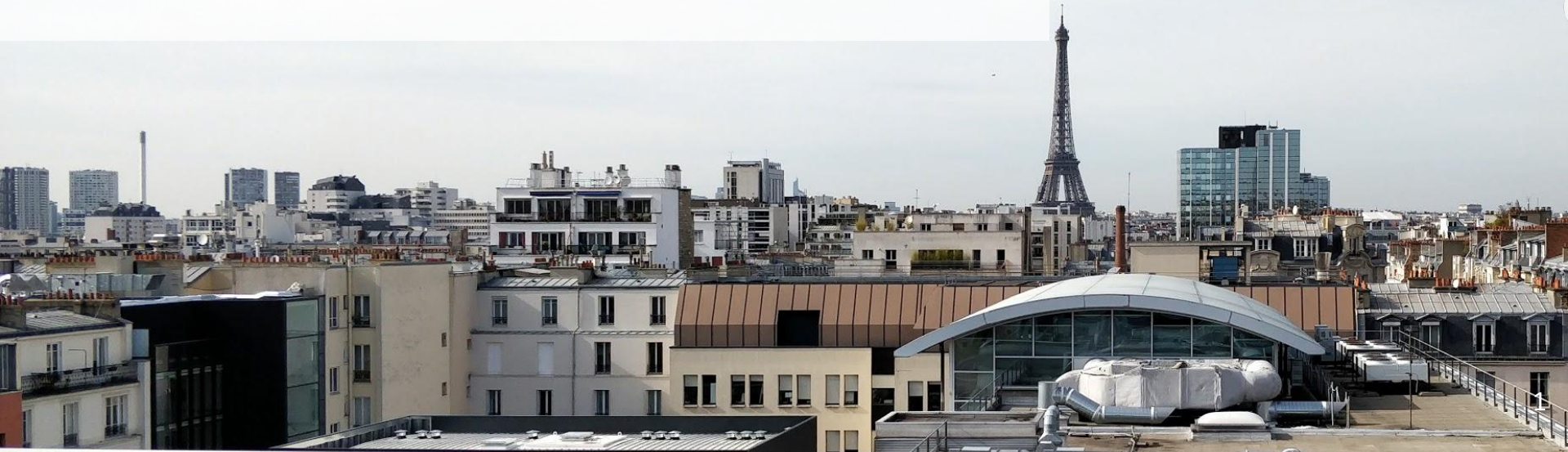


Amine Ghozlane, Ph.D.
Contact : amine.ghozlane@pasteur.fr
Hub de Bioinformatique et de Biostatistique, C3BI, IP
CNRS USR3756



Institut Pasteur

Shiny : développement d'applications brillantes pour la recherche, l'enseignement et les plateformes



First....



I am not paid by RStudio company



I don't develop shiny app every day
I am not an expert



I don't recommend SHINY in all your projects



I have a very basic knowledge in term security
= Not my job

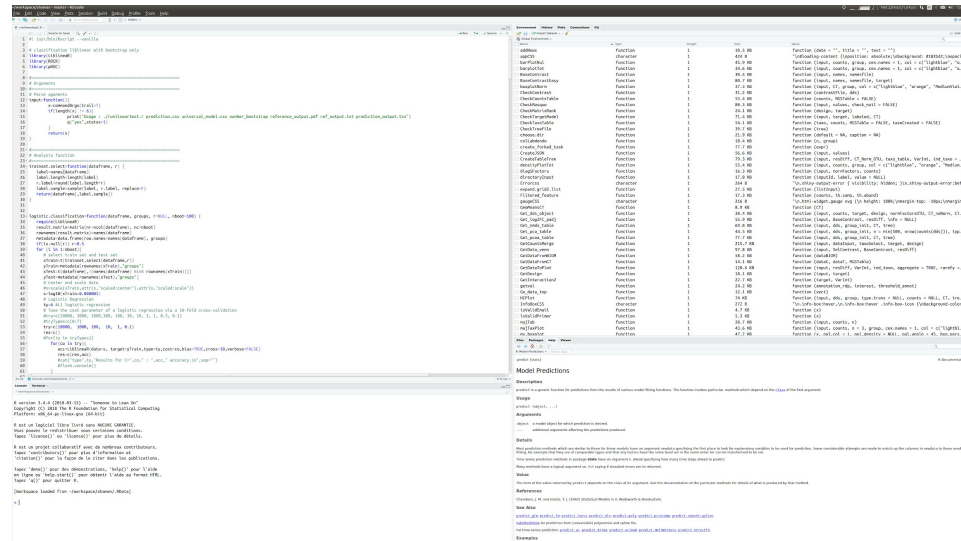


This presentation contains my personal opinion
and it involves only me

What is shiny ?

Shiny is an R package that makes it easy to build interactive web apps straight from R. You can host standalone apps on a webpage or embed them in [R Markdown](#) documents or build [dashboards](#). You can also extend your Shiny apps with [CSS themes](#), [htmlwidgets](#), and JavaScript [actions](#).

Developed by Rstudio
company:



You write R code and it's your website

What is shiny ?

Server.R

```
shinyServer(function(input, output, session) {  
  hide(id = "loading-content", anim = TRUE, animType = "fade", time=1.5)  
  hide(id = "loading-content-bar", anim = TRUE, animType = "fade", time=1.5)  
  #####  
  ##          LOAD FILES  
  ##  
  ## Create base for contrast  
  rand = floor(runif(1,0,1e9))  
  namesfile = tempfile(pattern = "BaseContrast", tmpdir = tempdir(), fileext = "")  
  file.create(namesfile, showWarnings=FALSE)  
  target = NULL  
  ## JSON name for masque  
  curdir = getwd()  
  json_name = tempfile(pattern = "file", tmpdir = paste(curdir, "www", "masque", "todo", sep = ".Platform$file.sep", fileext = ".json")  
  ## Pass for MASQUE  
  pass = gsub("file", "", basename(file_path_sans_ext(json_name)))  
  ## Popup messages  
  observe(if(input$addReg$scatter) info("By adding the regression line, you will lose interactivity."))  
  ## Reactive target  
  values <- reactiveValues(TargetWorking = target, labeled=NULL, fastq_names_only=NULL, R1fastQ=NULL, R2fastQ=NULL,  
    json_name=json_name, num=0, pass=pass, login_email = NULL, is_valid = NULL,  
    bion_masque = NULL, tree_masque=NULL, masque_key = NULL, count_table_masque = NULL,  
    rdg_annot_masque = NULL, rdg_thres_masque = NULL,  
    paths_fastq_tmp=NULL, curdir=curdir, error_progress=FALSE)  
  ## Counts file  
  dataInputCounts <- reactive({  
    data = NULL  
    inFile <- input$fileCounts  
    if (is.null(inFile) && is.null(values$count_table_masque)) return(NULL)  
    #if (is.null(inFile)) return(NULL)  
    if (is.null(values$count_table_masque) && file.exists(values$count_table_masque)){  
      tryCatch(read.csv(values$count_table_masque, sep = "\t", header=TRUE, check.names=FALSE)-->data,  
        error=function(e) sendSweetAlert(messageId="ErrorCounts",  
          title = "Oops",  
          text=paste("The count file can not be read in SHAMAN.\n {n}",e), type = "error"))  
    }  
    else{  
      tryCatch(read.csv(inFile$datapath, sep=input$sepcount, header=TRUE, check.names=FALSE)-->data,  
        error=function(e) sendSweetAlert(messageId="ErrorCounts",  
          title = "Oops",  
          text=paste("Your file can not be read in SHAMAN.\n {n}",e), type = "error"))  
    }  
  })  
}
```

Make them
communicate



User Interface.R

```
function(request) {  
  sidebar <- dashboardSidebar(  
    useShinyjs(),  
    inlineCSS(appCSS),  
    # tags$head(  
    #   tags$script(src = "custom.js")  
    # ),  
    div(id = "loading-content-bar",  
      p()),  
    div(  
      id = "app-content-bar",  
      sidebarMenu(id = "side",  
        menuItem("Home", tabName = "Home", icon = icon("home")),  
        menuItem("Tutorial", tabName = "Tutorial", icon = icon("book")),  
        menuItem("Download/Install", tabName = "Download", icon = icon("download")),  
        menuItem("Raw data", tabName = "RawData", icon = icon("upload")),  
        menuItem("Upload your data", tabName = "Upload", icon = icon("upload")),  
        #book$button(),  
        menuItemOutput("dymMenu"),  
        img(src = "logo.jpg", height = 49, width = 220, style="position:absolute;bottom:0;margin:0 15px 10px;")  
      )  
    )  
  )  
  body <- dashboardBody(  
    tags$style(type="text/css", Errorcss),  
    useFontAwesome(),  
    useShinyjs(),  
    inlineCSS(appCSS),  
    div(  
      id = "loading-content",  
      br(),  
      br(),  
      h2("Please wait while SHAMAN is loading..."),  
      div(  
        id = "app-content-bar",  
        tabItems(  
          tabItem(tabName = "Home",  
            fluidRow(  
              column(width=9,  
                div(style="width:100% ; max-width: 1200px; height: 550px",  
                  tabBox(title="Welcome to SHAMAN", id="tabset1", width=NULL,  
                    # tags$script(type="text/javascript", language="javascript", src="google-analytics.js"),  
                    tabPanel("About",  
                      p("SHAMAN is a Shiny application for Metagenomic Analysis including the normalization  
                        the differential analysis and multiple visualization.", style = "font-family  
                        p("SHAMAN is based on DESeq R package", a("[Anders and Huber 2010]", href="http://n  
                        ". SHAMAN robustly identifies the differential abundant genera with the Generalize  
                        Resulting p-values are adjusted according to the Benjamini and Hochberg procedure  
                        The PCOA is performed with the", a("ade4 R package", href="http://pbill.univ-lyon1.f  
                        A presentation about SHAMAN is available", a("here", target="_blank", href="shaman.p  
                        "SHAMAN is compatible with standard formats for metagenomic analysis. We also prov  
                        p("Hereafter is the global workflow of the SHAMAN application:");  
                        div(img(src = "Workflow_sh.png", width = "100%", height = "100%", style="max-width: 800  
                        );  
                    tabPanel("Authors", h3("The main contributors to SHAMAN:");  
                      p(a("Stevven Volant", href="mailto:stevven.volant@pasteur.fr"), "(Initiator, coding,  
                        p(a("Anine Ghozlane", href="mailto:anine.ghozlane@pasteur.fr"), "(Coding, testing, do
```

What is shiny ?

In one file

```
1 library(shiny)
2 library(shinydashboard)
3
4 # Define UI for application that draws a histogram
5 ui <- function(request) {
6   sidebar <- dashboardSidebar(
7     div(
8       sidebarMenu(id = "side",
9         menuItem("Home", tabName = "Home", icon = icon("home"))
10      )
11    )
12  )
13
14  body <- dashboardBody(
15    div(
16      tabItems(
17        tabItem(tabName = "Home",
18          column(width=12,
19            box(title="A box for the", width = 6, status = "primary",
20              # Input: Slider for the number of bins ----
21              sliderInput(inputId = "bins",
22                label = "Number of bins:",
23                min = 1,
24                max = 50,
25                value = 30, width = '100%')
26            ),
27            column(width=12,
28              column(width=6,
29                plotOutput(outputId = "distPlot", width = "100%")
30              )
31            )
32          )
33        )
34      )
35    )
36
37    dbHeader <- dashboardHeader(title = "Demo shiny")
38    # Put them together into a dashboardPage
39    dashboardPage(skin="blue",
40      dbHeader,
41      sidebar,
42      body)
43  }
44
45 # Define server logic required to draw a histogram
46 server <- function(input, output) {
47   output$distPlot <- renderPlot({
48     # Faithful provide data
49     x <- faithful[, 2]
50     bins <- seq(min(x), max(x), length.out = input$bins + 1)
51     # draw the histogram with the specified number of bins
52     hist(x, breaks = bins, col = 'darkgray', border = 'white')
53   })
54 }
55
56 # Run the application
57 shinyApp(ui = ui, server = server)
```

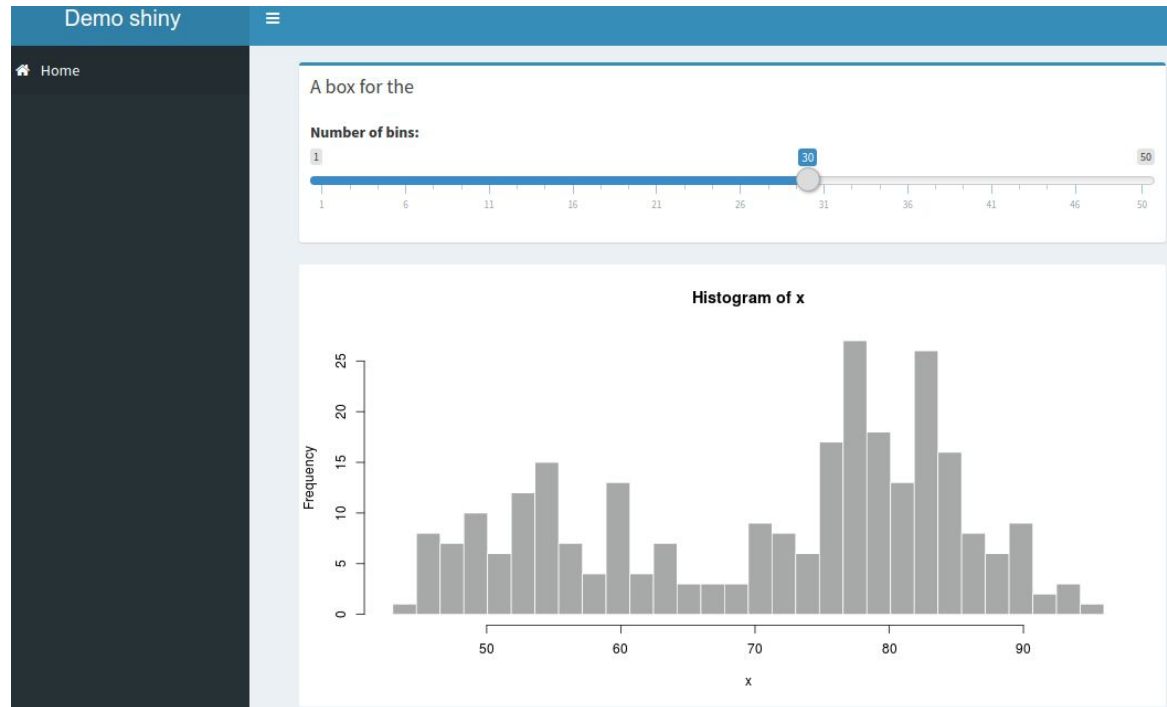
In three, with a global file to order library loading

```
# Allow to upload 50M files only shaman server
#if(Sys.info()["nodename"] == "ShinyPro"){
#  options(shiny.maxRequestSize=1000000000*1024^2)
#}else{
#  Limit with the raw data submission to 2Gb
options(shiny.maxRequestSize=2000000000)
#}
```

```
source('LoadPackages.R')
source("css/owncss.R")
source("Rfunctions/Data_Management.R")
source("Rfunctions/Stat_Model.R")
source("Rfunctions/DiagPlot.R")
source("Rfunctions/VisuPlot.R")
source("Rfunctions/CompPlot.R")
source("Rfunctions/DiffTable.R")
source('Rfunctions/directoryInput.R')
source('Rfunctions/internal_masque.R')
```

Just an insight of the basics

```
1 library(shiny)
2 library(shinydashboard)
3
4 # Define UI for application that draws a histogram
5 ui <- function(request) {
6   sidebar <- dashboardSidebar(
7     div(
8       sidebarMenu(id = "side",
9         menuItem("Home", tabName = "Home", icon = icon("home"))
10      )
11    )
12  )
13
14  body <- dashboardBody(
15    div(
16      tabItems(
17        tabItem(tabName = "Home",
18          column(width=12,
19            box(title="A box for the", width = 6, status = "primary",
20              # Input: Slider for the number of bins ----
21              sliderInput(inputId = "bins",
22                label = "Number of bins:",
23                min = 1,
24                max = 50,
25                value = 30, width = '100%')
26            )),
27          column(width=12,
28            column(width=6,
29              plotOutput(outputId = "distPlot", width = "100%")
30            )
31          )
32        )
33      )
34    )
35  )
36
37  dbHeader <- dashboardHeader(title = "Demo shiny")
38  # Put them together into a dashboardPage
39  dashboardPage(skin="blue",
40    dbHeader,
41    sidebar,
42    body)
43 }
44
45 # Define server logic required to draw a histogram
46 server <- function(input, output) {
47   output$distPlot <- renderPlot({
48     # Faithful provide data
49     x <- faithful[, 2]
50     bins <- seq(min(x), max(x), length.out = input$bins + 1)
51     # draw the histogram with the specified number of bins
52     hist(x, breaks = bins, col = 'darkgray', border = 'white')
53   })
54 }
55
56 # Run the application
57 shinyApp(ui = ui, server = server)
```



Personalize shiny

SHAMAN is a SHiny application for Metagenomic ANalysis including the normalization, the differential analysis and multiple visualization.

SHAMAN is based on DESeq2 R package [Anders and Huber 2010] for the analysis of metagenomic data, as suggested in [McMurdie and Holmes 2014, Jonsson2016]. SHAMAN robustly identifies the differential abundant genera with the Generalized Linear Model implemented in DESeq2 [Love 2014]. Resulting p-values are adjusted according to the Benjamini and Hochberg procedure [Benjamini and Hochberg 1995]. The PCOA is performed with the ade4 R package and plots are generated with ggplot2 or D3.js packages. A presentation about SHAMAN is available here and a poster here. SHAMAN is compatible with standard formats for metagenomic analysis. We also provide a complete pipeline for OTU picking and annotation named MASQUE used in production at Institut Pasteur.

Hereafter is the global workflow of the SHAMAN application:

```
graph LR
    subgraph Input_files [Input files]
        C[Counts]
        A[Annotation]
        M[Metadata target file]
        B[Biom]
    end
    subgraph Statistical_Analysis [Statistical Analysis]
        N[Normalization at OTU level  
modified RLE approach]
        M2[Merging normalized counts  
at the user selected level]
        F[Filtering the features  
optional step]
        R[Run DESeq2]
    end
    subgraph Differential_Analysis [Differential Analysis]
        D[Define contrasts vectors  
comparisons]
        G[Get differential abundant  
features]
    end
    subgraph Diagnostic_plots [Diagnostic plots]
        P[Heatmap]
        B[Barplot]
        S[Stacked barplot]
        A2[Abundance tree]
    end
    subgraph Visualiz [Visualiz]
        V[Visualization]
    end

    Input_files --> Statistical_Analysis
    Statistical_Analysis --> Differential_Analysis
    Differential_Analysis --> Diagnostic_plots
    Diagnostic_plots --> Visualiz
```

Y aghozlane / shinydashboard
forked from rstudio/shinydashboard

Shiny Dashboarding framework <https://rstudio.github.io/shinydashbo...>

Manage topics

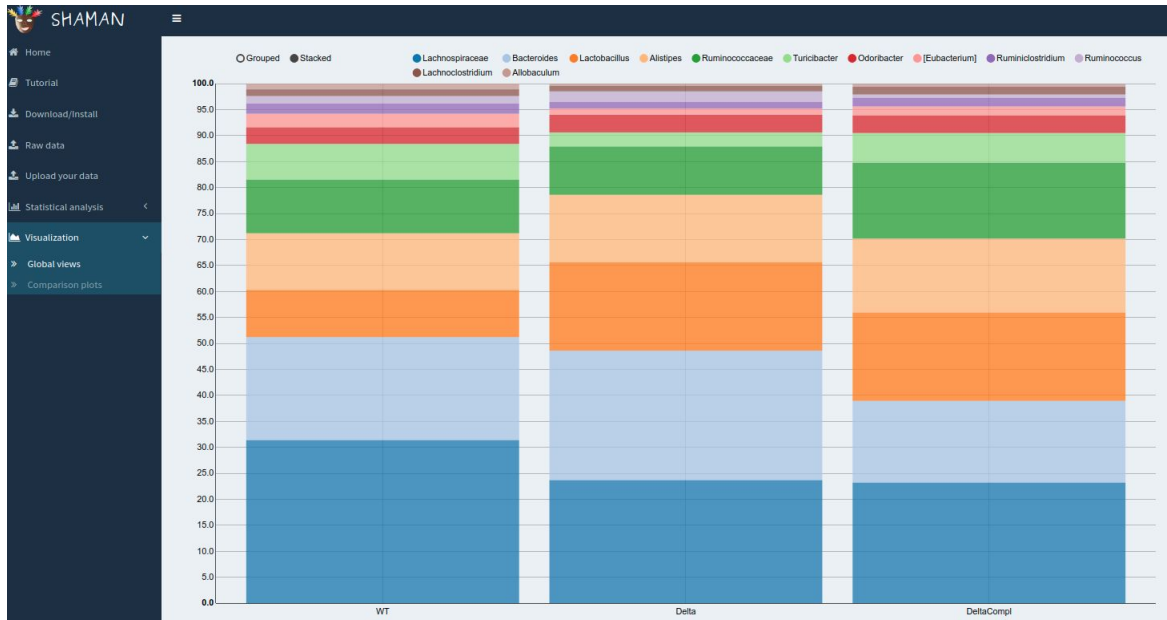
240 commits 2 branches 5 releases 3 contributors

Branch: master New pull request Create new file Upload files Find file Clone or download

This branch is 1 commit ahead, 68 commits behind rstudio:master. Pull request Compare

File	Description	Last commit
R	Don't try to restore tabs if there's no ID. Closes #160	2 years ago
inst	Add Pasteur theme	2 years ago
man	Mention that id is required for bookmarking tabs	2 years ago
tests-manual	Improve description file, and also add more comments for manual tests.	3 years ago
tools	Minify AdminLTE files	4 years ago
.Rbuildignore	Use AppVeyor	2 years ago
.gitattributes	Treat minified files as binary	4 years ago
.gitignore	Ignore Rnb.cached	3 years ago
.travis.yml	Update Travis config	2 years ago
DESCRIPTION	Update NEWS and bump version to 0.5.3	2 years ago
LICENSE	Update DESCRIPTION and LICENSE	4 years ago
NAMESPACE	roxygenize + update description file	3 years ago
NEWS.md	Update NEWS and bump version to 0.5.3	2 years ago
README.md	Use AppVeyor	2 years ago
appveyor.yml	Add appveyor.yml	2 years ago
shinydashboard.Rproj	Rename Rproj file	4 years ago

Insert Javascript



Server.R

```
plotd3 <- nvd3Plot(Proportions ~ AllVar | Taxonomy,  
plotd3$chart(stacked = TRUE)  
if(input$SensPlotVisu == "Vertical") {  
  plotd3$chart(reduceXTicks = FALSE)  
  plotd3$xAxis(rotateLabels = XRotate)  
}
```

User Interface.R

```
uiOutput("TaxoToPlotVisu")
```

Sometimes interaction between javascript variables

Shiny-ception



Github aghozlan Kronarshy: `tags$iframe(src = "http://Url/KronaRShy/?parameter=/tmp/text.txt",height = "1000px",width = "1000px")`

Server.R

```
if(Sys.info()["nodename"] == "ShinyPro"){  
  res = tags$iframe(src=paste0("http://hub05.hosting.pasteur.fr/aghozlane/KronaRShy/?parameter=",Krona()),  
  ]
```

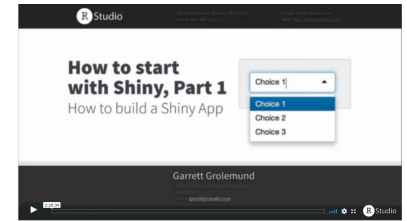
User Interface.R

```
uiOutput("TaxoToPlotVisu")
```

On the developer side



5 min coding and you have a website
= Any intern student can do it



Documentation is great
Tutorial / Video / API / Stackoverflow



Very few difference between local and
production



The only issue is R

R for web development is a bad idea

In large project like SHAMAN, we have 44 R packages in interaction

- Updates are an issue
- Packages developers never check for backward compatibility

```
Package: nlme
Version: 3.1-131.1
Date: 2018-02-16
Priority: recommended
Title: Linear and Nonlinear Mixed Effects Models
Authors@R: c(person("José", "Pinheiro", role = "aut", comment = "S version"),
  person("Douglas", "Bates", role = "aut", comment = "up to 2007"),
  person("Saikat", "DebRoy", role = "ctb", comment = "up to 2002"),
  person("Deepayan", "Sarkar", role = "ctb", comment = "up to 2005"),
  person("EISPACK authors", role = "ctb", comment = "src/rs.f"),
  person("Siem", "Heisterkamp", role = "ctb", comment = "Author fixed sigma"),
  person("Bert", "Van Willigen", role = "ctb", comment = "Programmer fixed sigma"),
  person("R-core", email = "R-core@R-project.org",
    role = c("aut", "cre")))
Description: Fit and compare Gaussian linear and nonlinear mixed-effects models.
Depends: R (>= 3.1.2)
Imports: graphics, stats, utils, lattice
Suggests: Hmisc, MASS
LazyData: yes
ByteCompile: yes
Encoding: UTF-8
License: GPL (>= 2) | file LICENCE
BugReports: https://bugs.r-project.org
NeedsCompilation: yes
Packaged: 2018-02-16 16:42:40 UTC; ripley
Author: José Pinheiro [aut] (S version),
  Douglas Bates [aut] (up to 2007),
  Saikat DebRoy [ctb] (up to 2002),
  Deepayan Sarkar [ctb] (up to 2005),
  EISPACK authors [ctb] (src/rs.f),
  Siem Heisterkamp [ctb] (Author fixed sigma),
  Bert Van Willigen [ctb] (Programmer fixed sigma),
  R-core [aut, cre]
Maintainer: R-core <R-core@R-project.org>
Repository: CRAN
Date/Publication: 2018-02-16 17:39:29 UTC
```

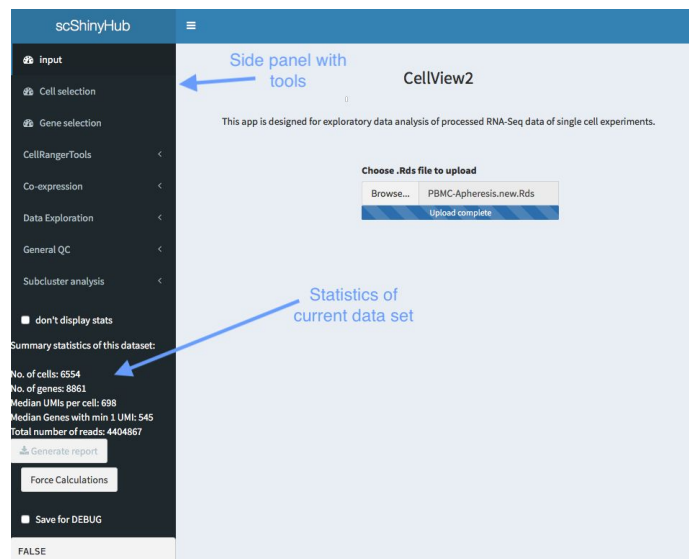
Deploy a shiny app

- Shiny server open source
 - 1 server or 1 docker = 1 application
 - 1 user click at a time
 - Used in Pasteur by some platforms



✗ Not a way to make your application popular
Practical sessions are infeasible
99% of user will not use your docker !

<https://github.com/baj12/scShinyHub>



scShinyHub

Side panel with tools

CellView2

This app is designed for exploratory data analysis of processed RNA-Seq data of single cell experiments.

Choose .Rds file to upload

Browse... PBMC-Apheresis.new.Rds

Upload complete

Statistics of current data set

Summary statistics of this dataset:

No. of cells: 6554
No. of genes: 8861
Median UMIs per cell: 698
Median Genes with min 1 UMI: 545
Total number of reads: 4404867

Generate report

Force Calculations

Save for DEBUG

FALSE

Deploy a shiny app

- Shinyproxy
1 server = N application
Deploy docker on the fly

I did not manage to make it work on my desktop




<https://www.shinyproxy.io>

ABOUT

ShinyProxy
About
Getting Started
Deploying Apps
Configuration
ShinyProxy in a Container
Security
Usage Statistics
Downloads
Troubleshooting
Support

Java Server Side
ShinyProxy uses time-tested and mature enterprise Java technology bundled nicely as a Spring boot web application.



Docker-based technology
When deploying a Shiny application with ShinyProxy, the application is simply bundled as an R package and installed into a Docker image. Every time a user runs an application, a container spins up and serves the application. This has numerous advantages:

- fully isolated 'workspace' per session
- plug and play different docker images (even with different R versions or different Shiny versions)
- control on memory and cpu usage via the Docker API
- monitoring and debugging using standard Docker tooling




Table of contents
What is ShinyProxy?
Why use it?
Open Source
Java Server Side
Docker-based technology
Open Source Shiny Package

Deploy a shiny app

- Shinyapps
No server
Limited active hours / apps
Used by teams in Pasteur for teachings
Easy to deploy



Only packages that are in official repository



FREE	STARTER	BASIC	STANDARD	PROFESSIONAL
\$0 /month	\$9 /month (or \$100/year)	\$39 /month (or \$440/year)	\$99 /month (or \$1,100/year)	\$299 /month (or \$3,300/year)
New to Shiny? Deploy your applications for FREE.	More applications. More active hours!	Take your users to the next level!	Password protection? Authenticate your users!	Professional has it all! Personalize your domains.
5 Applications	25 Applications	Unlimited Applications	Unlimited Applications	Unlimited Applications
25 Active Hours	100 Active Hours	500 Active Hours	2,000 Active Hours	10,000 Active Hours
● Community Support	● Premium Support	● Performance Boost ● Premium Support	● Authentication ● Performance Boost ● Premium Support	● Authentication ● Account Sharing ● Performance Boost ● Custom Domains ● Premium Support
● Studio Branding				
Sign Up Now	Sign Up Now	Sign Up Now	Sign Up Now	Sign Up Now



Deploy a shiny app

RStudio Shiny Server Pro Pricing

Publish Shiny applications on RStudio Shiny Server Pro.
Contact Sales

RStudio Shiny Server Pro
\$9,995 per year

BUY NOW

Concurrent Users	20
Upgrade Path	Add Concurrent User packs of 20 for \$4,995 and 150 for \$14,995
Commercial License (not AGPL)	●
RStudio Support	●
Deploy Shiny apps and interactive documents to the internet	●
Controlled access via SSL and LDAP, Active Directory, Google OAuth, PAM, proxied authentication, or passwords	●
Tune & Scale applications across multiple processes	●
Metrics & Session Management	●
Pricing	\$9,995/yr



- Shinypro
- 1 server = N application
Easy to deploy / manage for IT
5000€ for academics
Support is not good at all
20 users max at same time
Solution deployed at Pasteur



Deploy a shiny app

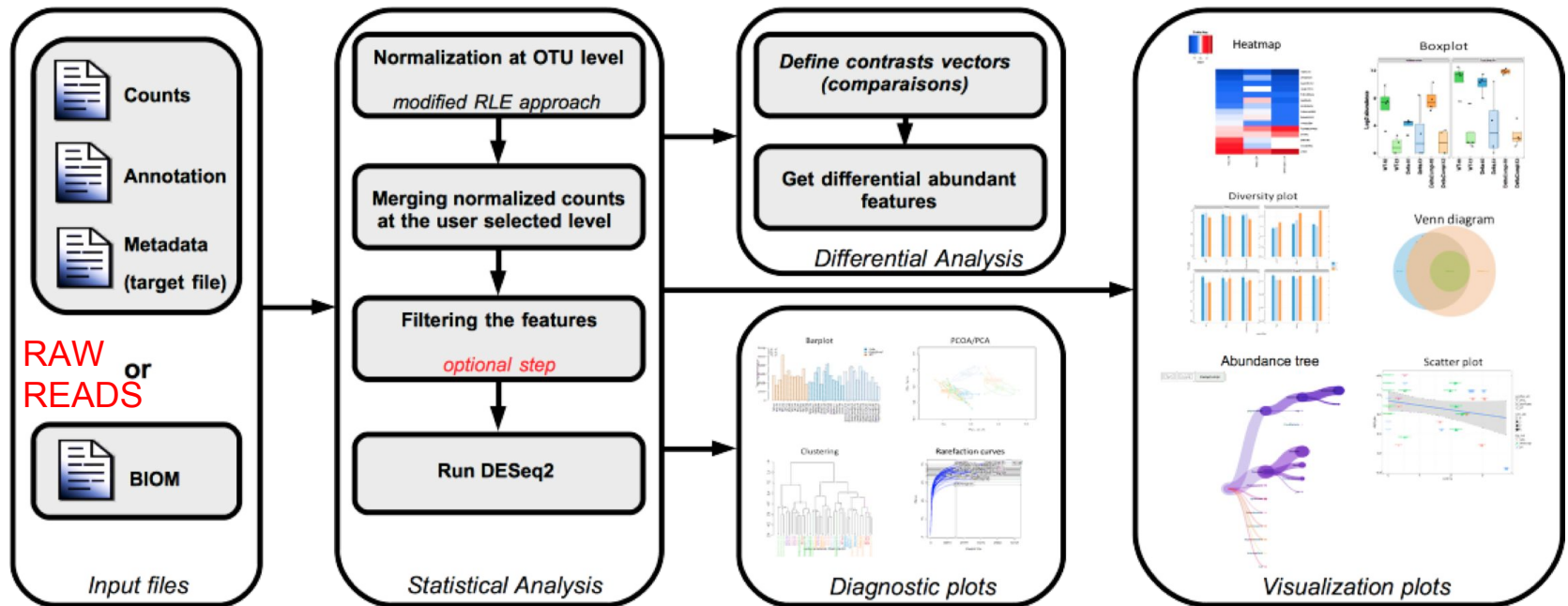
	RStudio Connect Base \$14,995 per year 50 per user/month	RStudio Connect Standard \$24,995 per year 121 per user/month	RStudio Connect Enterprise* \$74,995 per year 3620 per user/month
	CONTACT SALES	CONTACT SALES	CONTACT SALES
Named Users <small>Named Users are publishers of content or have authenticated access to published content.</small>	20	100	1,000
Upgrade Path	Upgrade to Standard	Add Named User Packs of 50 for \$4,995 and 250 for \$14,995	Add Named User Packs of 250 for \$14,995
Scaling <small>Run across a multi-node cluster, providing an option to scale compute horizontally and ensure high availability.</small>	N/A	Add an Execution Server for \$9,995	Please contact sales
Commercial License	●	●	●
RStudio Support	●	●	●
One convenient place to share shiny apps, dashboards, R Markdown reports, and plots	●	●	●
Push-button publishing from RStudio IDE	●	●	●
Scheduled updates and distribution of reports	●	●	●
Self-managed content – view and manage what you've published or can access	●	●	●
Controlled access via SSL and LDAP, Active Directory, Google OAuth, PAM, proxied authentication, or passwords	●	●	●
Tune & scale applications across multiple processes	●	●	●
Metrics & Session Management	●	●	●
Organize, Search, & Tag Content	●	●	●
Host R functions as REST APIs	●	●	●
Pricing	\$14,995/yr	\$24,995/yr	\$74,995/yr



- Rstudio connect
1 server = N application
Easy to deploy / manage for IT
15000€ /year minimum
Deploy apps/markdown from Rstudio



SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



Proudly maintained
since september 2015

SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



30a47fca2dc3

The screenshot shows the SHAMAN web application interface. On the left is a dark sidebar with navigation links: Home, Tutorial, Download/Install, Raw data, and Upload your data. The main content area is divided into three horizontal sections: 'GET A KEY' (Require a valid email address), 'FASTQ FILES' (Load the fastq files), and 'MATCH THE PAIRS' (Only for paired-end sequencing). The 'GET A KEY' section includes a form for email address, a 'Get key' button, and options for 'Paired-end sequencing?' and 'Select the host'. The 'FASTQ FILES' section has a 'Browse...' button and shows 'No file selected'. The 'MATCH THE PAIRS' section has input fields for 'Suffix R1' and 'Suffix R2', and 'Match' and 'Remove file(s)' buttons. On the right side, there are three panels: '0 % Waiting for the data...' with a progress indicator, 'Enter the key' with a text input and 'Check project' button, and 'Summary of your analysis' showing 'Type of data: 16S', 'Paired-end sequencing: n', 'Number of samples: 0', and 'Removed samples: 0' with a 'Save' button. At the bottom center is a 'Check and submit' button. The footer contains logos for Institut Pasteur, CBM, and STTECM.

SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



Your project is done !

OTU building process

4248638

Number of amplicons



1629789

Remaining amplicons after dereplication



40537

Remaining amplicons after removing singletons



34496

Remaining amplicons after removing chimera



63

Number of OTU



16S annotation process

39

Number of OTU annotated by SILVA



39

Number of OTU annotated by Greengenes



62

Number of OTU annotated by RDP



Start statistical analysis

Load the results

Select the database

Silva

Upload the results

Download .zip file

Download the results

Detailed process table

Show 10 entries

Search:

sample	Raw_reads_fwd	Raw_mean_length_fwd	Raw_median_length_fwd	Raw_reads_rev	Raw_mean_length_rev	Raw_median_length_rev	Trimmed	Trimmed_fwd	Trimmed_rev	Removed	Removed_fwd	Removed_rev
1 5ng-25cycles-1_S26_L001_001	216807	300	301	216807	300	300	403438	196888	206550	27842	17587	10255
2 20ng-25cycles-1_S2_L001_001	302678	300	301	302678	300	300	560043	274679	285364	42410	25097	17313
3 1ng-30cycles-1_S50_L001_001	275152	300	301	275152	300	300	509447	250179	259268	37693	21809	15884
4 zero5ng-25cycles-1_S62_L001_001	308283	300	301	308283	300	300	569407	277786	291621	43427	26767	16660

SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



The screenshot displays the SHAMAN web application interface. On the left is a dark sidebar with navigation links: Home, Tutorial, Download/Install, Raw data, and Upload your data. The main content area is divided into several panels:

- 0% Annotated features**: A panel showing the progress of data processing.
- COUNT TABLE**: A panel with an upload icon and the text "Load the count table".
- TAXONOMY TABLE**: A panel with an upload icon and the text "Load the taxonomy table".
- PHYLOGENETIC TREE**: A panel with an upload icon and the text "Load the phylogenetic tree (optional)".

Below these panels are three detailed configuration boxes:

- Select your file format**: A dropdown menu set to "Count table & taxonomy (*.csv or *.tsv)" and a checkbox for "No taxonomy table".
- Load the count table**: Includes "Type" (radio buttons for "OTU/Gene table" and "MGS table"), "Separator" (dropdown set to "Tab"), and "Select your file" (Browse... button, "No file selected").
- Load the taxonomy file**: Includes "Format" (radio buttons for "Table" and "RDP"), "Separator" (dropdown set to "Tab"), and "Select your file" (Browse... button, "No file selected").

A fourth panel, "Load phylogenetic tree (optional)", is partially visible on the right with a plus sign.

SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



100%
Labeled features

TAXONOMY
OTU/Gene, nb features: 39

STATISTICAL ANALYSIS
Differential analysis is done !

CONTRASTS
At least one contrast (non null) must be defined

Experimental design

Select your target file
Browse... Experimental_plan.tsv
Upload complete

Separator: Tab
Select the taxonomy level: OTU/Gene

Select the variables: StartDNA CyclePCR
Add interactions

Run analysis

Options

Contrasts (New)

Compare: 05ng To: 1ng + Add

Contrasts (advanced user)

Select a file of contrasts: Browse... No file selected
Separator: Space

Define contrasts by yourself
Contrast name: + Add contrast

Defined contrasts

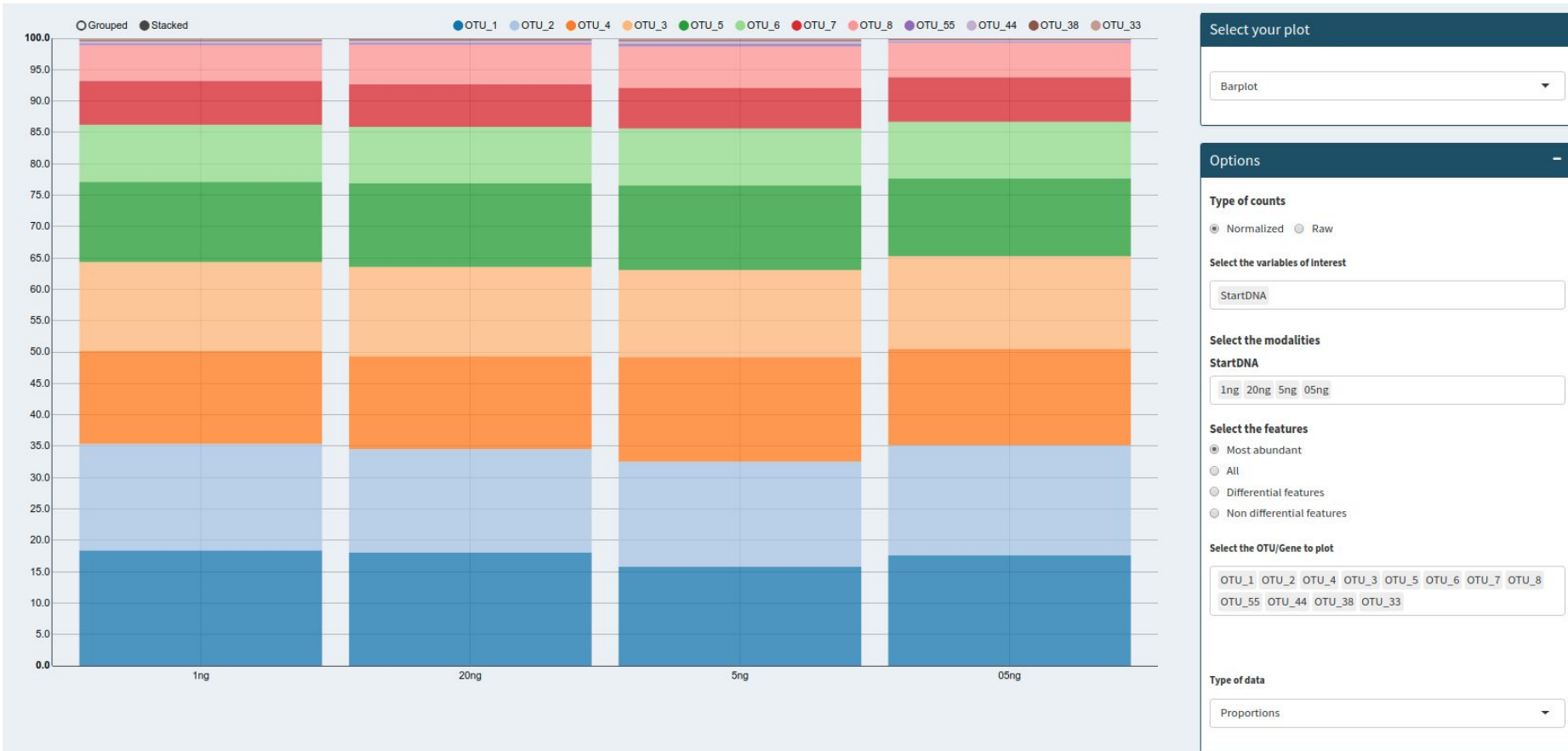
Contrasts

Remove Export

Target file overview +

Count table (OTU/Gene) +

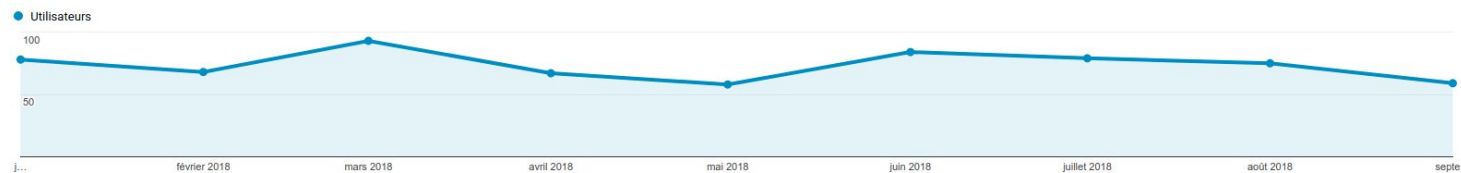
SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



SHAMAN: SHiny Application for Metagenomic - shaman.pasteur.fr



- ✓ We did 5 publications with SHAMAN including Nature microbiology | PNAS | Science Advances
- ✓ 3 publications with no intervention from our part
3 teachings using shaman
- ✓ SHAMAN is also used by private company
- ✓ 499 unique users since January 2018 / 624 downloads



Structural analysis: memhdx.c3bi.pasteur.fr

MEMHDX: Mixed Effects Models for HDX-MS analysis

developed by Stevnn Volant & Veronique Hourdel (Institut Pasteur)

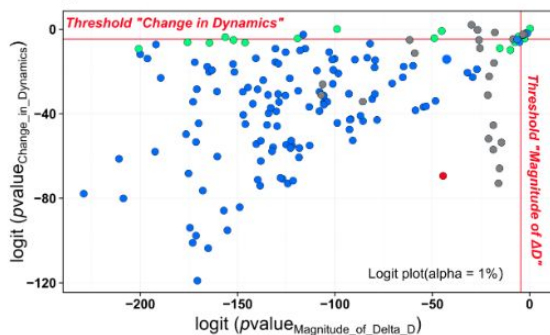
contact us at: [memhdx\[at\]pasteur.fr](mailto:memhdx[at]pasteur.fr)

This tool allows users to perform an automated workflow to analyze, validate and visualize large HDX-MS datasets. The input file is the output of **DynamX software** from Waters and of **HDX Workbench** http://hdx.florida.scripps.edu/hdx_workbench/Home.html. Output files provide a plot of the data, the fitted model for each peptide, a plot of the calculated p -values, and a global visualization of the experiment. User could also obtain an overview of all peptides on the 3D structure.

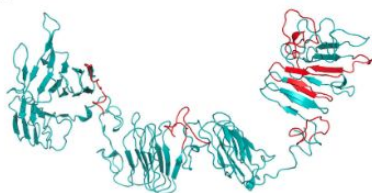


Example of MEMHDX results

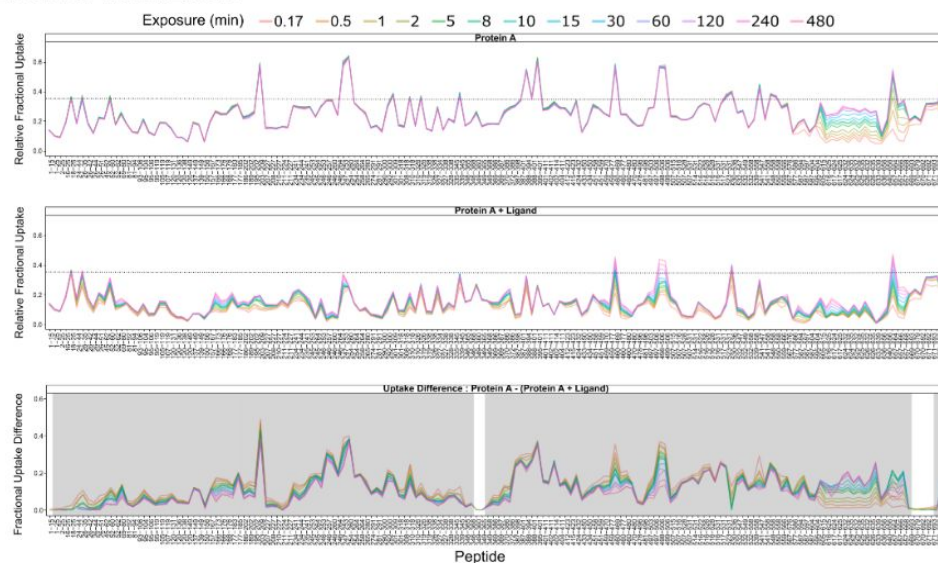
A. Logit Plot



C. 3D View



B. Global Visualization



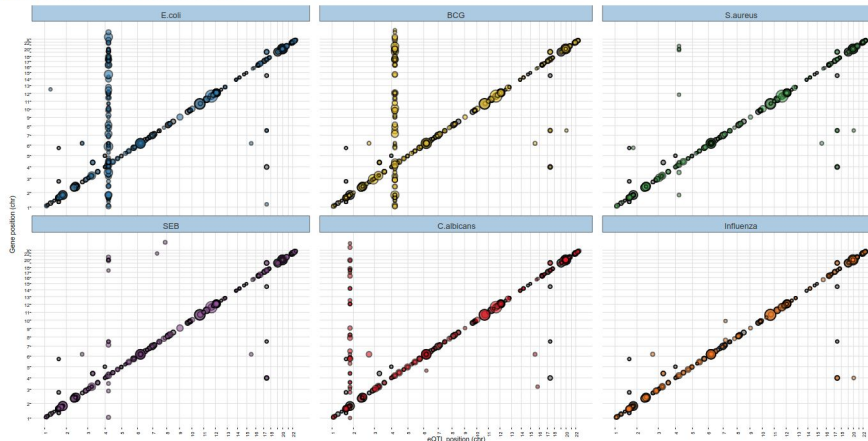
Illustrate your data / Let other biologists take a look at it

misage.pasteur.fr

Overview of genotypic effects on gene expression

135 Genes were found with local Cis eQTLs in the unstimulated state and around 140 genes presenting an eQTL after stimulation. On the other hand, trans-regulation was noticeably stronger after stimulation, particularly with E. coli, BCG, C. albicans and SEB.

Genome wide distribution of eQTLs



mithymus.pasteur.fr

Milieu Interieur sjTREC Prediction Service

Welcome! This work is brought to you by the Milieu Interieur Consortium and is published by Clave et al., 2018.

Guide

The Simple Prediction Service (SPS) is designed to give quick access to study results and outcomes. Use the basic controls on the right to predict sjTREC levels based on an individual's age, gender, and genotype. If you get stuck, please refer to the help section on the left. Full citation and author details may be found in the about section.

Parameters

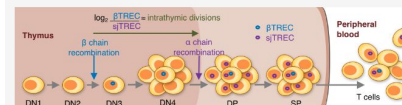
Age: 20-70 (slider set to 40)

Genotype: AA (dropdown)

Gender: Female Male

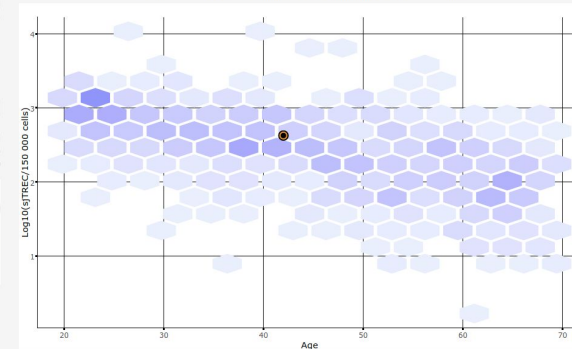
Predict sjTREC levels

Plot height: 200-1,000 (slider set to 200)



Prediction

Predicted sjTREC levels (points) in relation to background data (hex). Use mouse to interact.



Plot background data Plot history Group by gender Group by genotype

DOWNLOAD | PREVIEW | ADD 10 RANDOM

Conclude....

Pro:



Most R developers like shiny



EASY / PRODUCTIVE / FRIENDLY

Cons:



Shinyserver is expensive



Shinyserver is not perfect for production



That's all Folks!