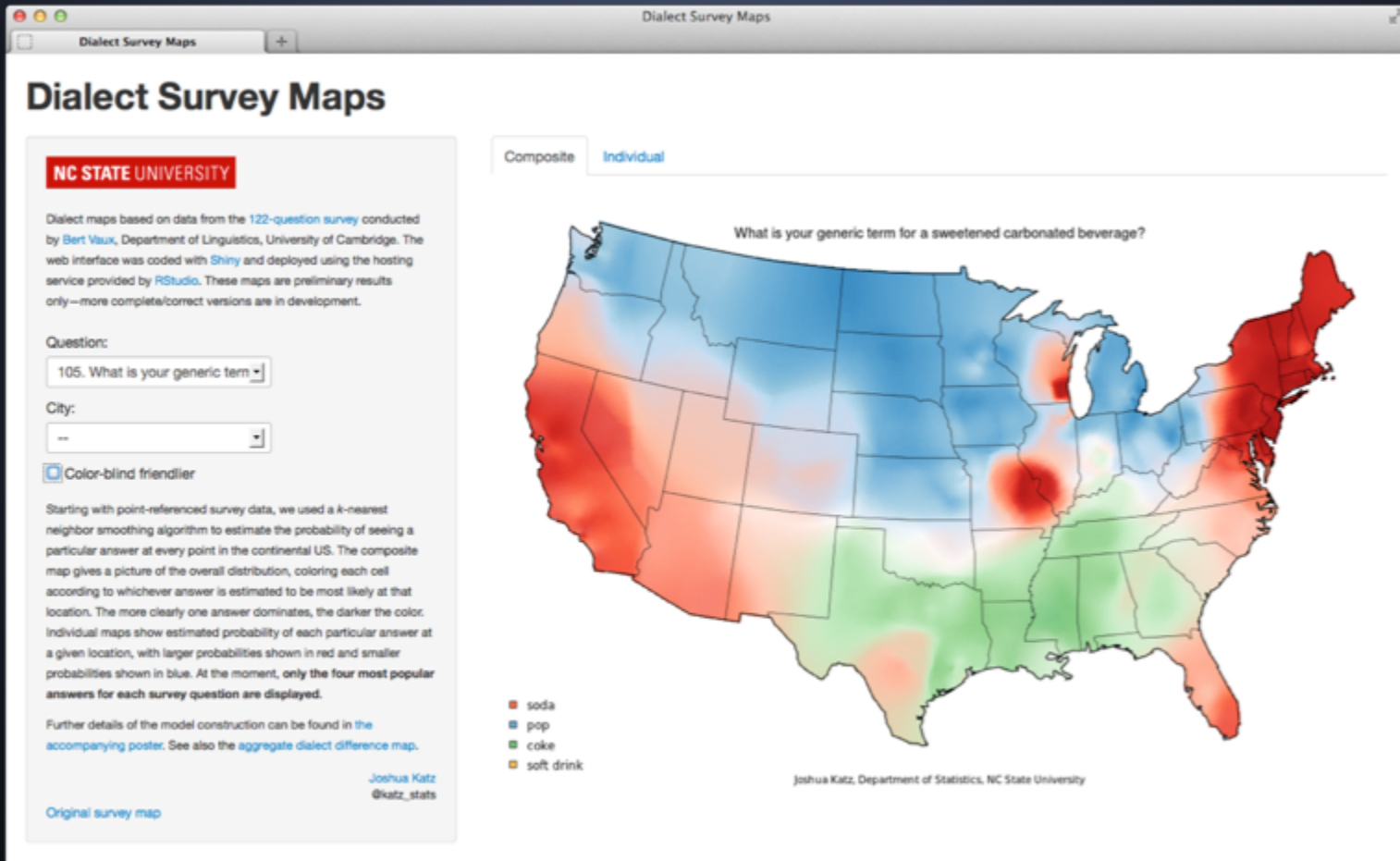
<http://glimmer.rstudio.com/qbrc/grn/>

Interactive Plotting



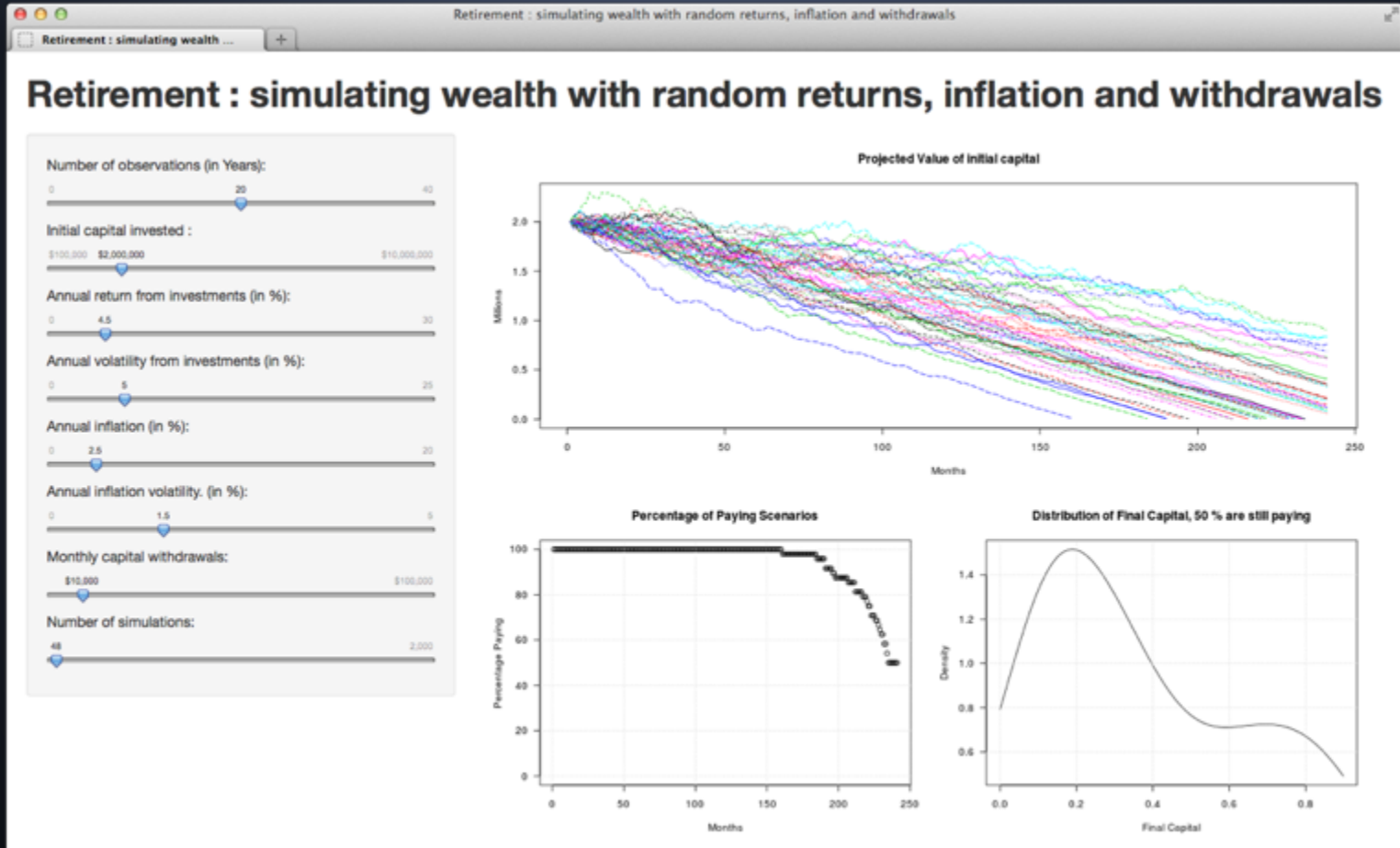
<http://glimmer.rstudio.com/qbrc/heatmap/>

Analytics That Go Viral

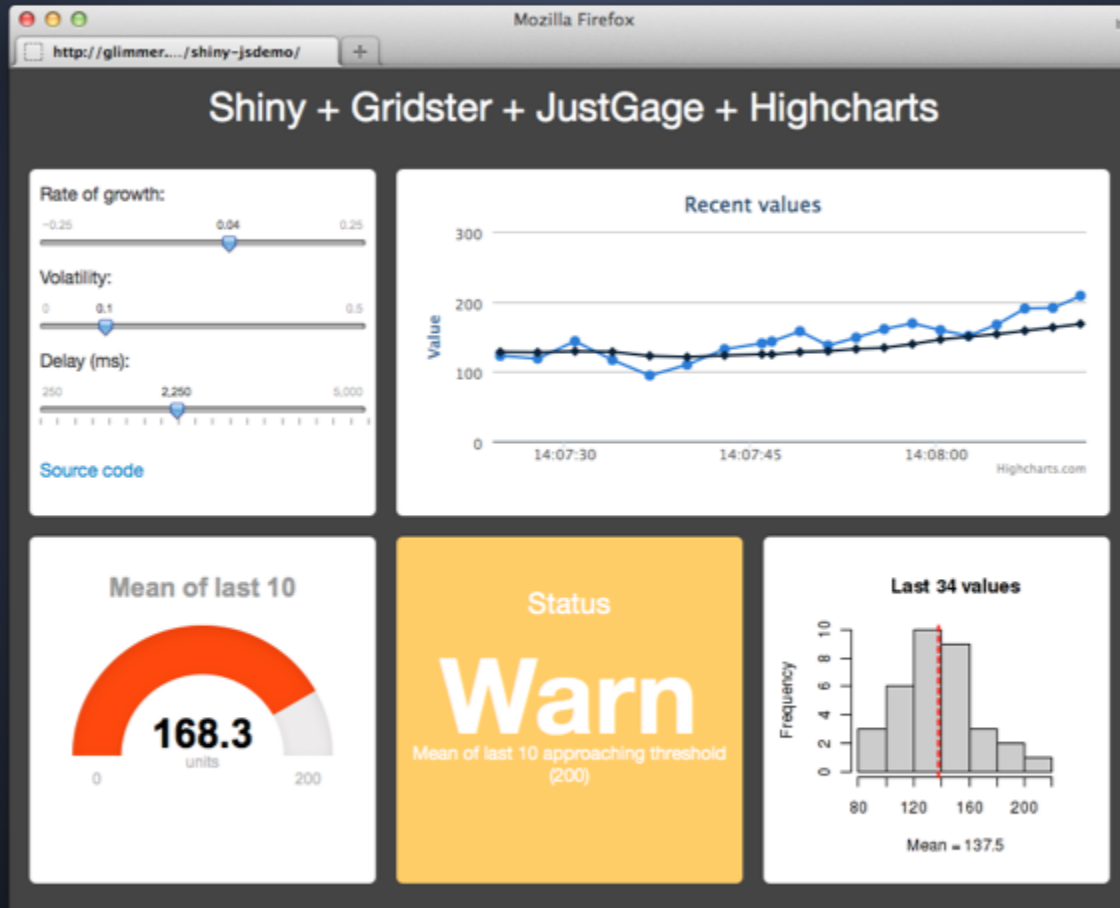


<http://spark.rstudio.com/jkatz/SurveyMaps/>
http://www.huffingtonpost.com/2013/06/06/dialect-maps_n_3395819.html

Build Practical Tools

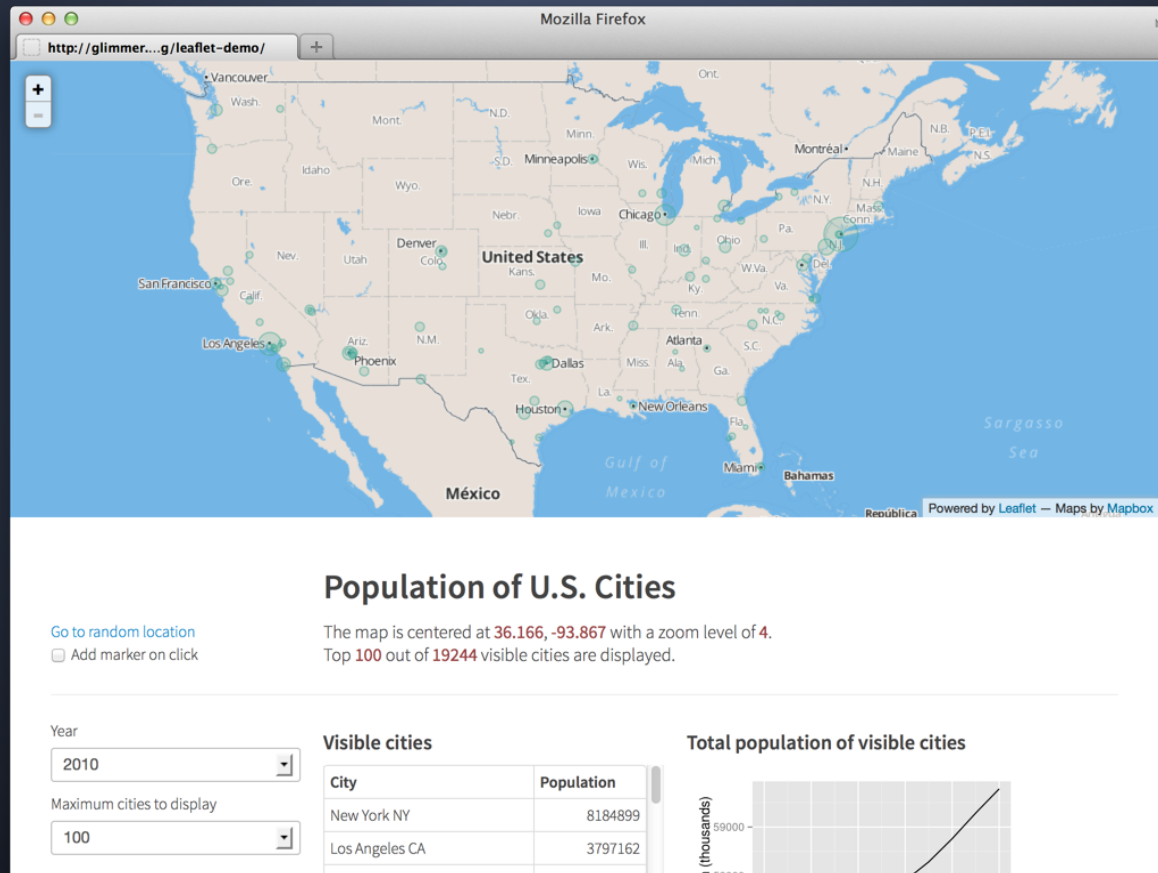


Customizable Dashboards



<http://glimmer.rstudio.com/winstontest/shiny-jsdemo/>

Control JavaScript Visualizations



<http://glimmer.rstudio.com/jcheng/leaflet-demo/>

displayR

Shawn Balcome
University of Minnesota

Shiny Walkthrough

Jeff Allen
RStudio, Inc.

Download Examples

Update Shiny

```
install.packages("devtools")  
library(devtools)  
install_github("shiny", "rstudio")
```

Download Examples

```
source("http://bit.ly/DLBIOOC")
```

Shiny Examples

- Data from `curatedOvarianData`
- 100s of MB of microarray data
- We extract two matrices:
 - 8 Normal samples x 8 genes
 - 20 Tumor samples x 8 genes
- Store as `ExpressionSet` objects
- Save as `.Rds` files

Example 1

- Comparison of normal expression vs. tumor expression
- Allow user to select gene to visualize
- Render as boxplot

<http://bit.ly/biocon1>

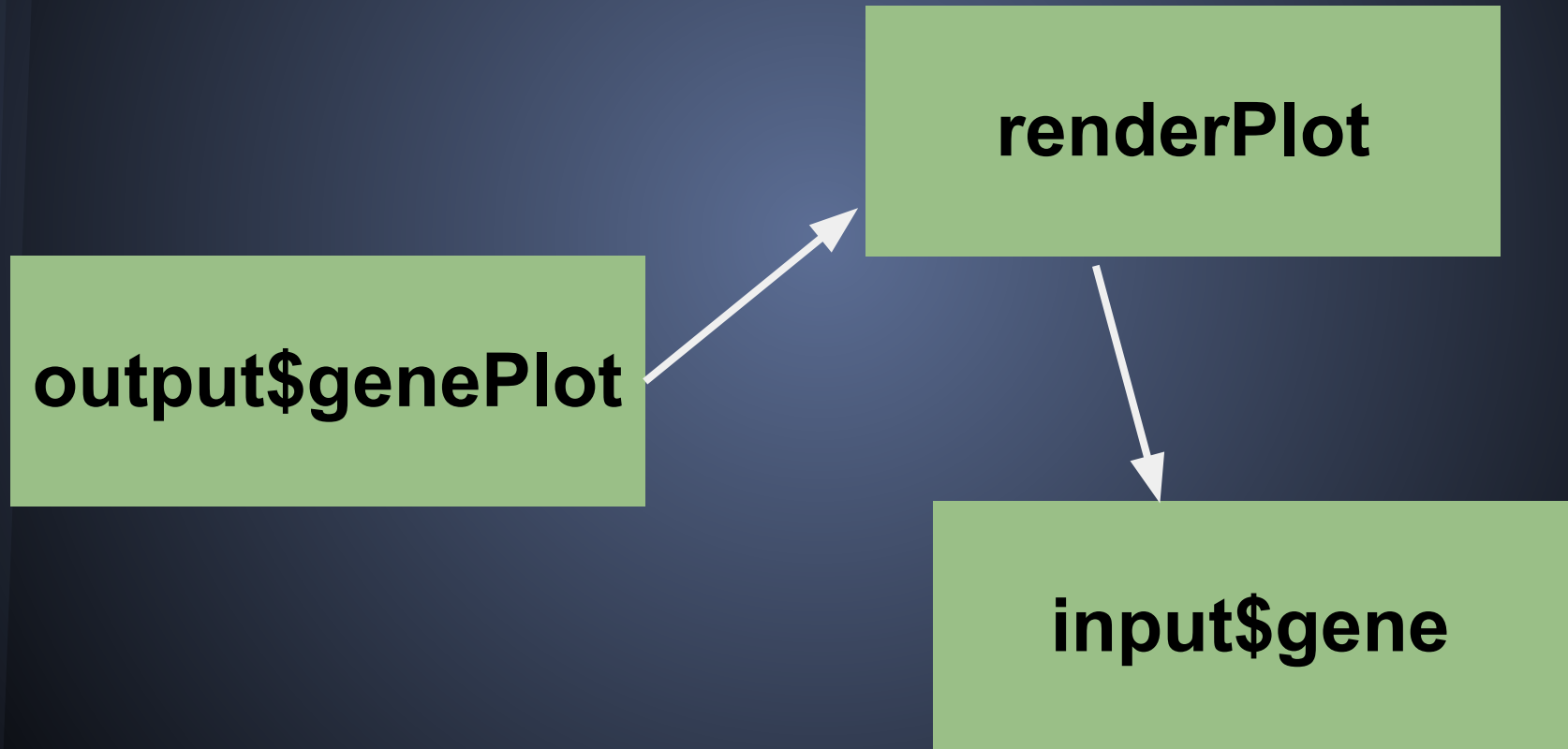
Prepare Workspace

```
library(shiny)
options(shiny.launch.browser=FALSE)

tumor
normal
library(Biobase)
exprs(tumor)
boxplot(list(Tumor=exprs(tumor),
Normal=exprs(normal)))
```


Let's Do it!

Dependency Graph - Example 1



Shiny Reactivity

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Reactivity

- Reactive programming is a way of organizing your code that emphasizes values that can change over time...
- ...and expressions that depend on such values...
- ...so that changes to those values naturally “flow” through your system.

Reactivity Demo

Reactivity

- Reactive values are values that vary over time
- Reactive expressions are expressions that may depend on reactive values and other reactive expressions
- Detailed explanation in the tutorial: <http://rstudio.github.io/shiny/tutorial/#reactivity-overview>

Shiny Examples, Cont'd.

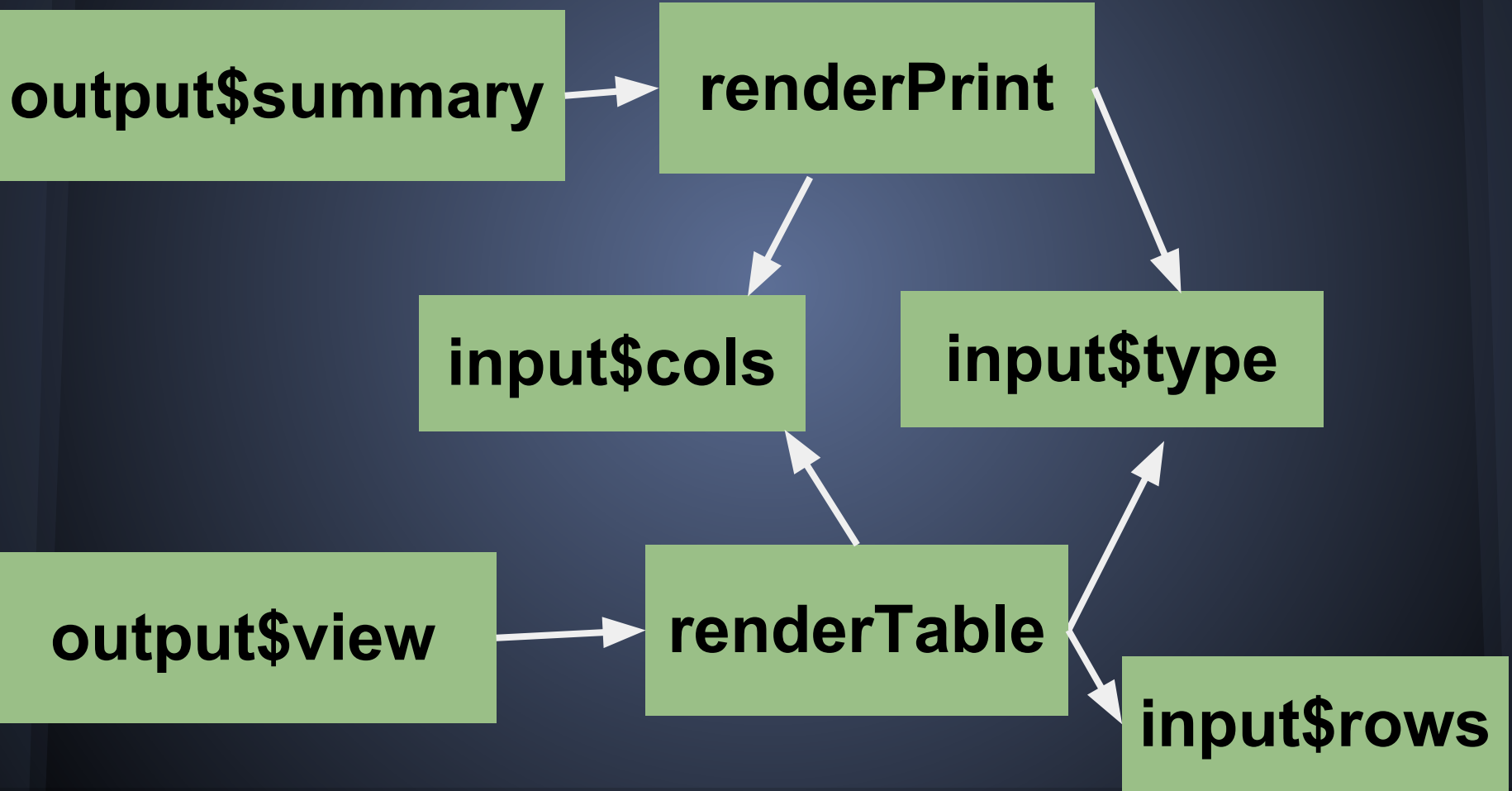
Jeff Allen
RStudio, Inc.

Shiny Example 2

- Shiny offers text-based inputs and outputs
- View tables
- Print R output directly
- Let's create an app that can preview the gene expression data in each set

<http://bit.ly/biocon2>

Dependency Graph - Example 2



Dependency Graph - Example 2

output\$summary

renderPrint

input\$cols

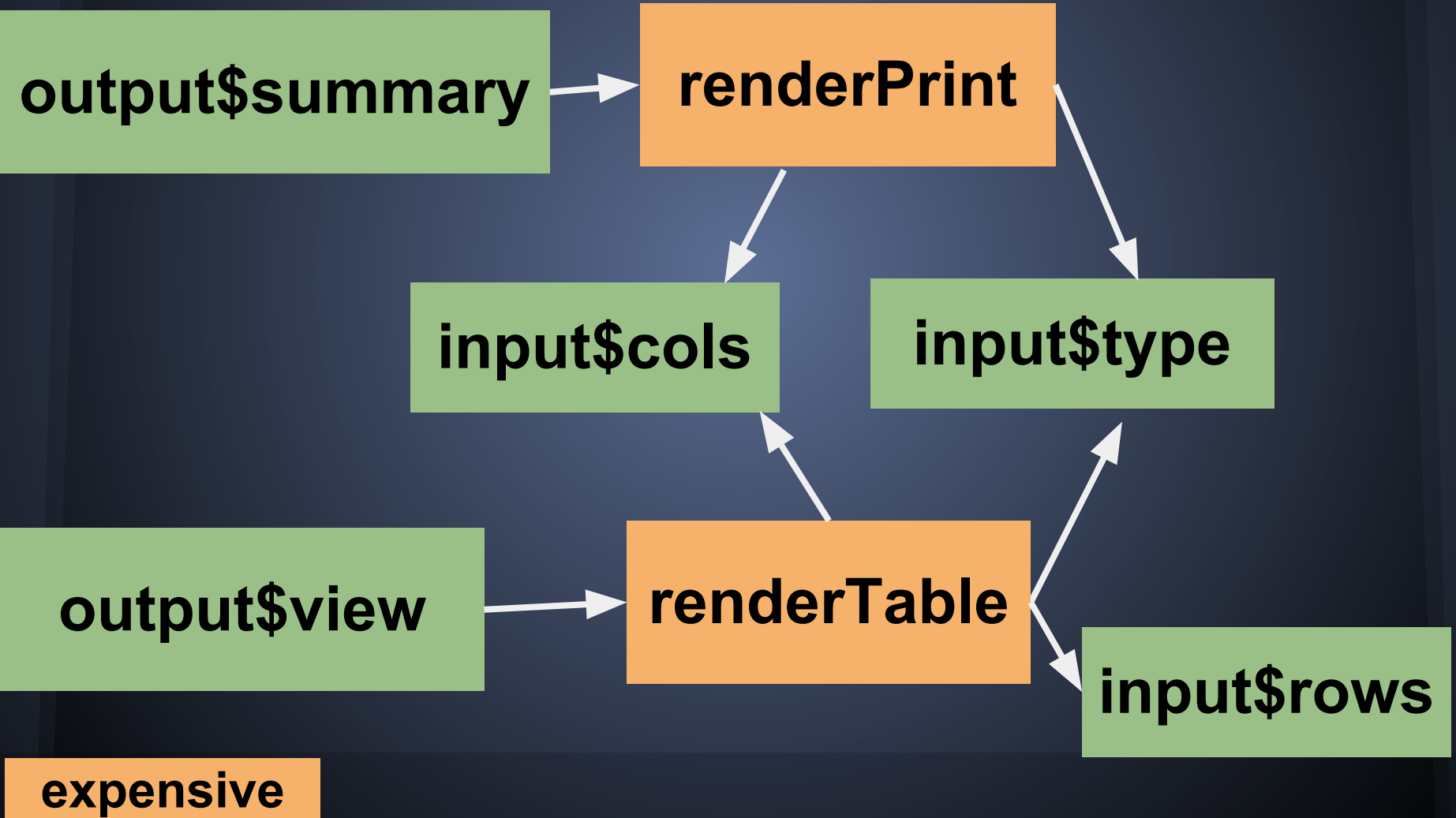
input\$type

output\$view

renderTable

input\$rows

expensive



Dependency Graph - Example 2

output\$summary

renderPrint

input\$cols

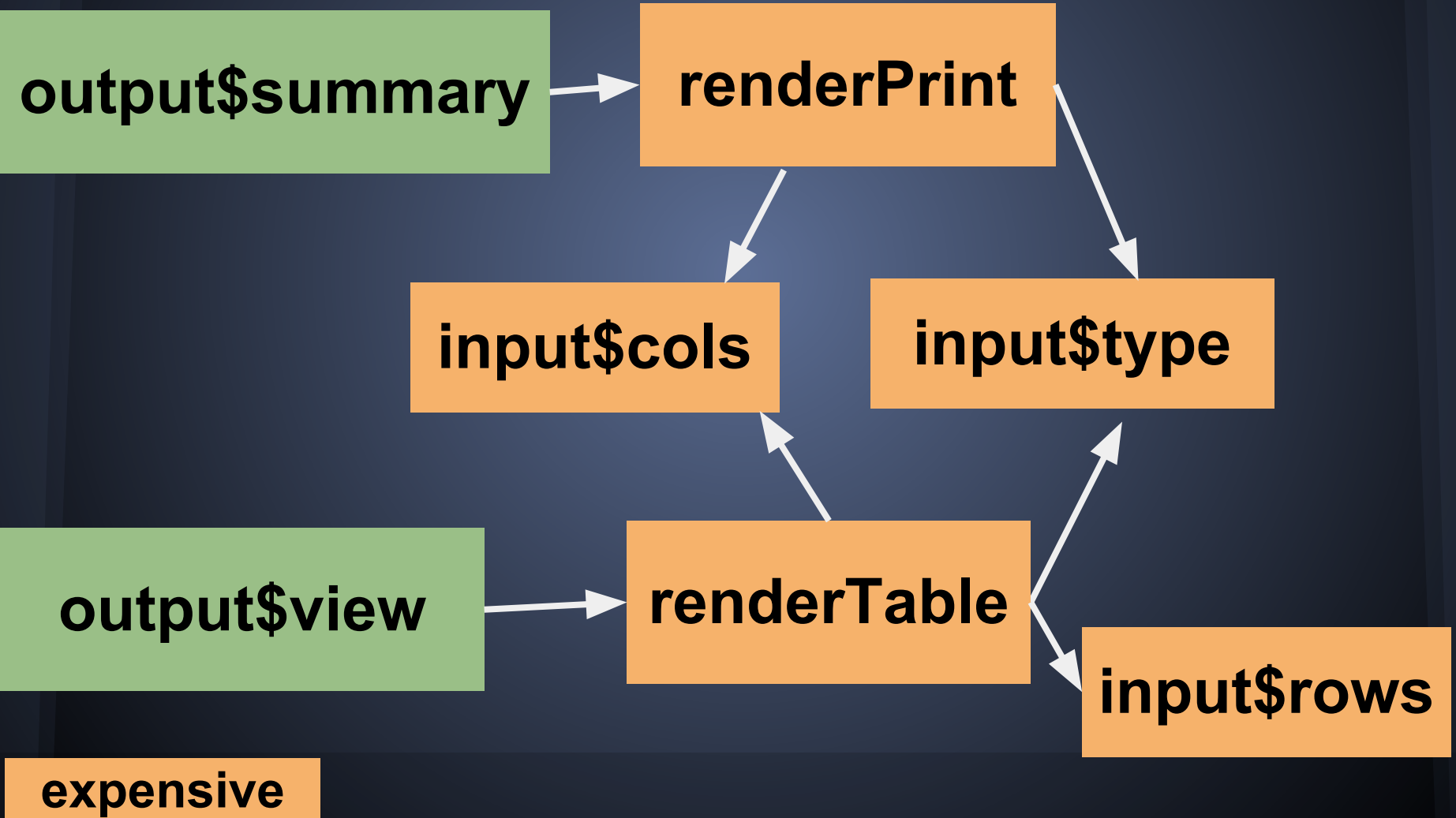
input\$type

output\$view

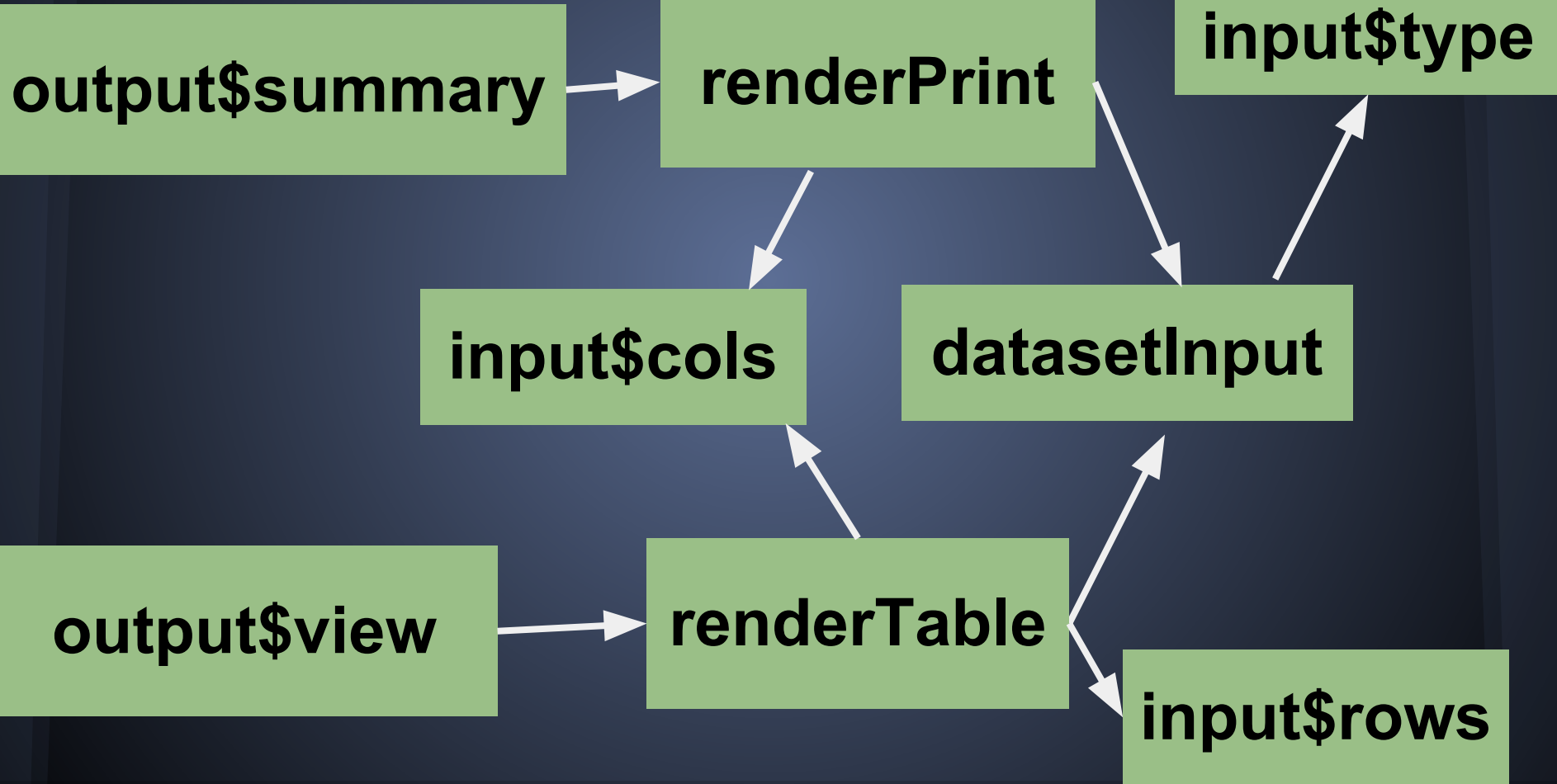
renderTable

input\$rows

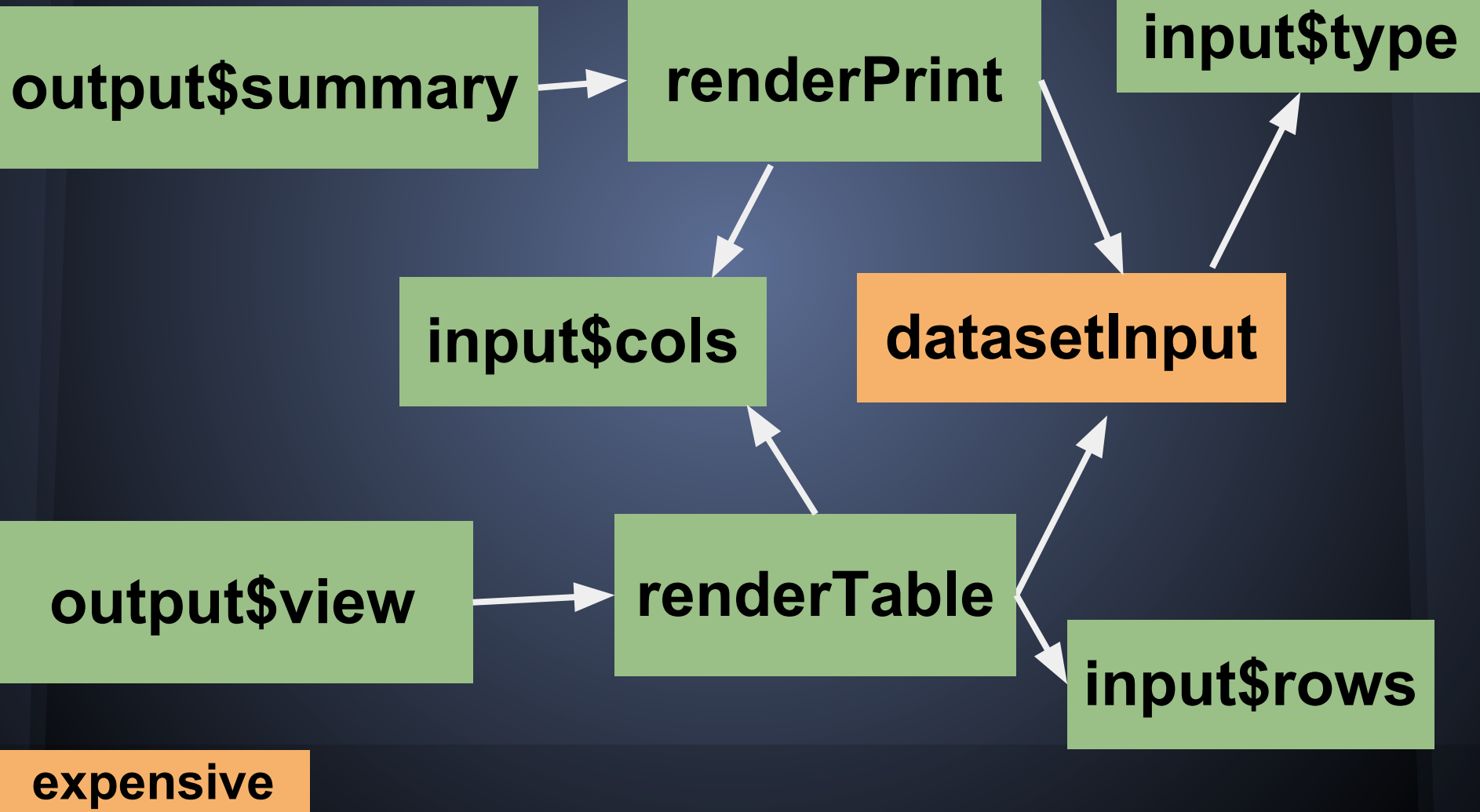
expensive



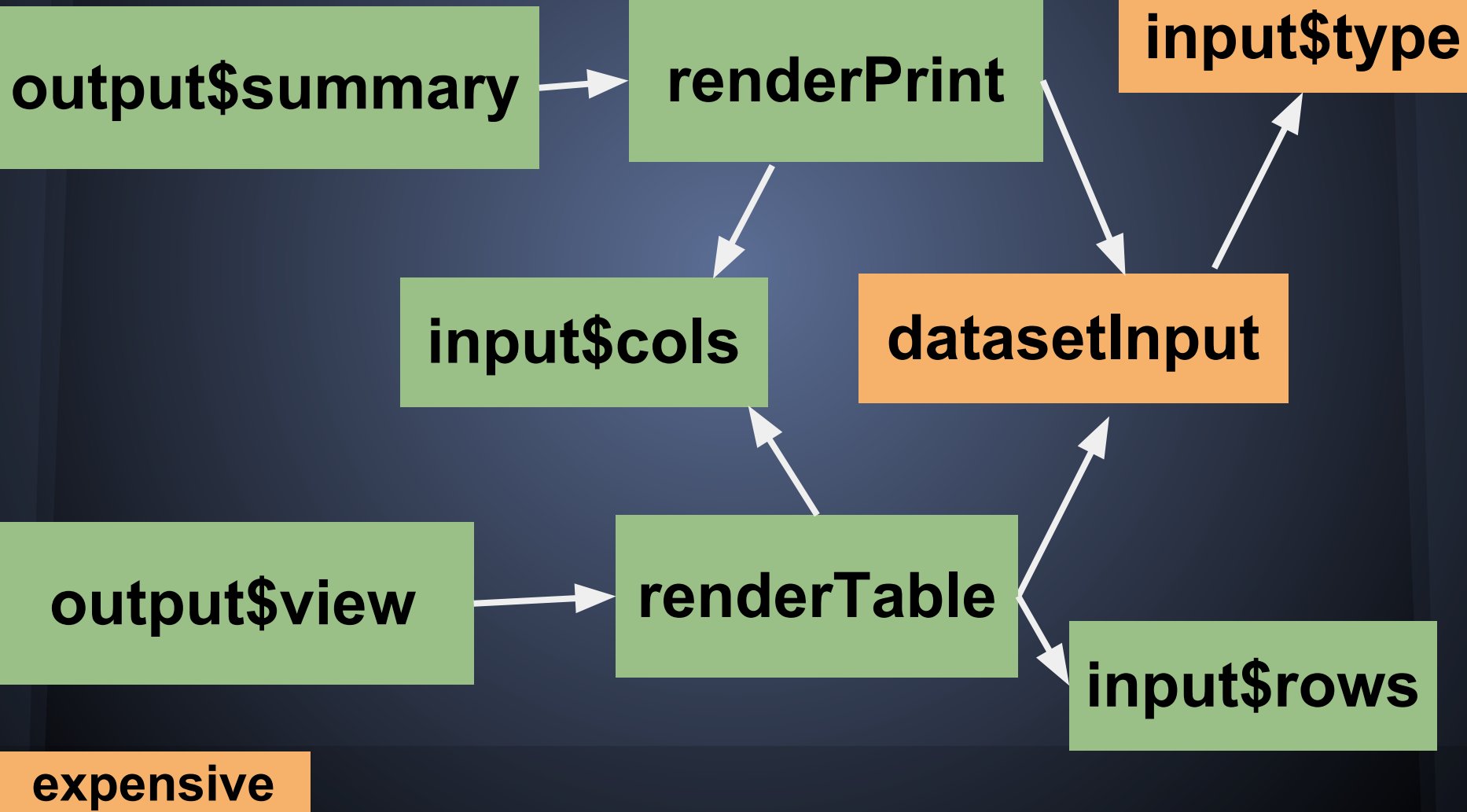
Dependency Graph - Example 2



Dependency Graph - Example 2



Dependency Graph - Example 2



Shiny Example 3

- No limits to computational power of Shiny
- Anything you can do in R, you can do in `server.R`

<http://bit.ly/biocon3>

Shiny Example 4

- Shiny not only used in isolation
- Great for injecting some interactivity at key points in a larger analysis workflow
- Use `stopApp()` to return some data from a Shiny app

<http://bit.ly/biocon4>

Next Steps

- Shiny homepage
<http://rstudio.com/shiny>
- Shiny Tutorial
<http://rstudio.github.io/shiny/tutorial>
- Discussion list
<http://groups.google.com/group/shiny-discuss>

Thanks!

Q&A