VisRseq: R-based visual analytics software for sequencing data

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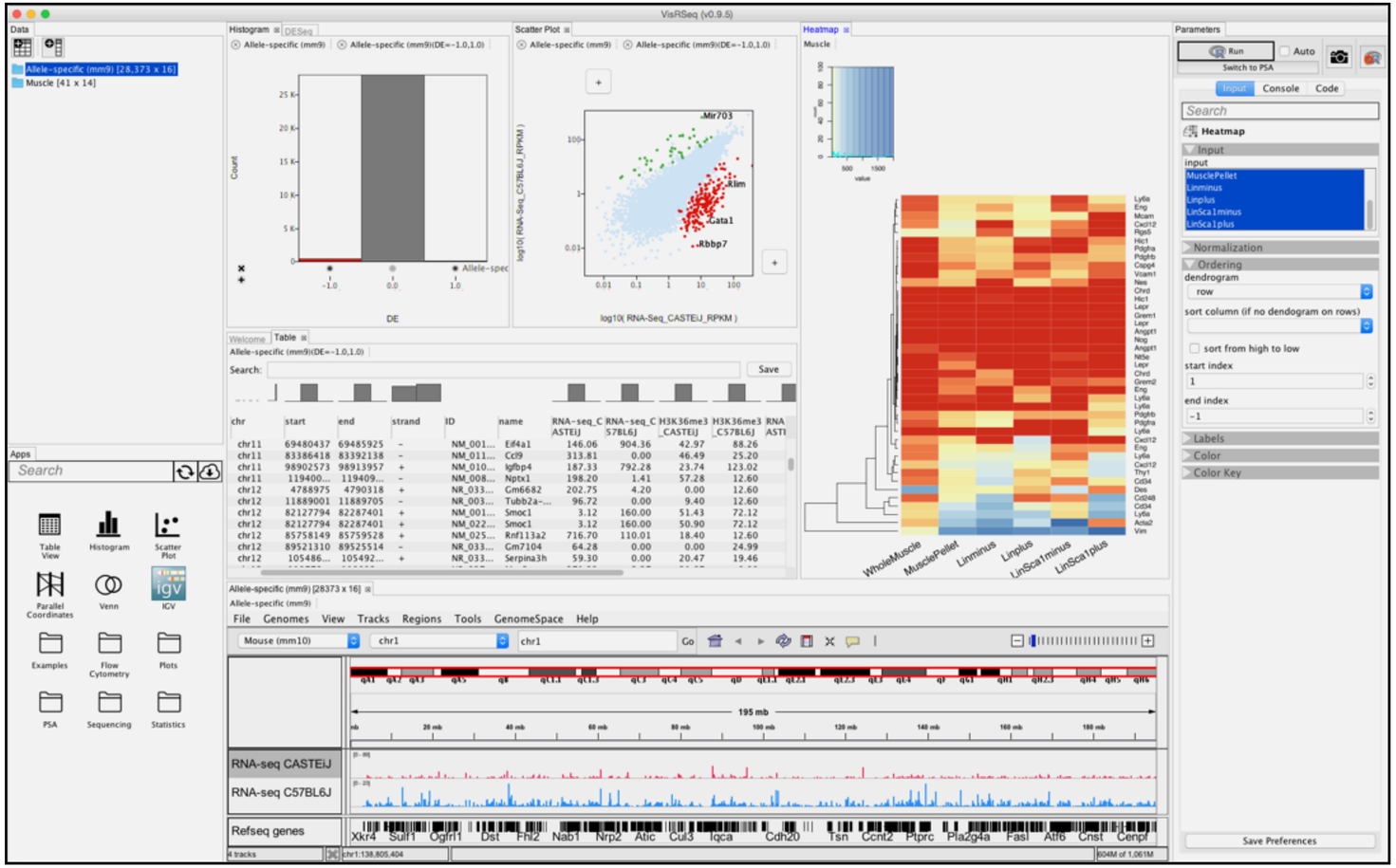
Mohammad M. Karimi — *Biomedical Research Centre, The University of British Columbia, Canada*
Steven J.M. Jones — *Genome Sciences Centre, BC Cancer Agency, Canada*

Overview

- introduction
- motivation
- VisRseq
- case study
- future works



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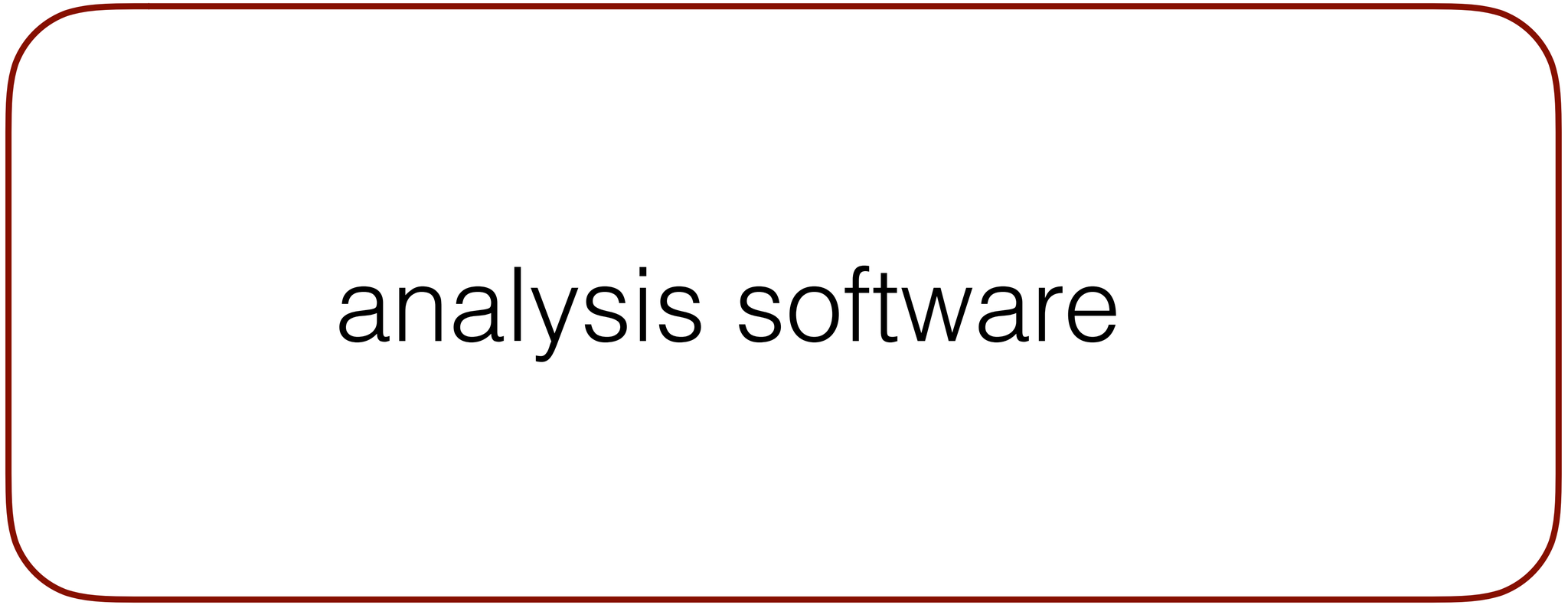

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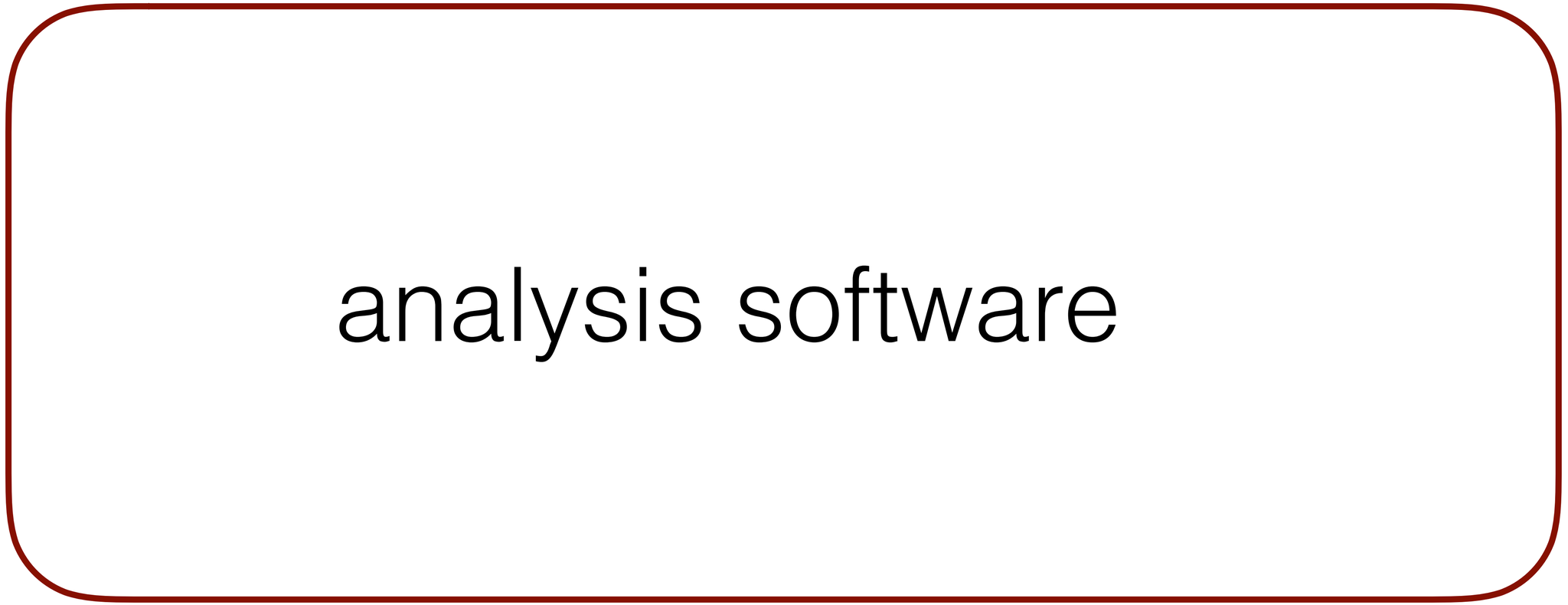

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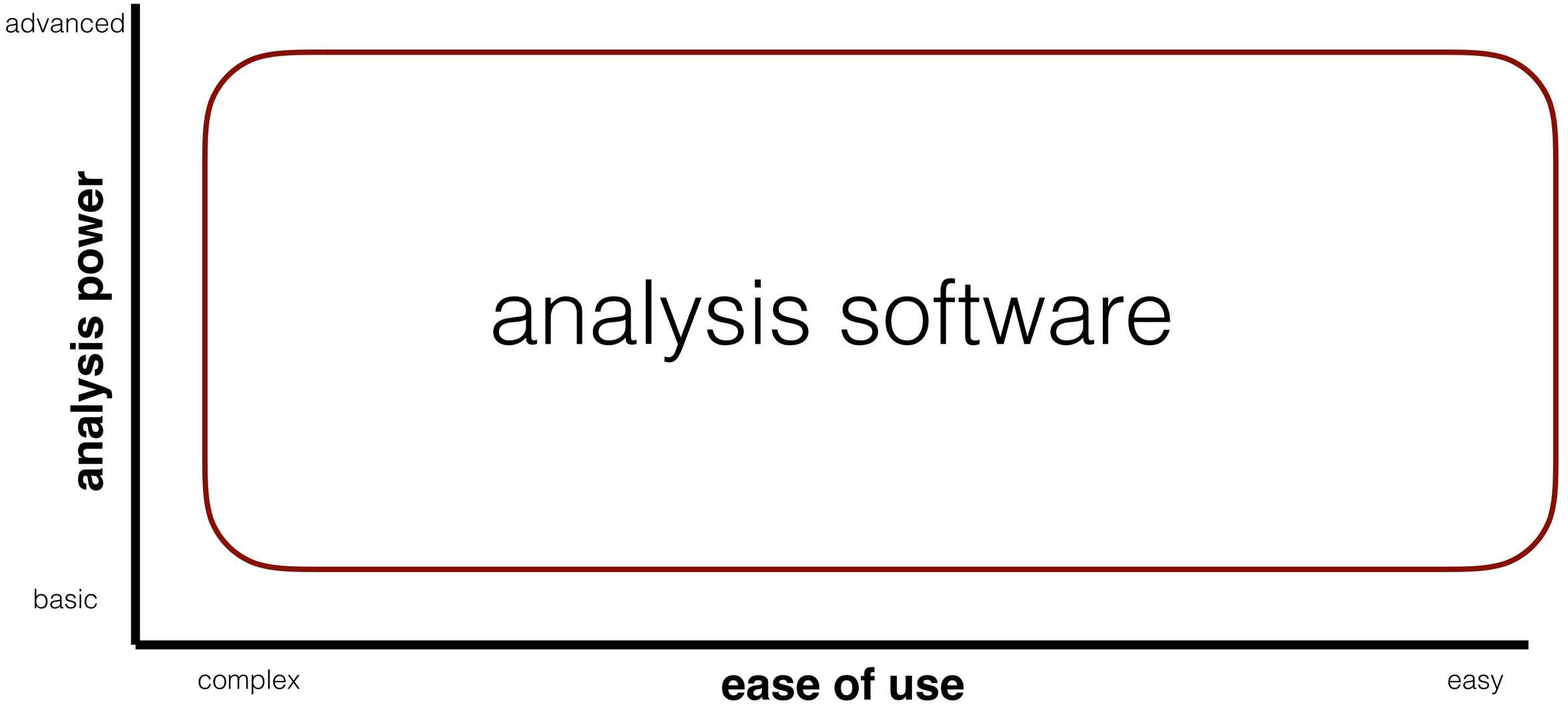
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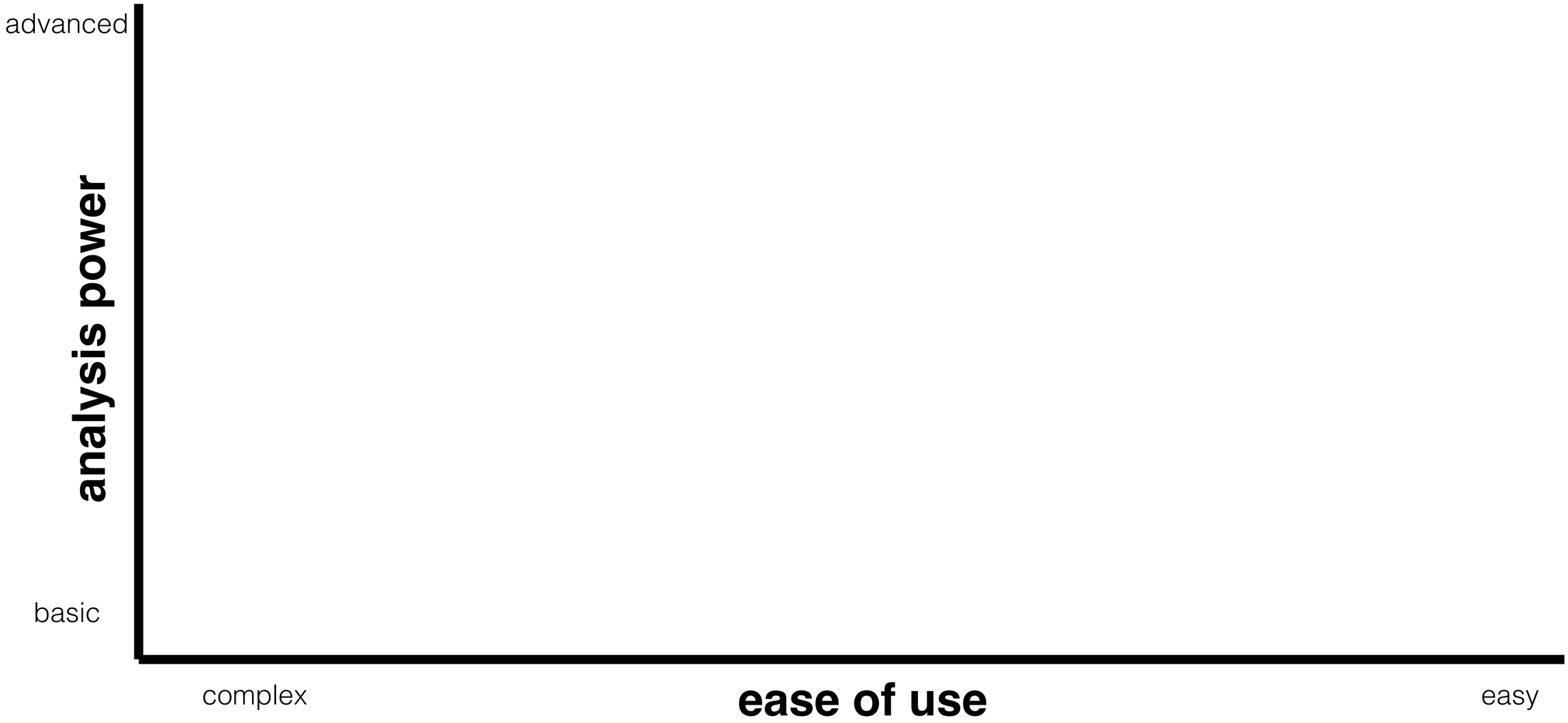
motivation



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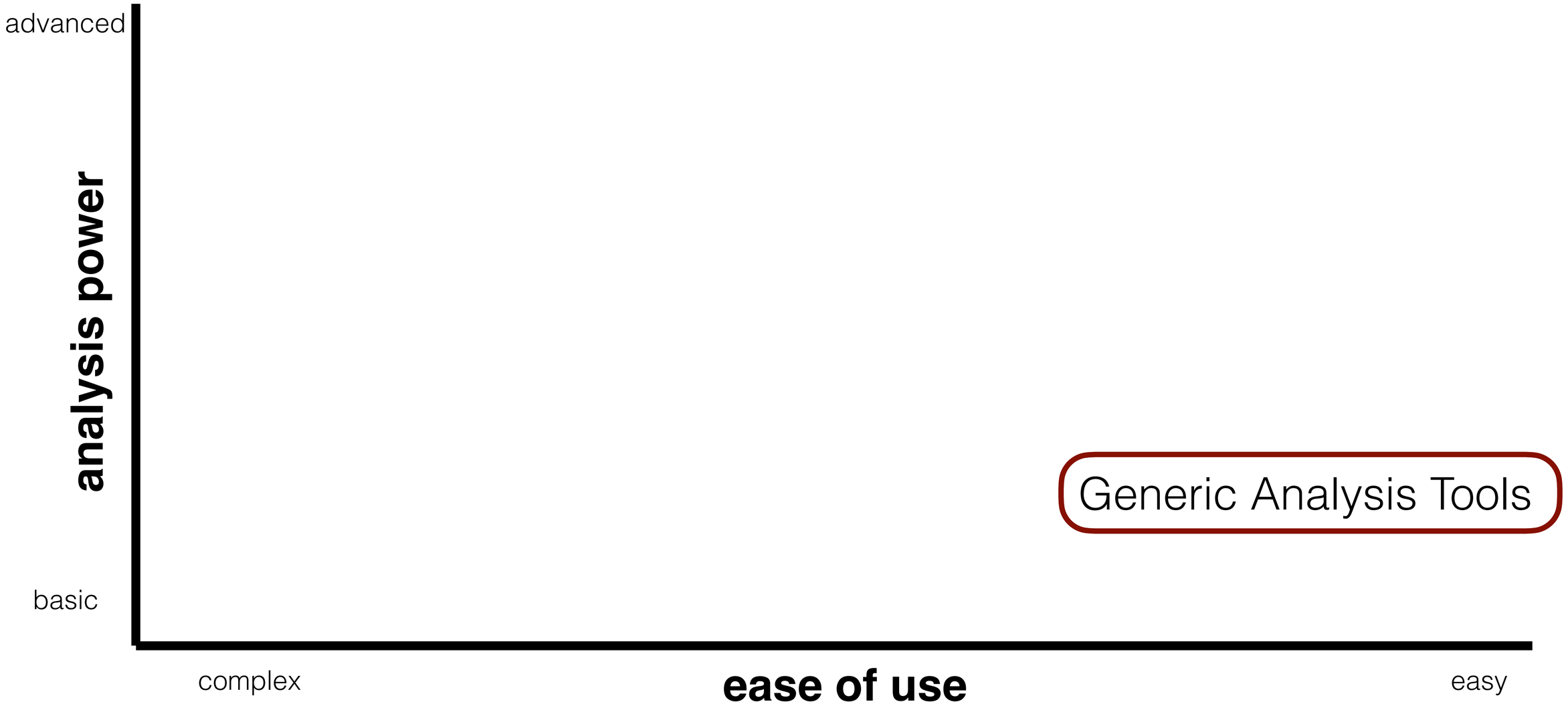
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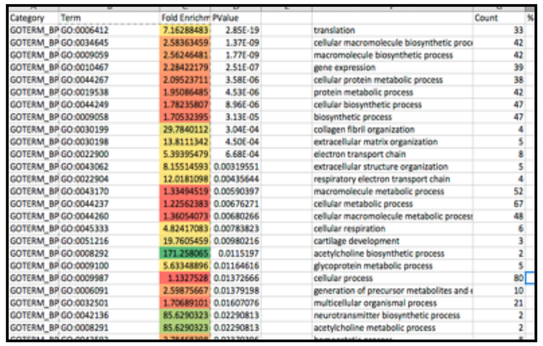

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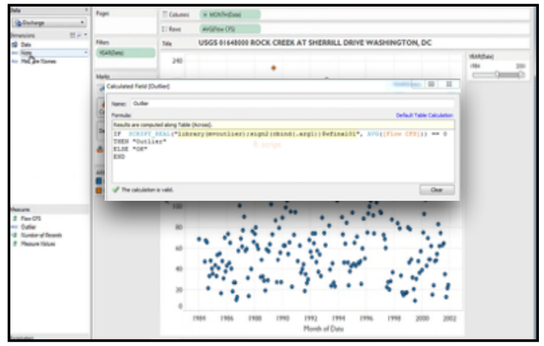

Tableau

Generic Analysis Tools

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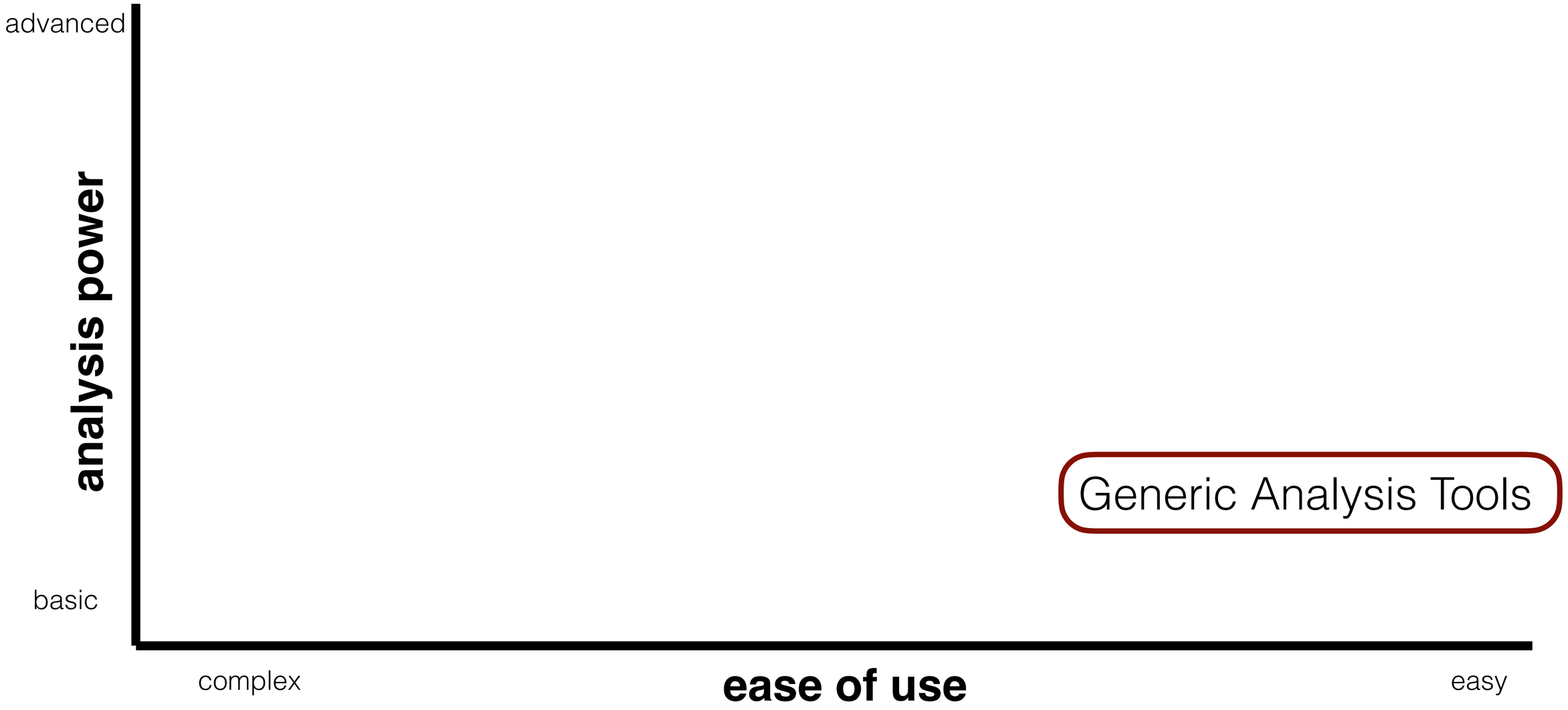
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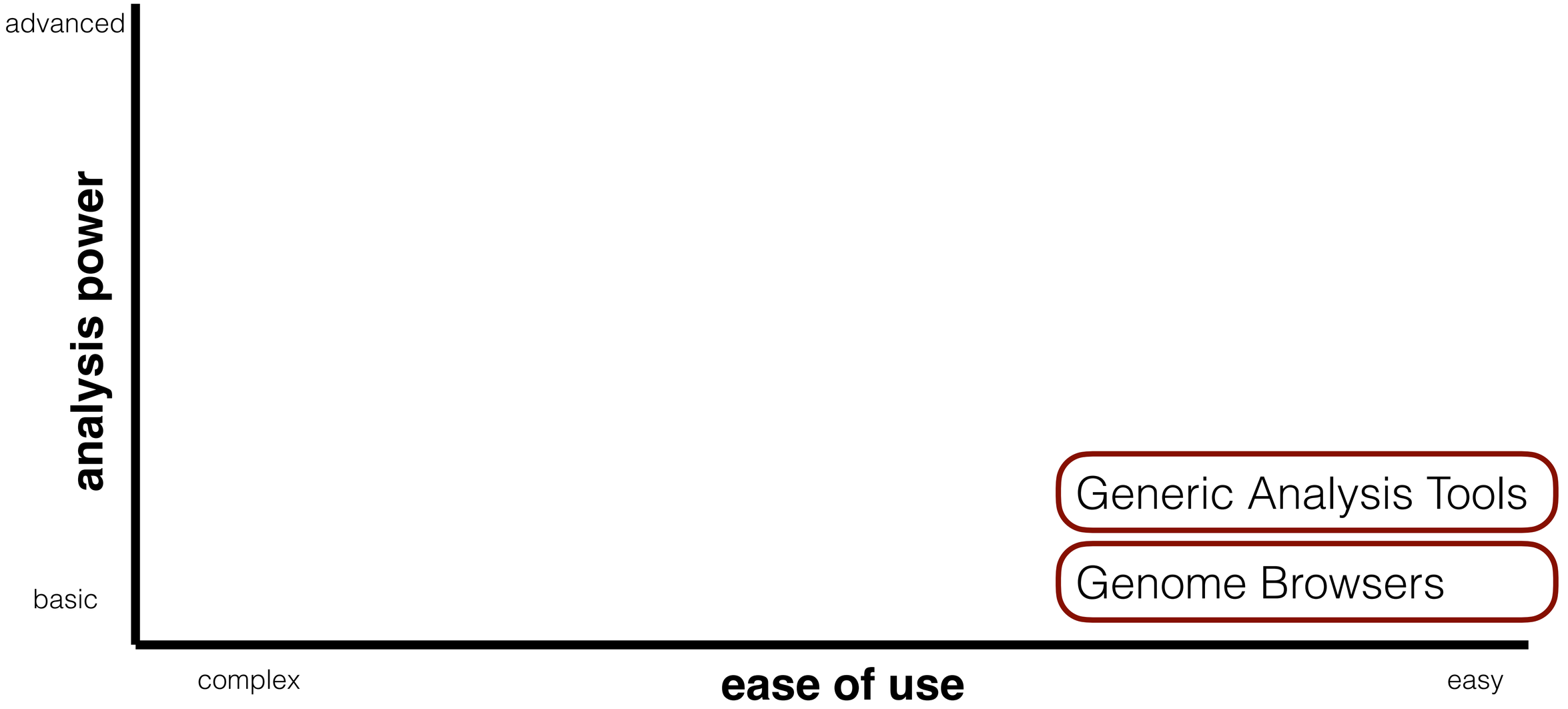
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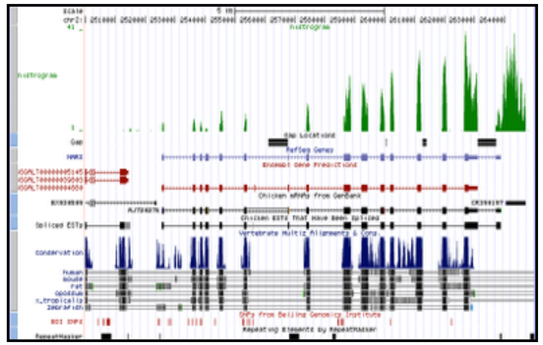
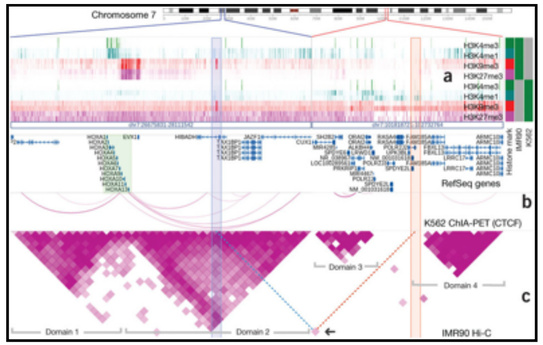
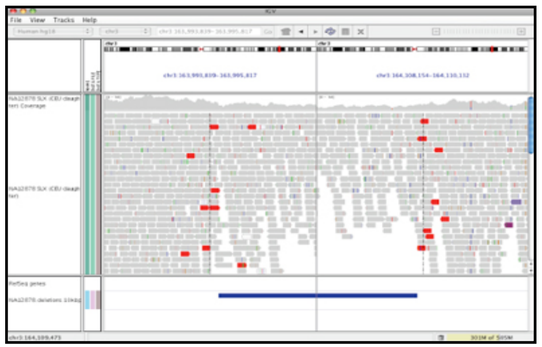


UCSC Genome Browser



WashU Epigenome Browser



Integrated Genome Viewer

Generic Analysis Tools

Genome Browsers

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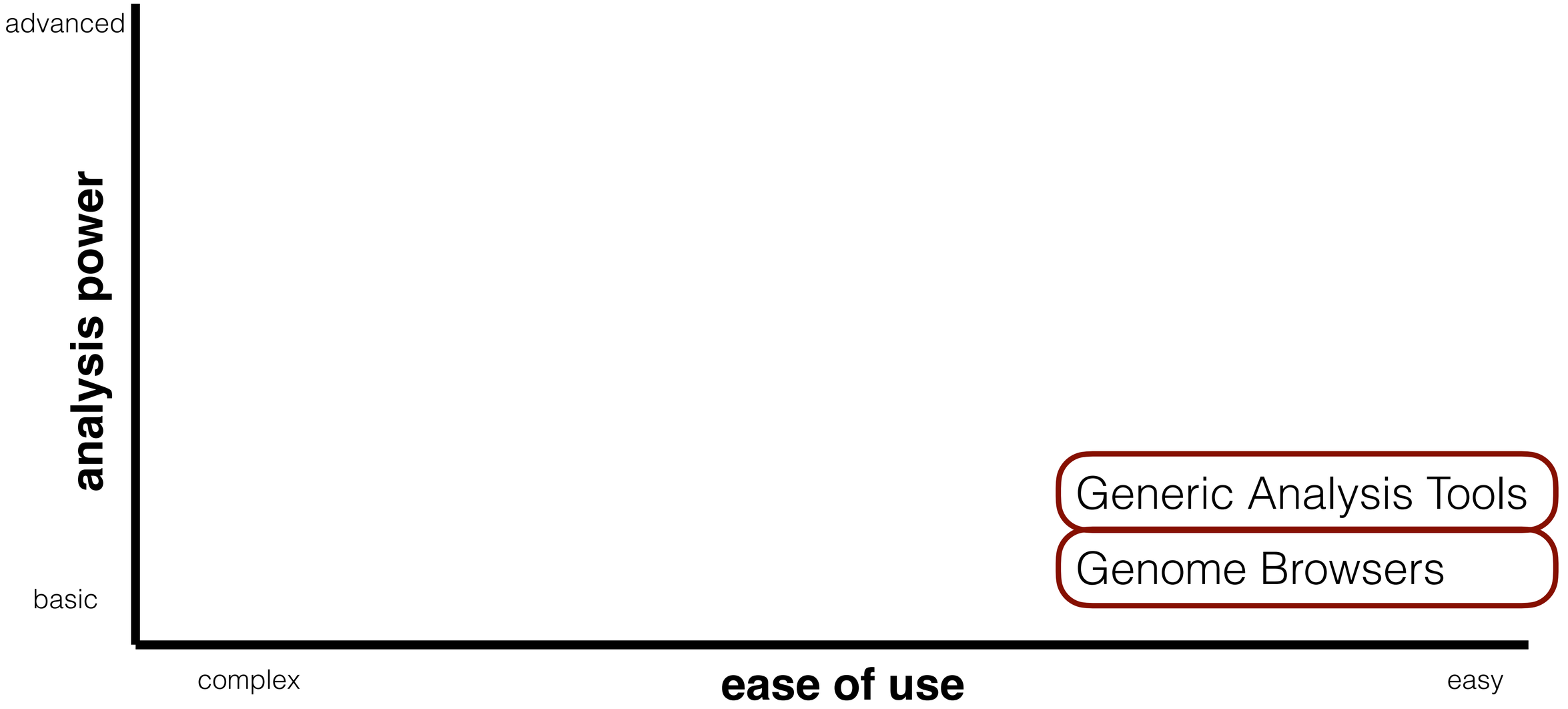
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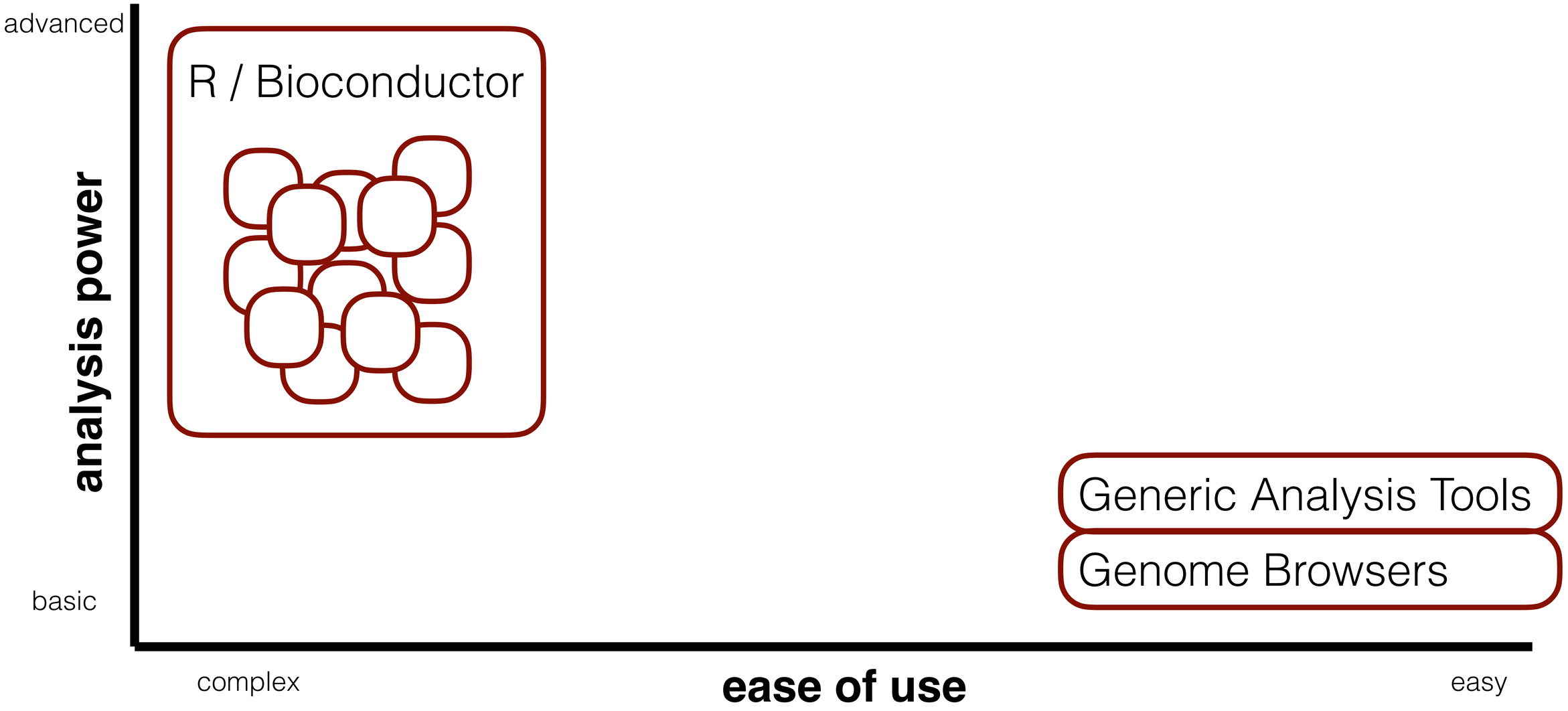
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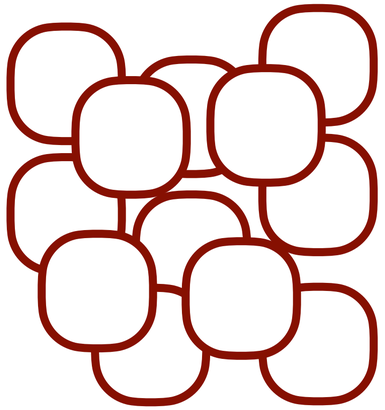
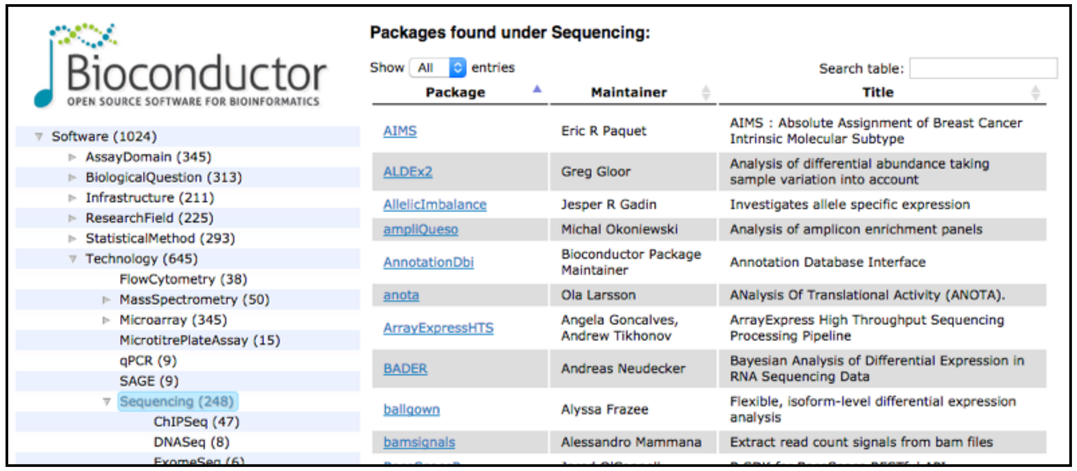
R / Bioconductor





Bioconductor Repository

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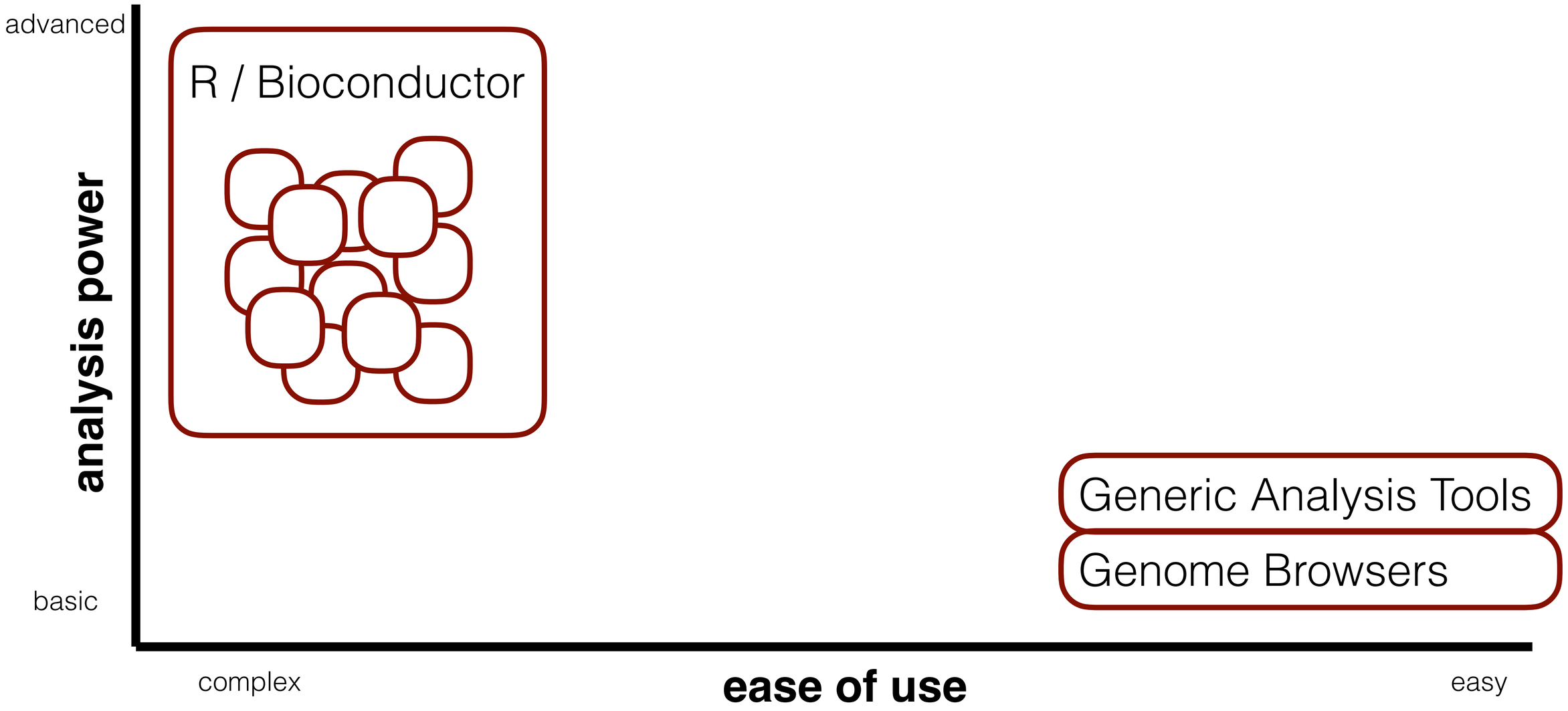
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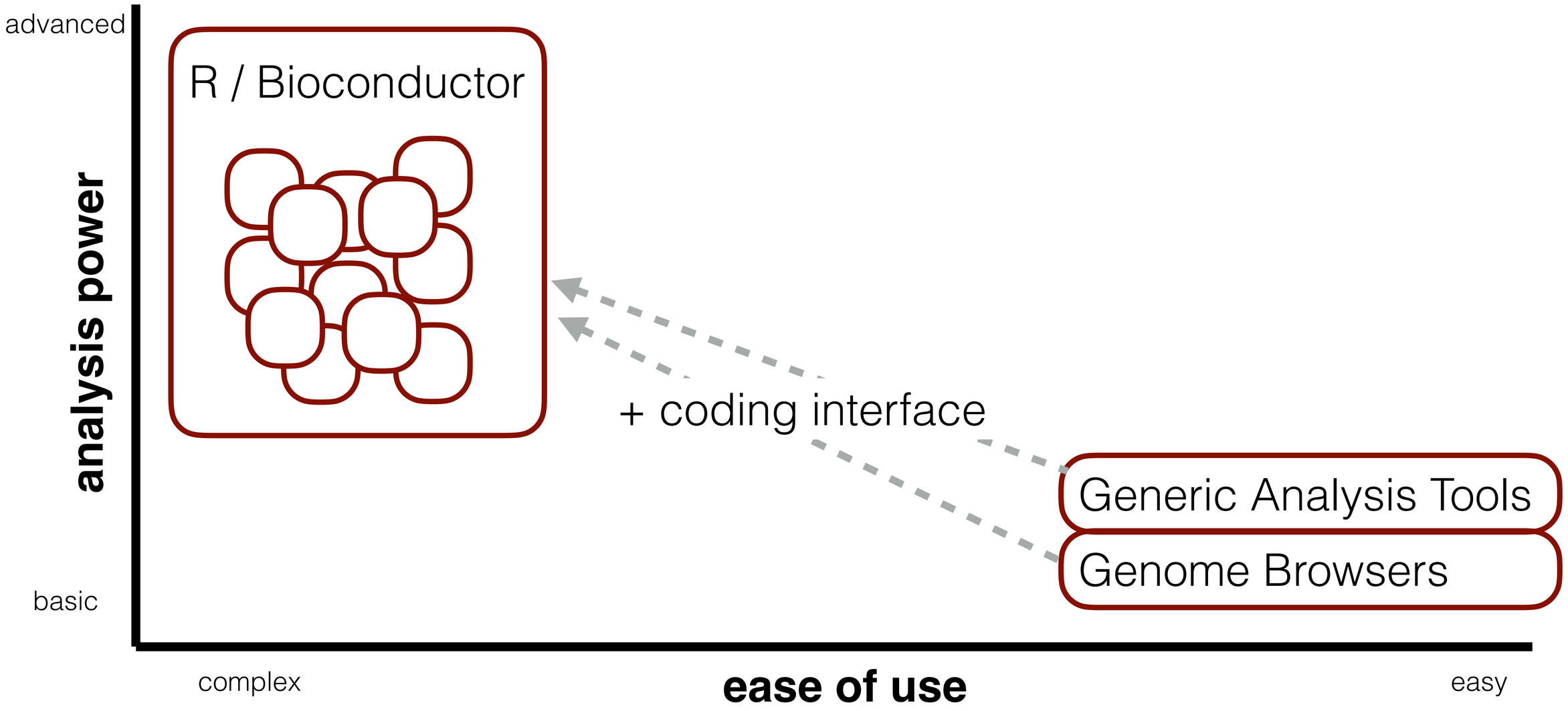
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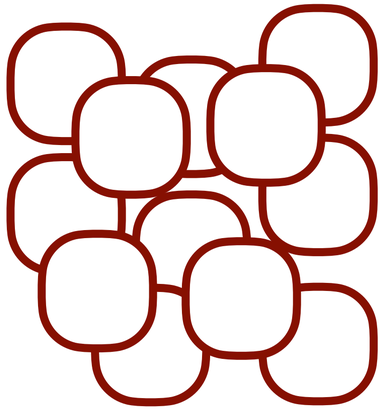
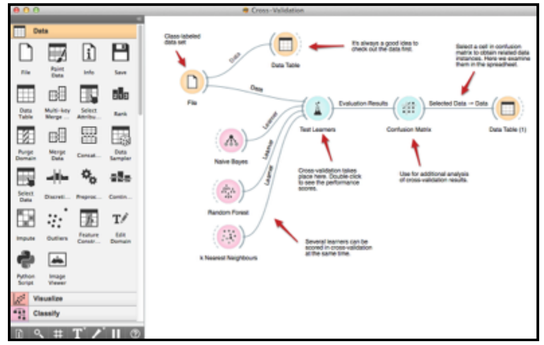


KNIME



Orange

+ coding interface

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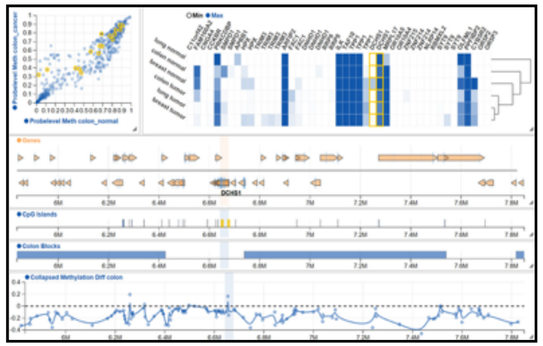

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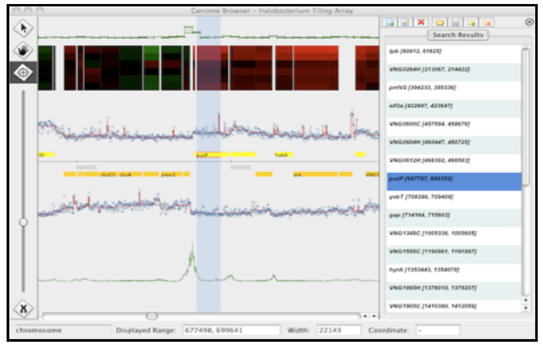
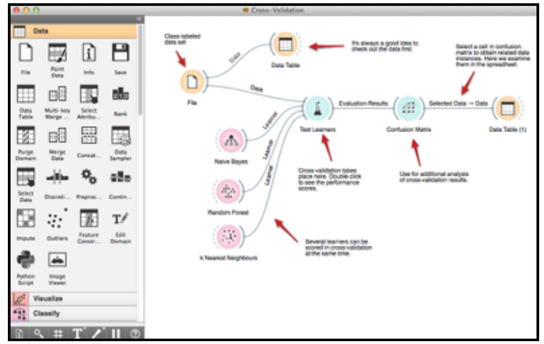


Gaggle Genome Browser

KNIME



Orange

+ coding interface

Generic Analysis Tools

Genome Browsers

ease of use

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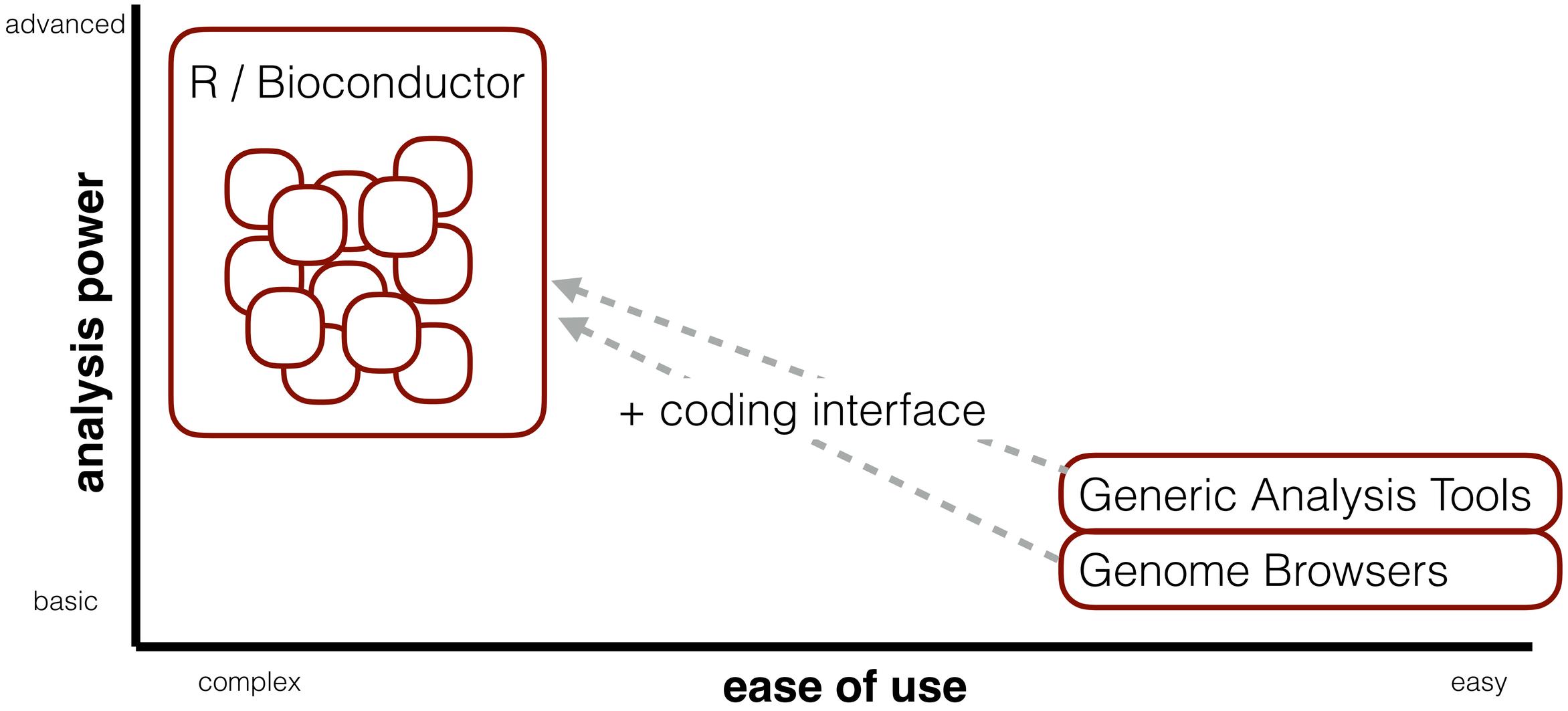
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easy

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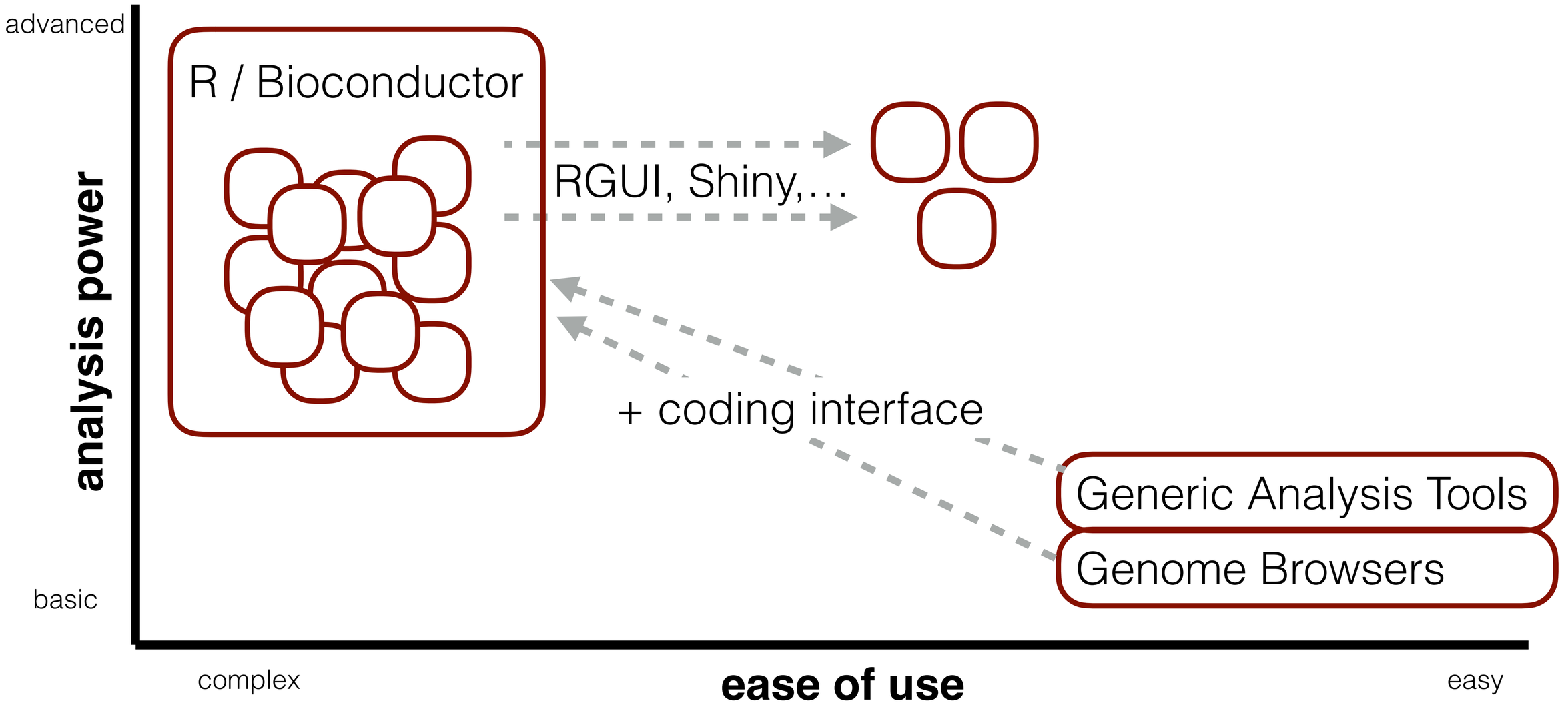
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RGUI, Shiny,…
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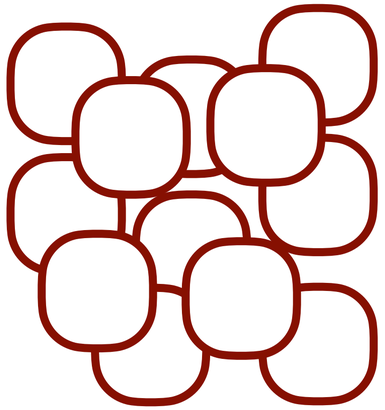

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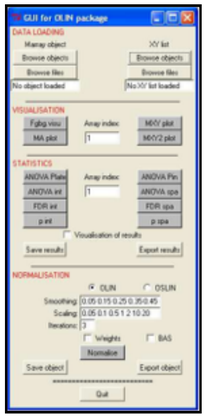

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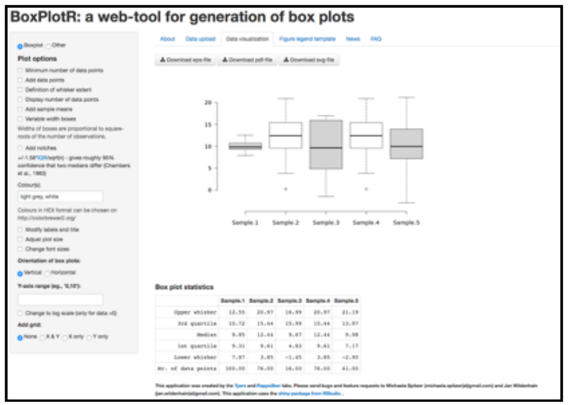

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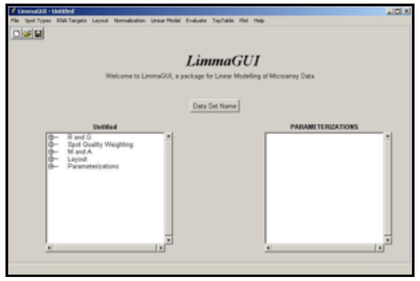

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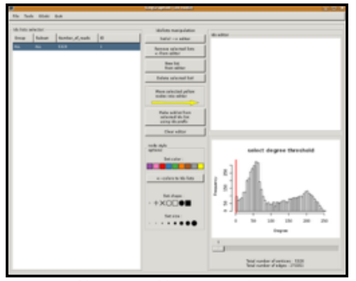

SeqGraphR

Generic Analysis Tools

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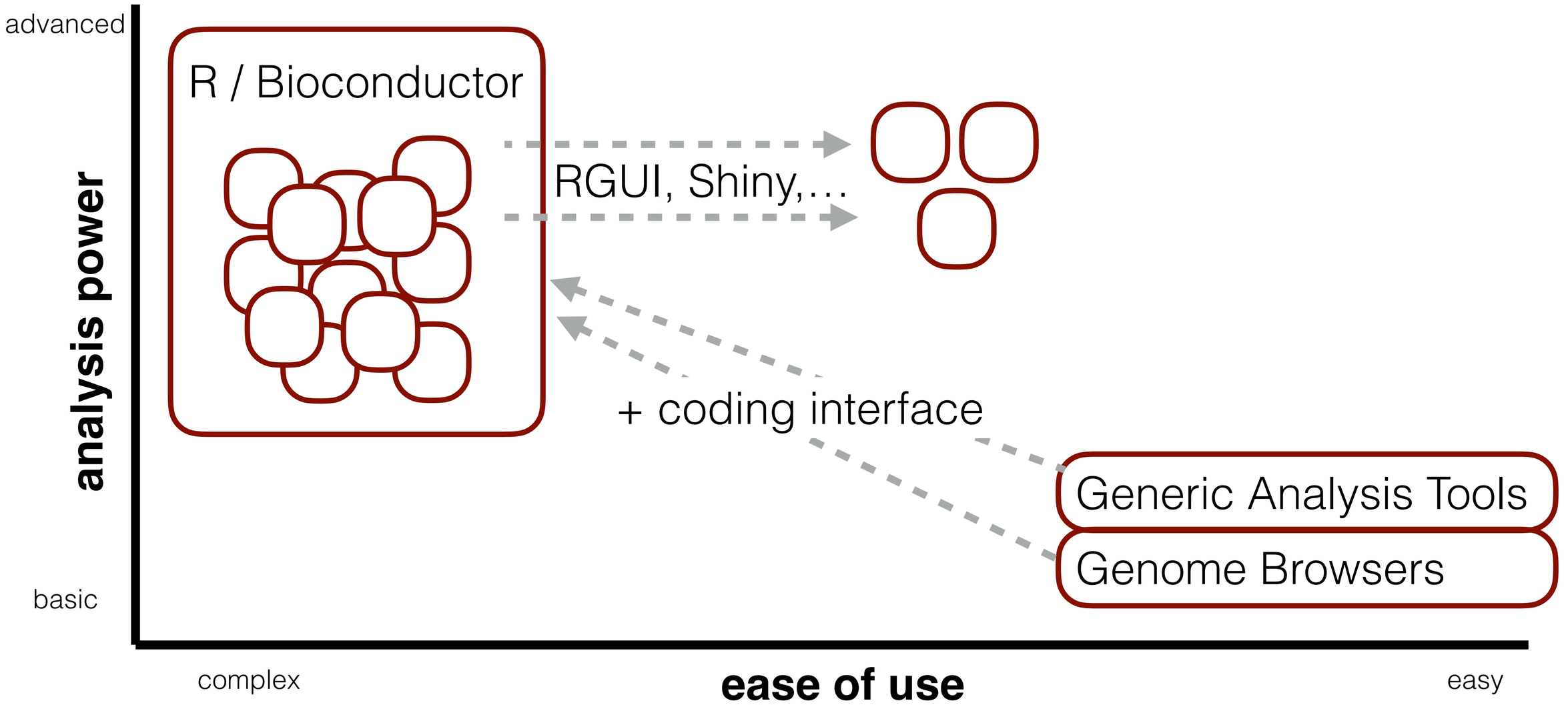
motivation


advanced
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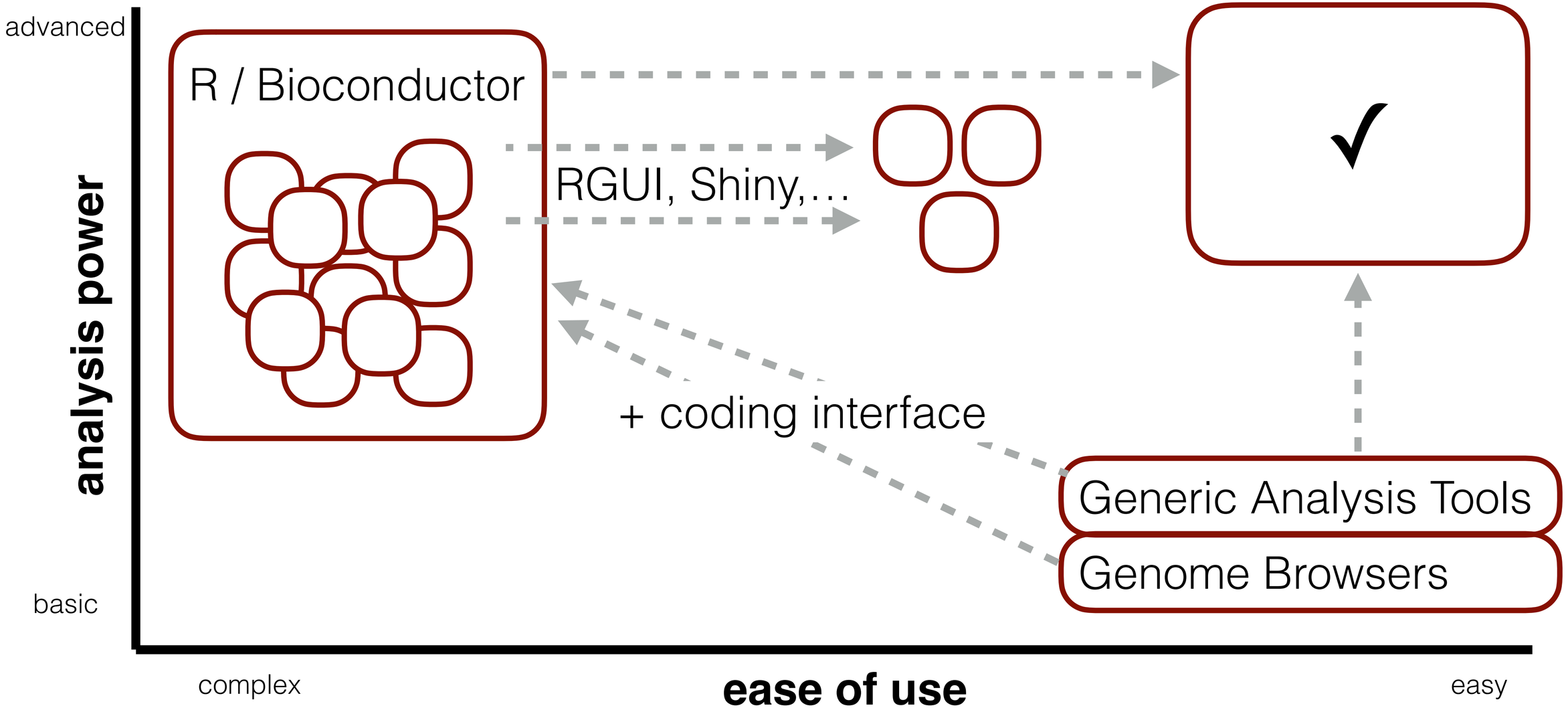
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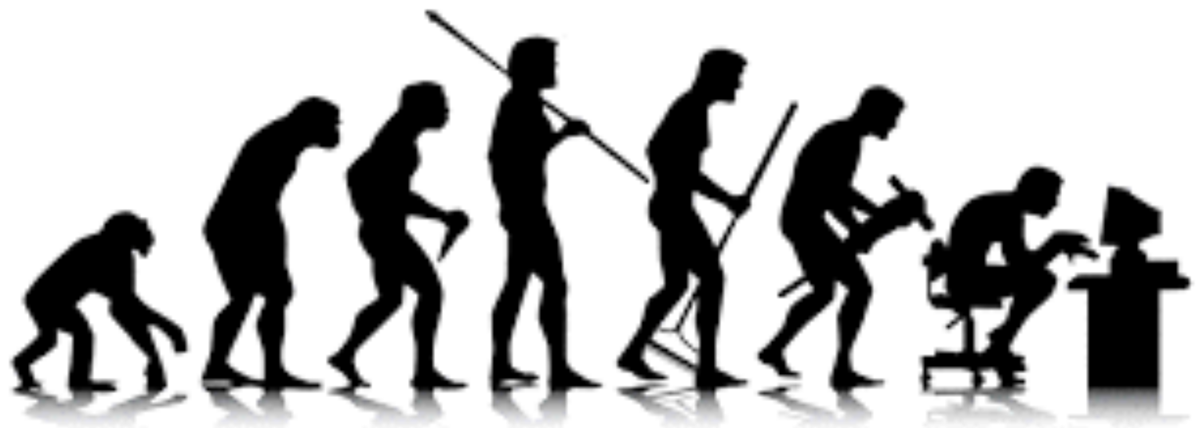
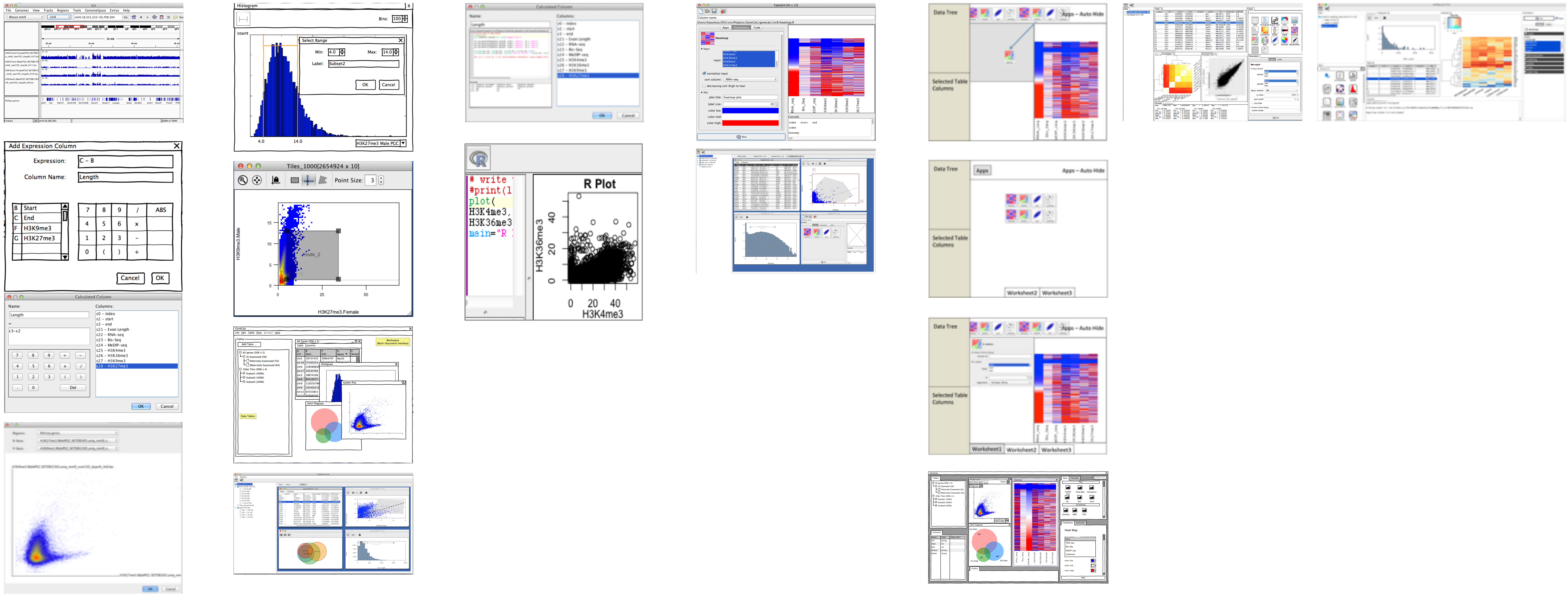
VisRseq

design evolution

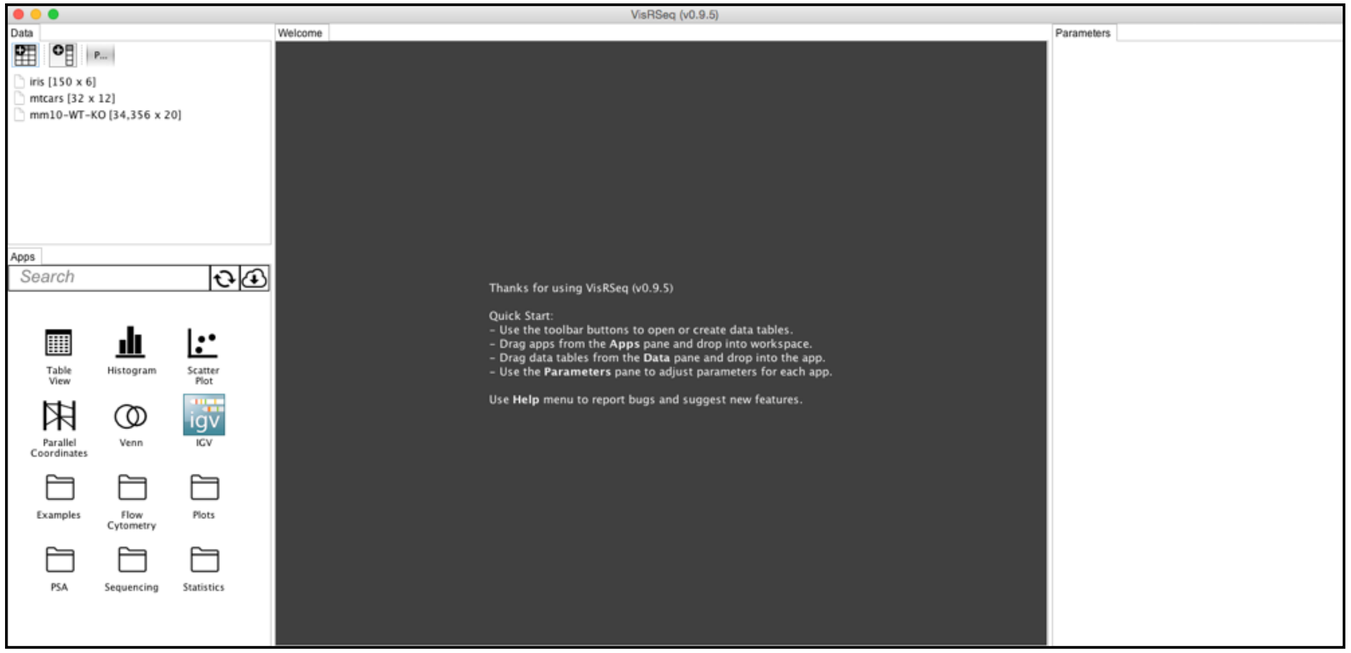


IGV plugin (2013) — workspace — R integration — BioVis Poster (2014) — Redesigned Layout — BMC Bioinf (2015) — **open beta**

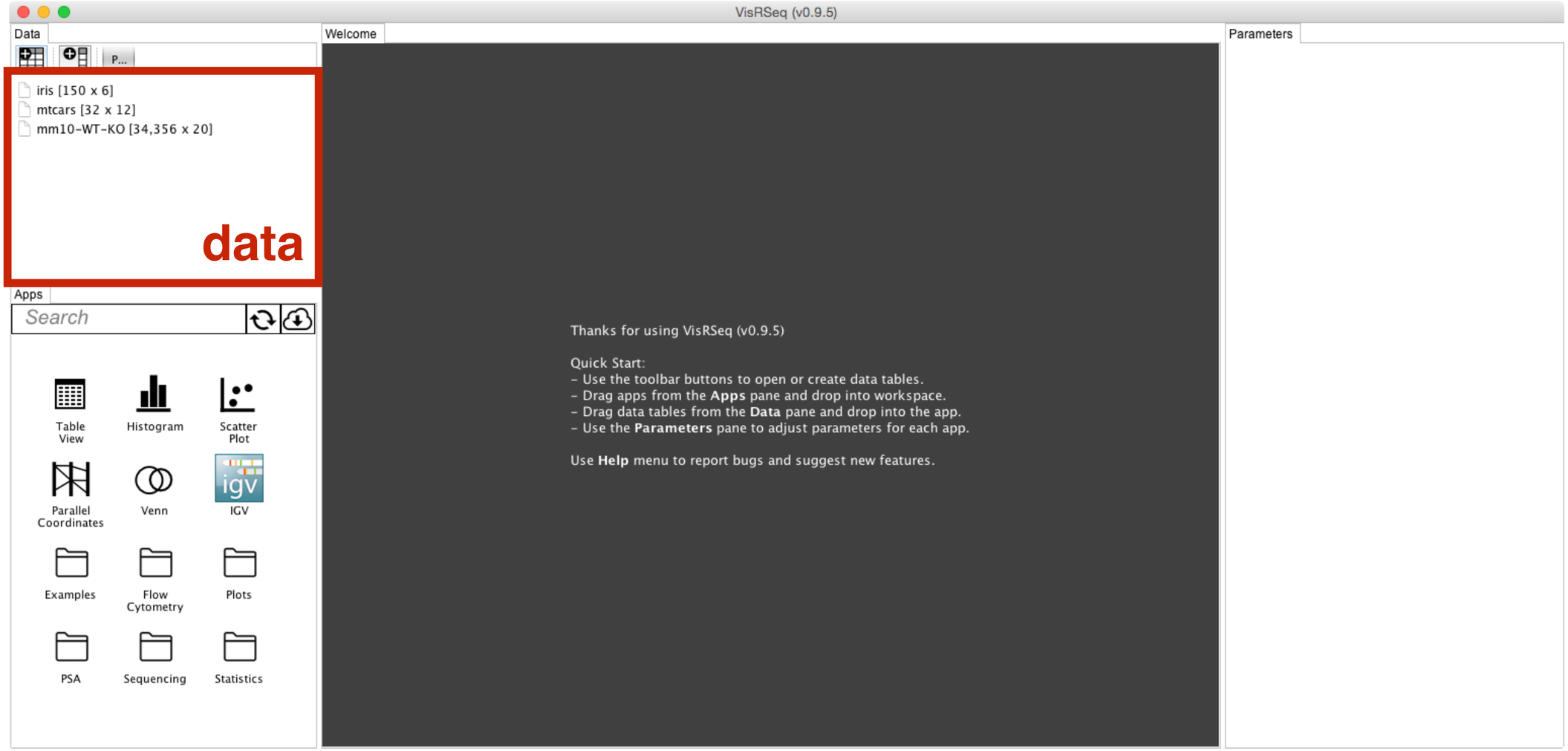


interface

- Installation Requirements:
  - Java SE 7
  - R
- Auto installs required packages
- Open Beta: http://visrseq.github.io



interface: data



interface: data

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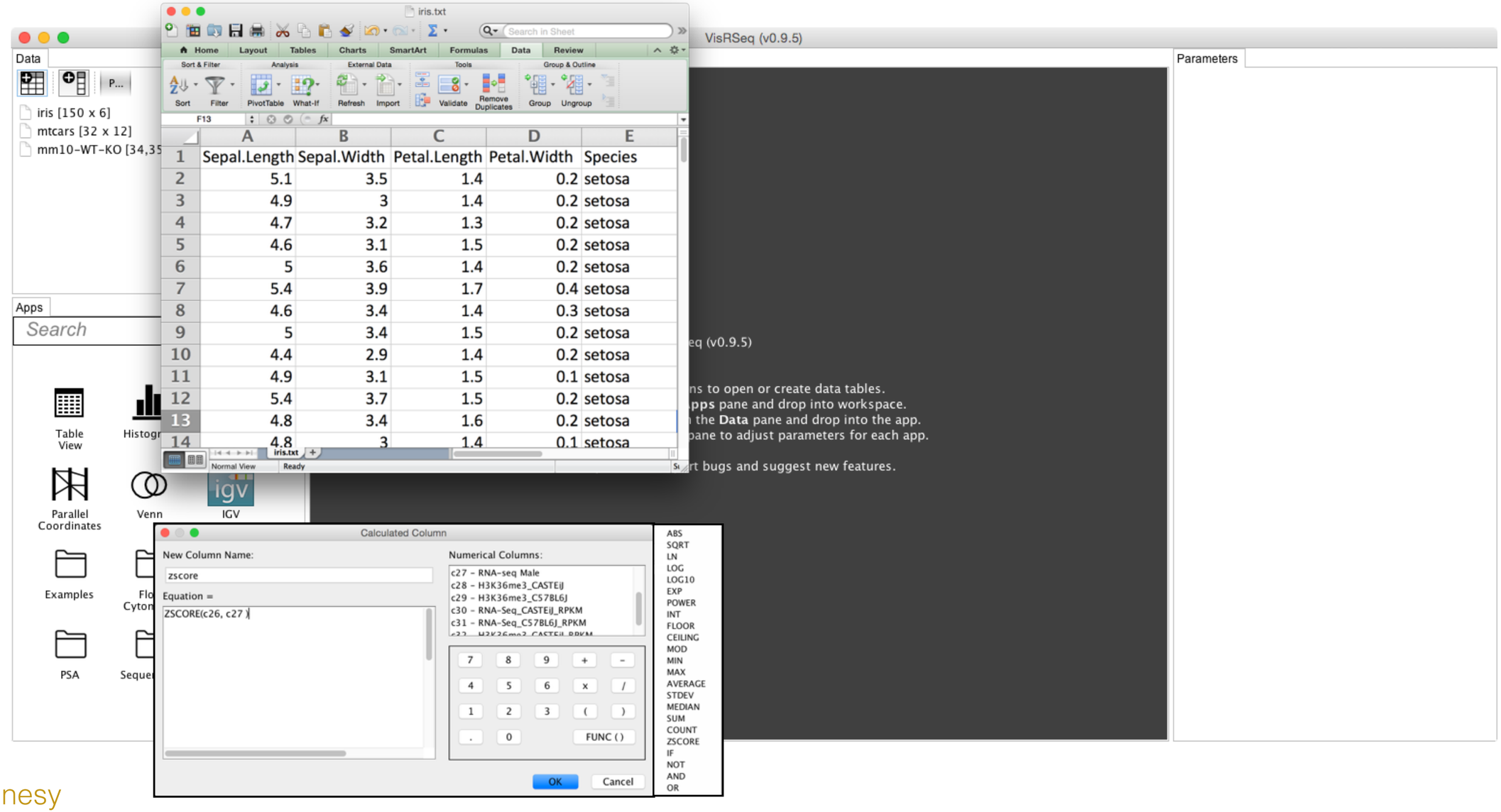

interface: data

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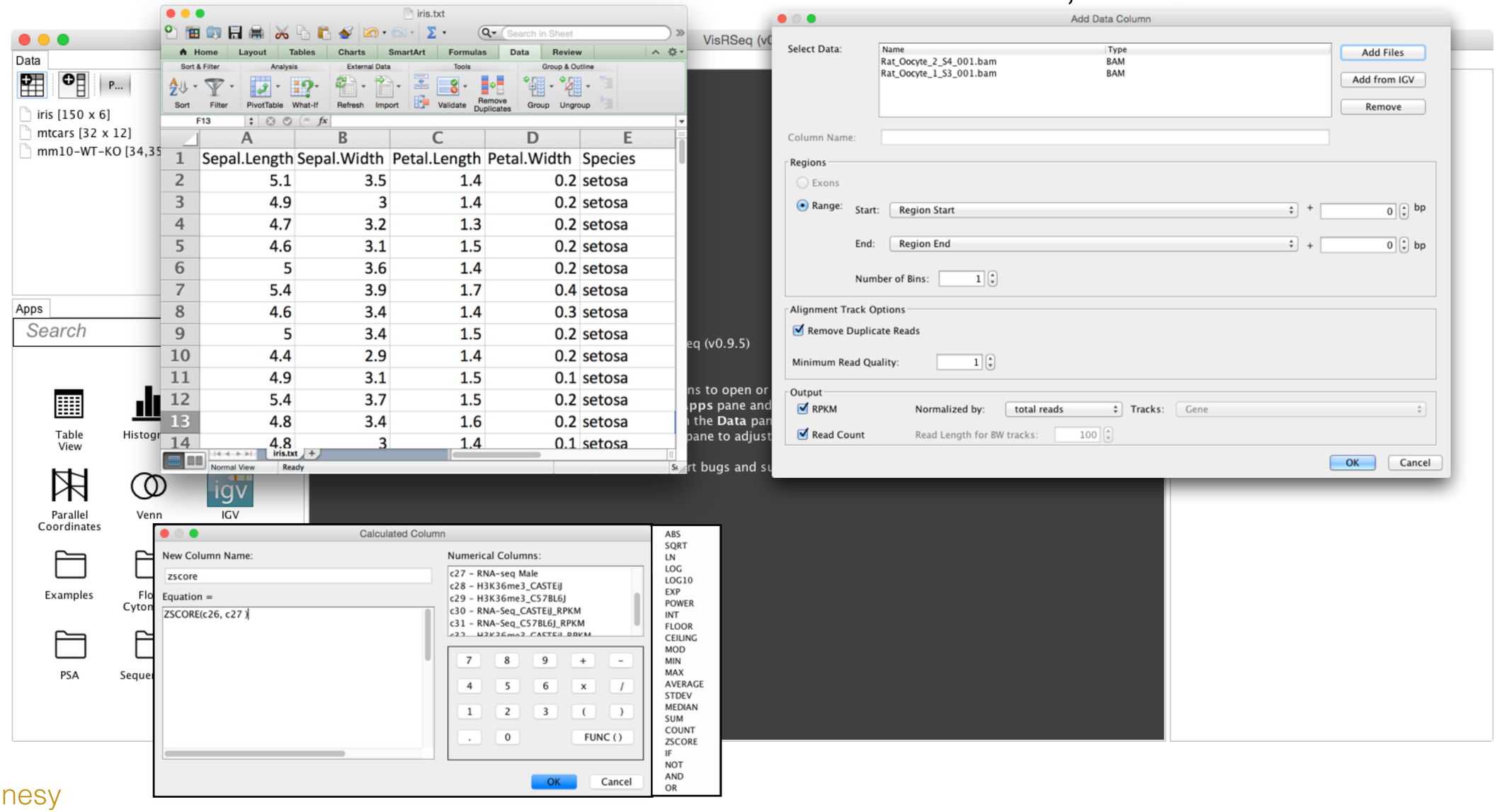
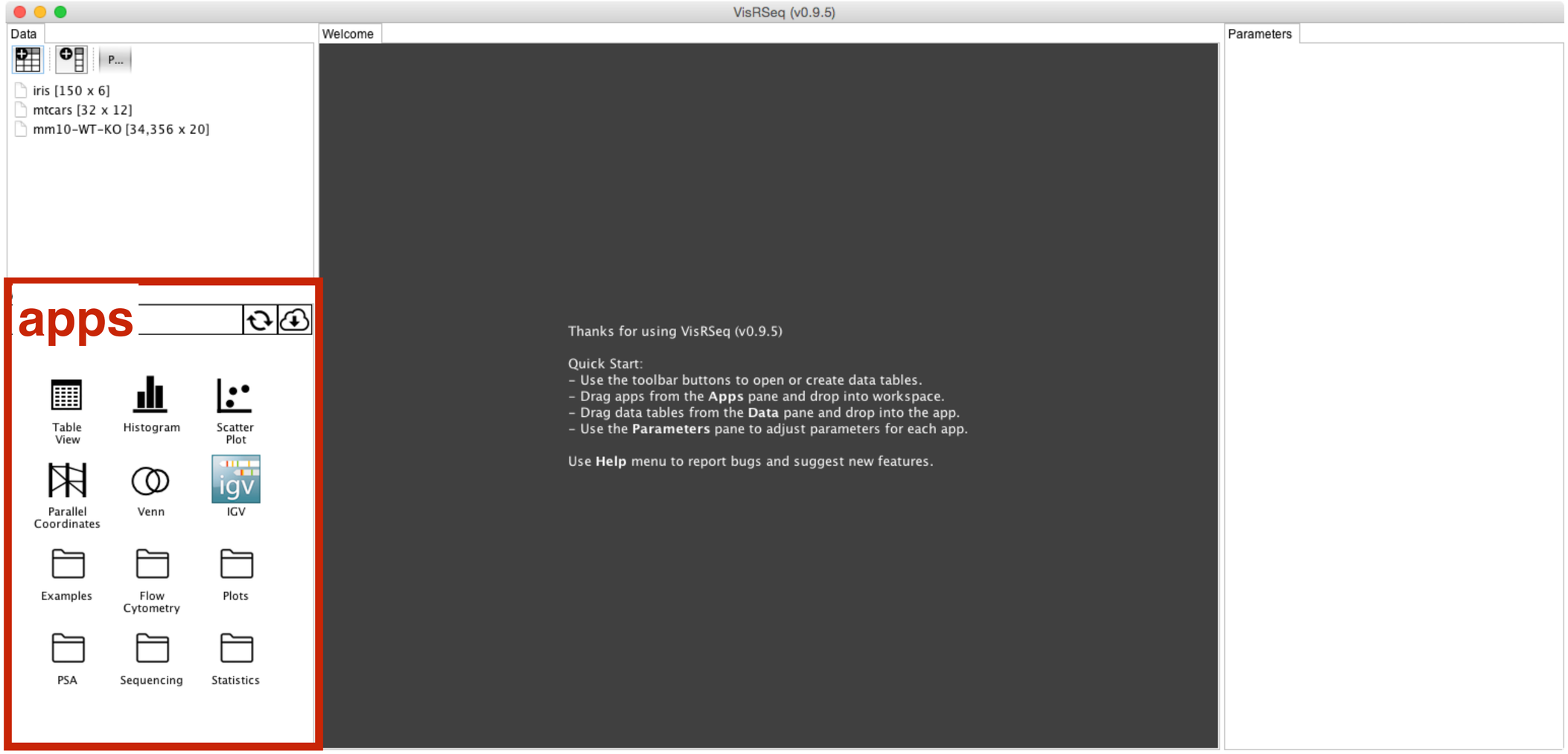


interface: apps



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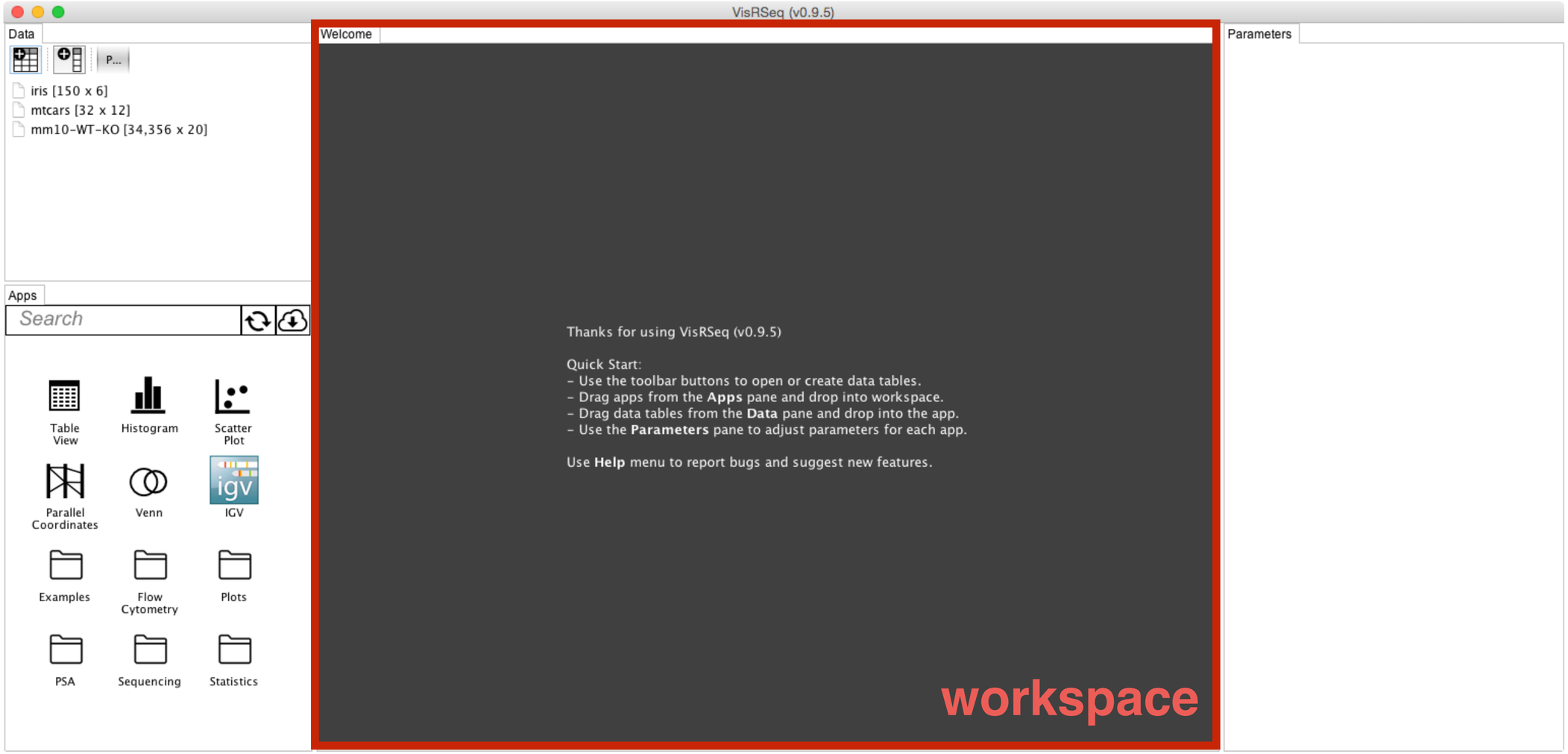
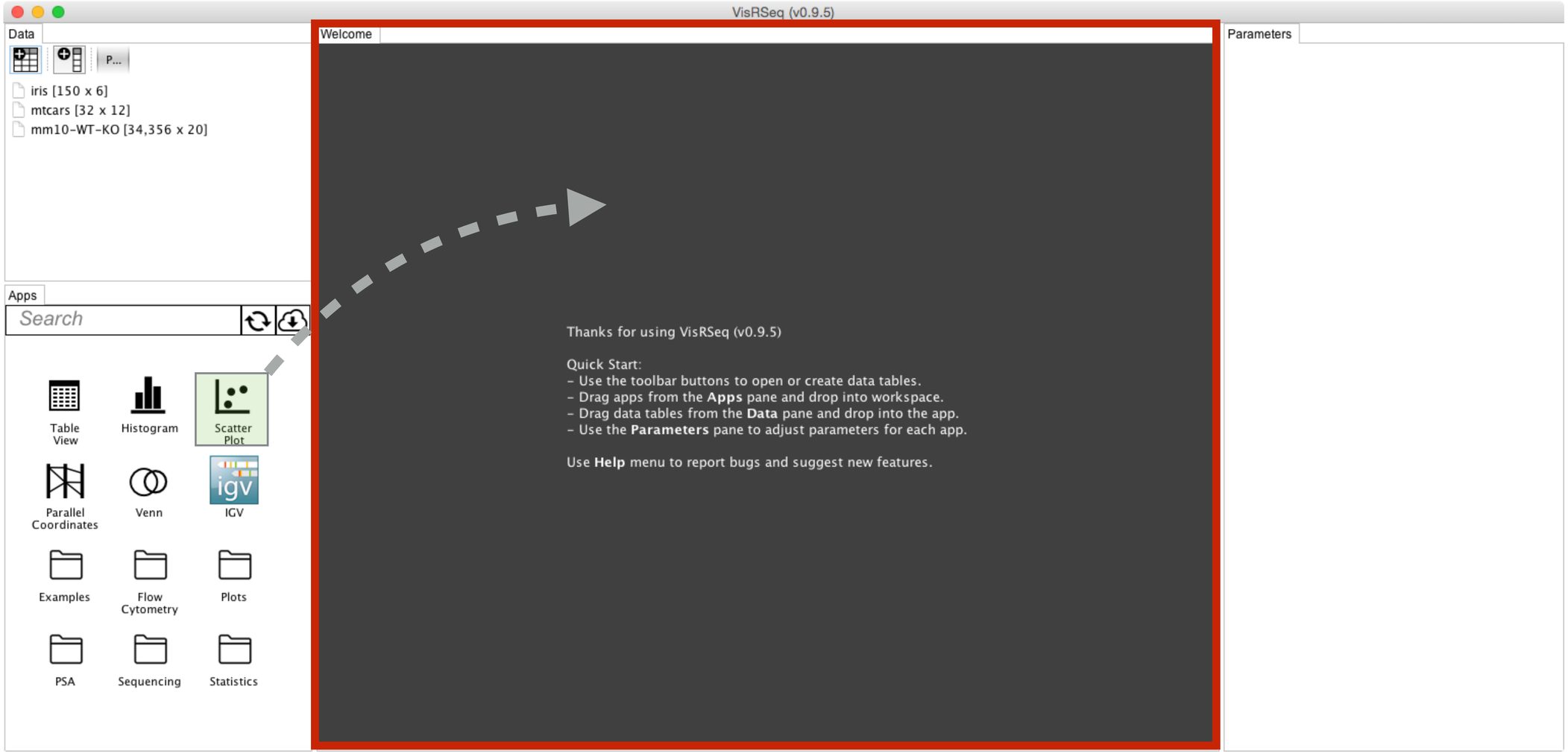
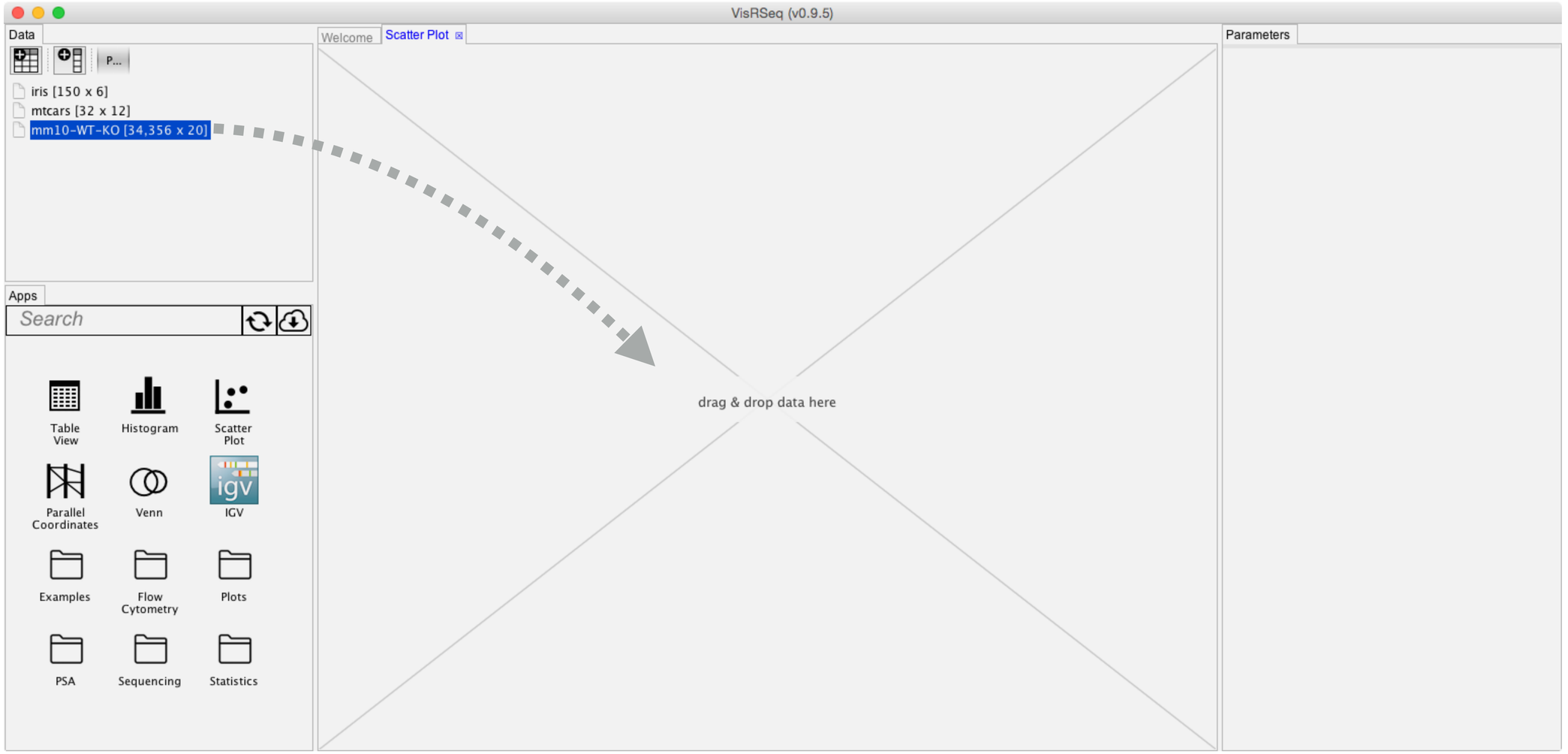


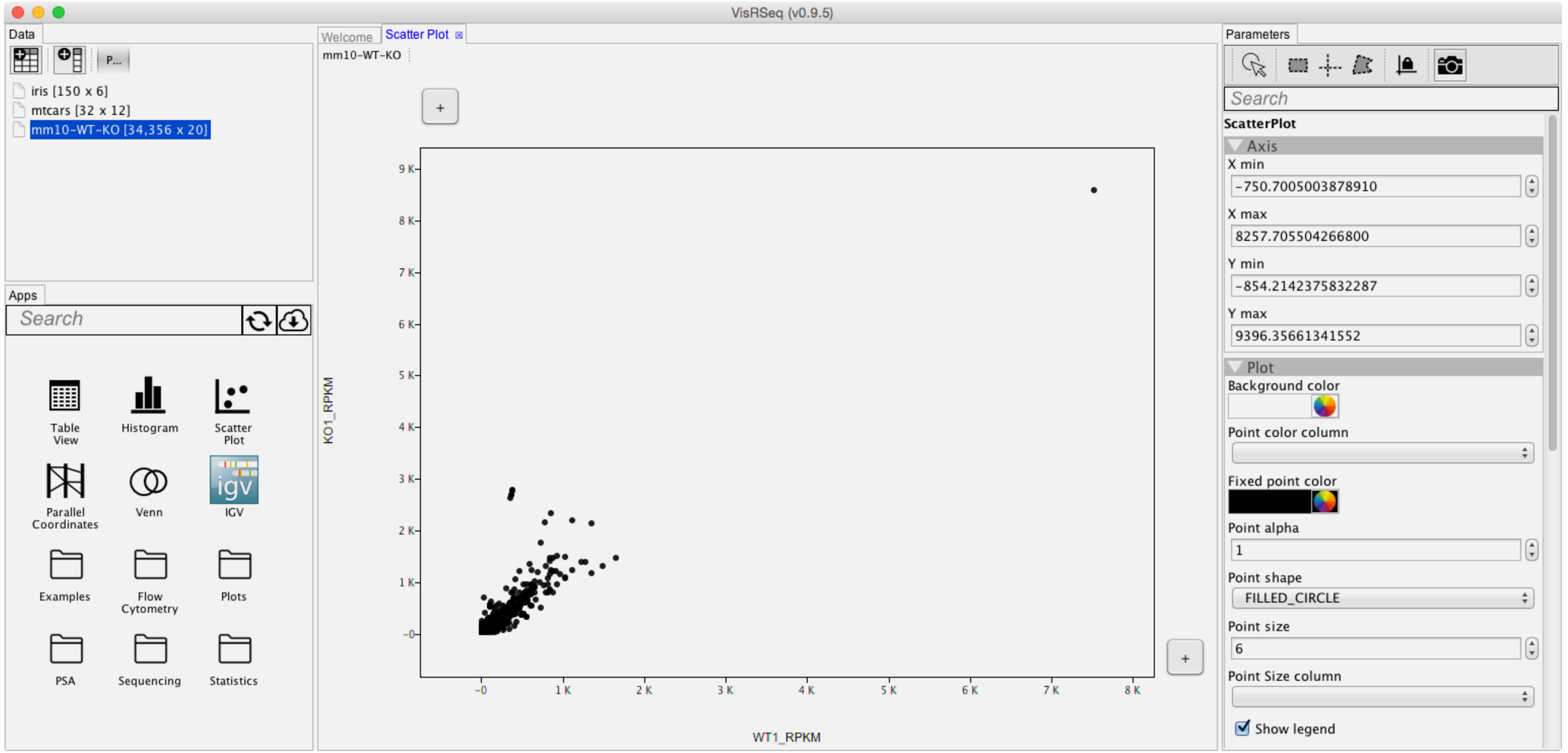
interface: workspace



interface: workspace

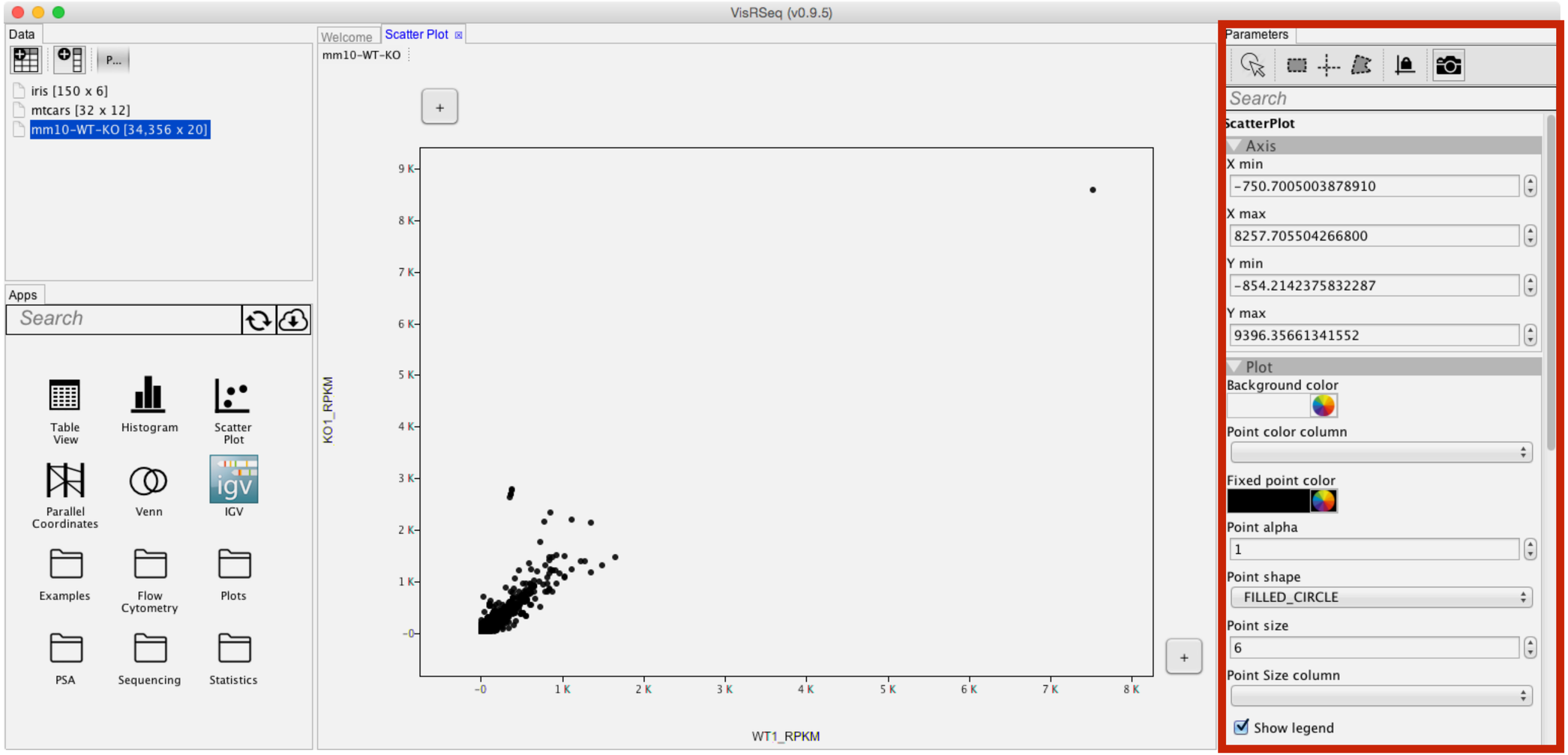


interface: workspace

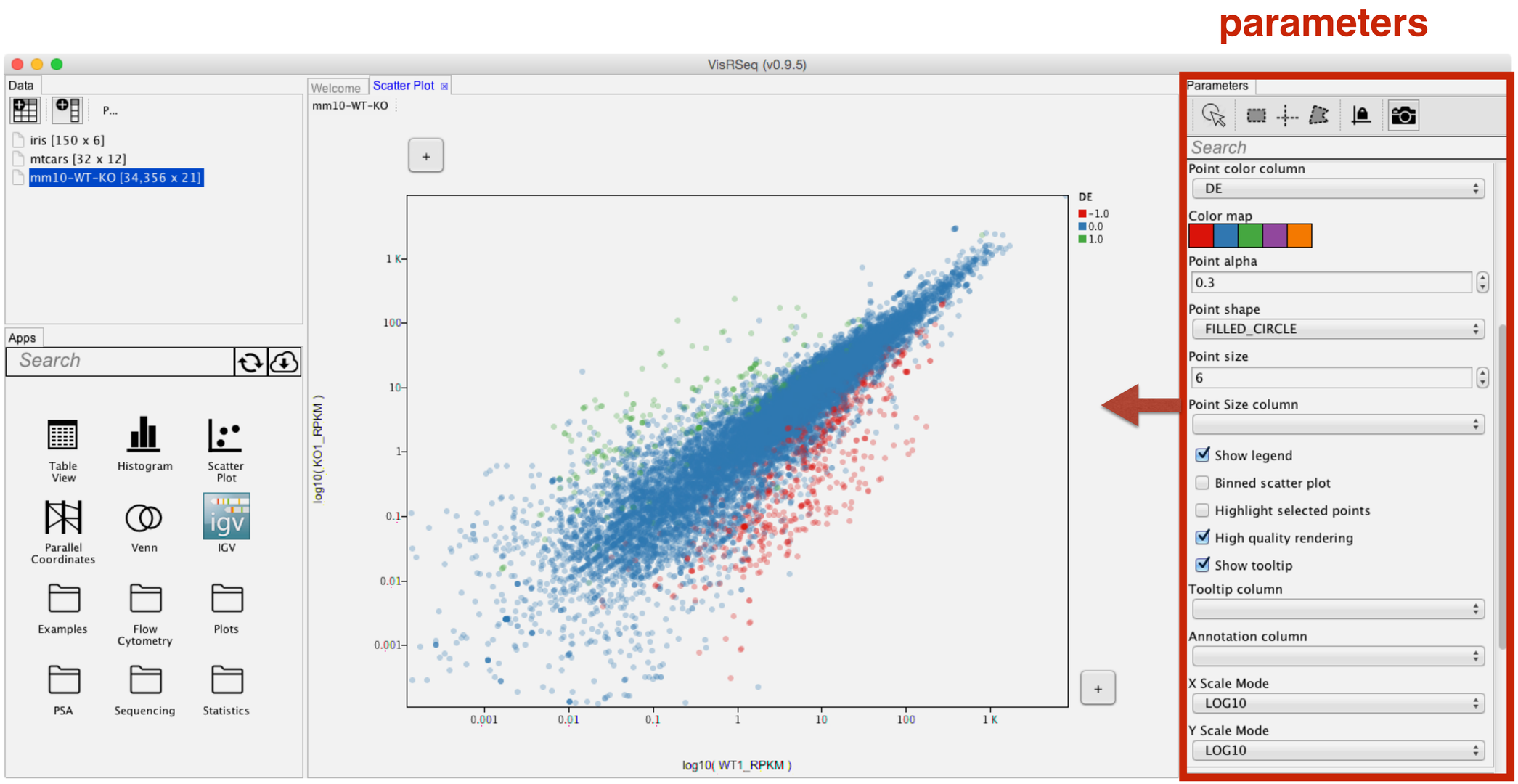


interface: parameters

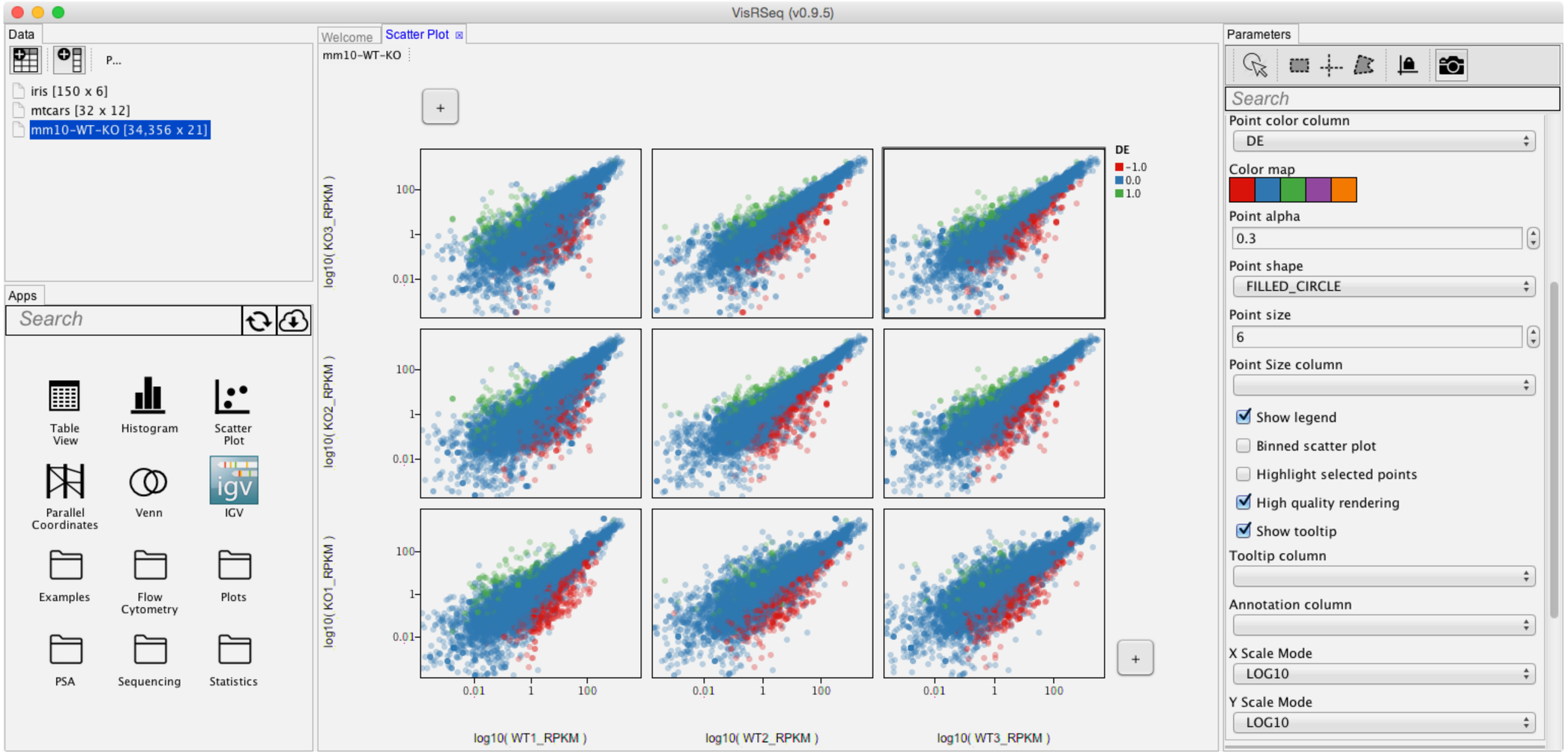
parameters



interface: parameters

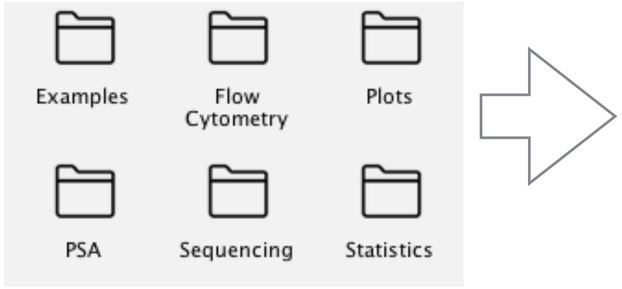


Apps: interactive

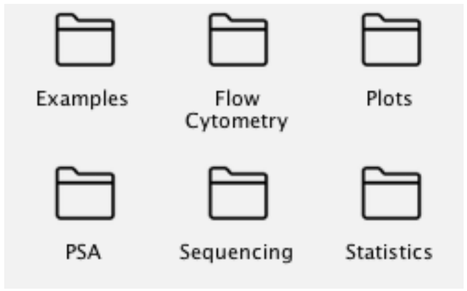


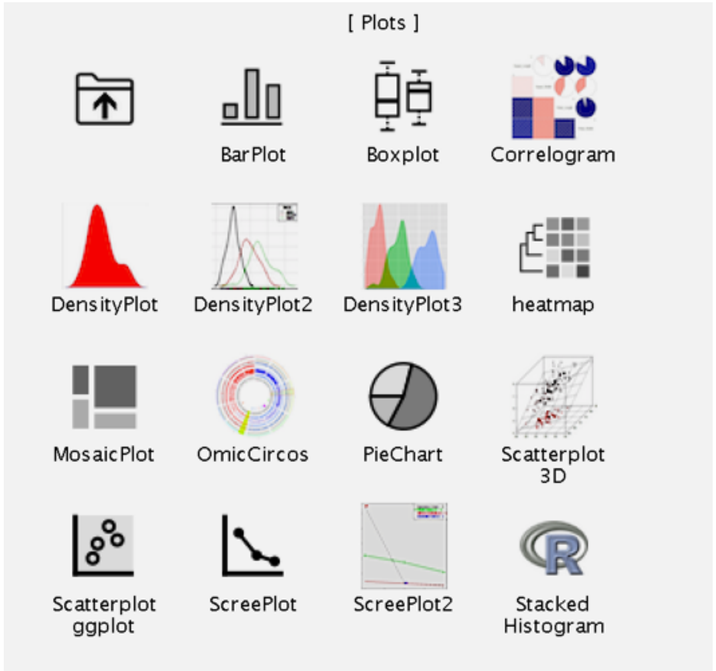
R - apps

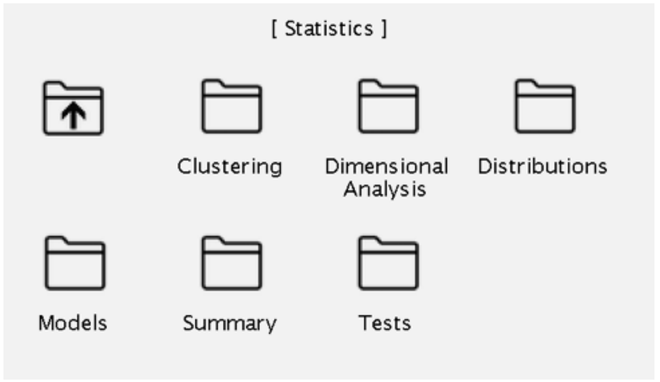
R Apps

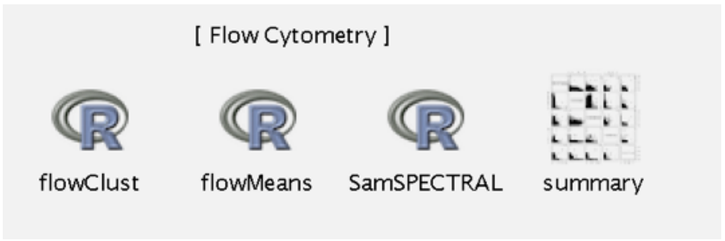


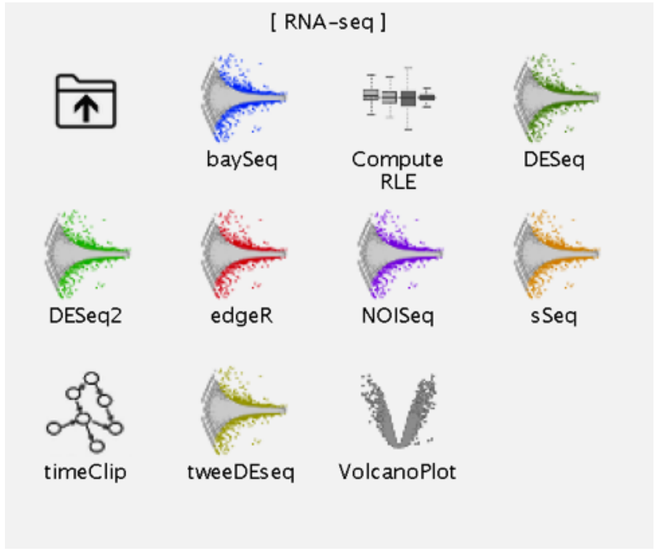
R Apps


Examples
Flow Cytometry
Plots
PSA
Sequencing
Statistics

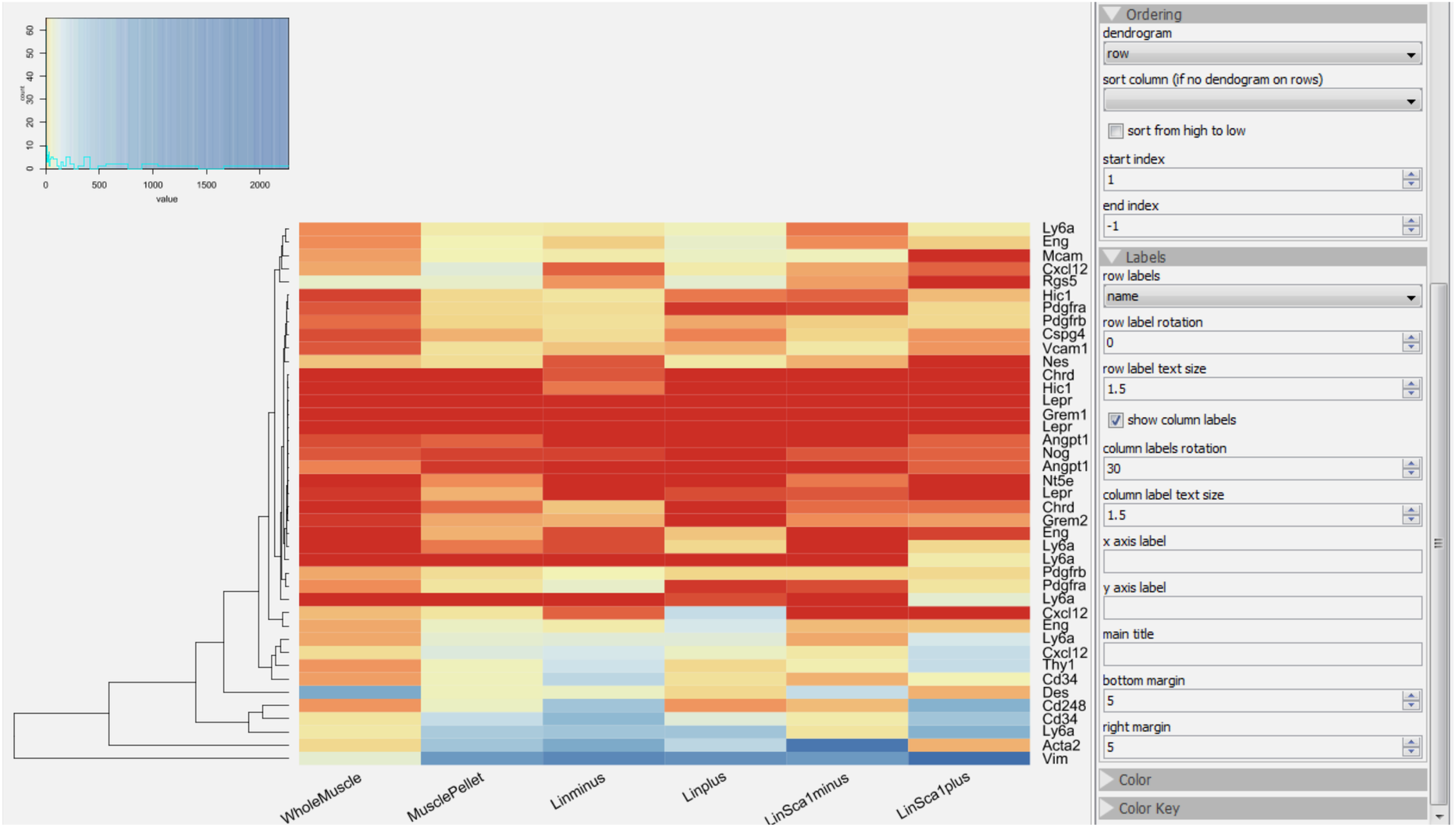

[Plots]
BarPlot
Boxplot
Correlogram
DensityPlot
DensityPlot2
DensityPlot3
heatmap
MosaicPlot
OmicCircos
PieChart
Scatterplot 3D
Scatterplot ggplot
ScreePlot
ScreePlot2
Stacked Histogram


[Statistics]
Clustering
Dimensional Analysis
Distributions
Models
Summary
Tests


[Flow Cytometry]
flowClust
flowMeans
SamSPECTRAL
summary


[RNA-seq]
baySeq
Compute RLE
DESeq
DESeq2
edgeR
NOISeq
sSeq
timeClip
tweeDEseq
VolcanoPlot

R – Apps example: heatmap



Anatomy of an R app

R code

kmeans.R

```
source("visrutils.R")

visr.applyParameters()

cluster_data<-subset(visr.input, select = param.columns)

output.clusterid <- kmeans(cluster_data, param.k,
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plot(cluster_data, main = param.plot.title,
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parameters

kmeans.json

```
{  "label":"kmeans", "categories":[
   { "variables":{
      "param.columns":    {"type":"multi-column-numerical" },
      "param.k":          {"type":"int", "default":3 },
      "param.algorithm": {"items":["Hartigan-Wong", "Lloyd",
                                   "Forgy", "MacQueen"]},
      "param.plot.title":{"default":"kmeans result"},
      "output.clusterid":{"type":"output-column"}
   }}
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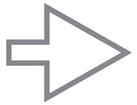
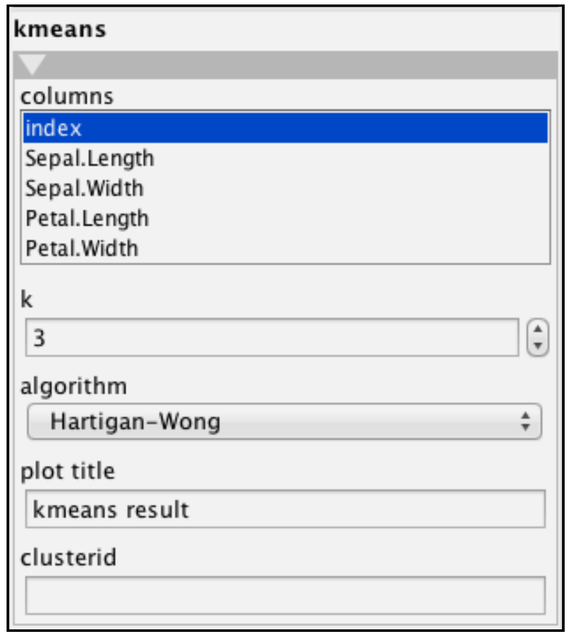
                                   "Forgy", "MacQueen"]},
      "param.plot.title":{"default":"kmeans result"},
      "output.clusterid":{"type":"output-column"}
   }}
]}
```



auto generated UI



Anatomy of an R app

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kmeans.R

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```

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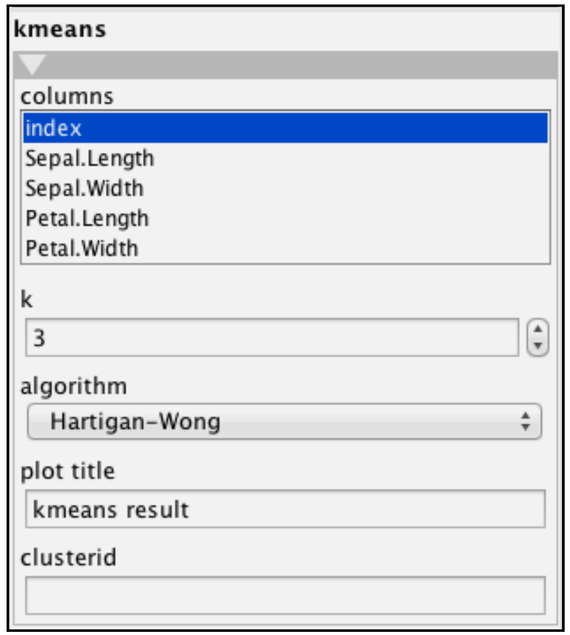
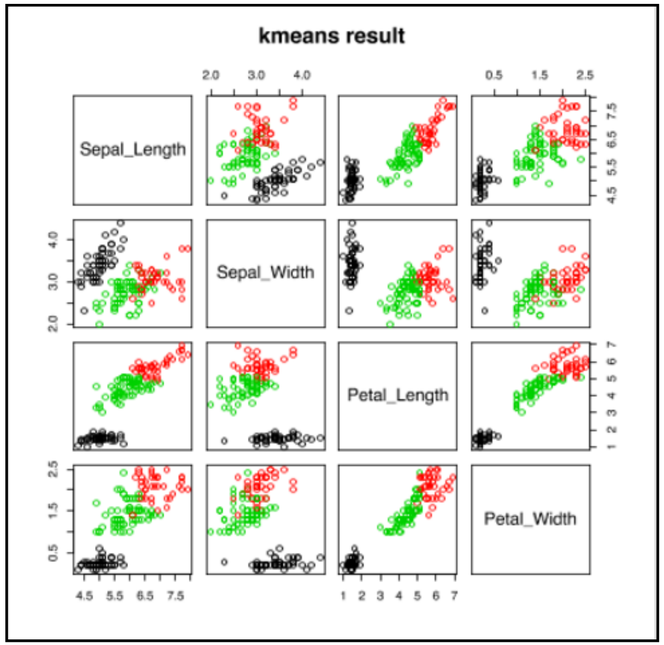
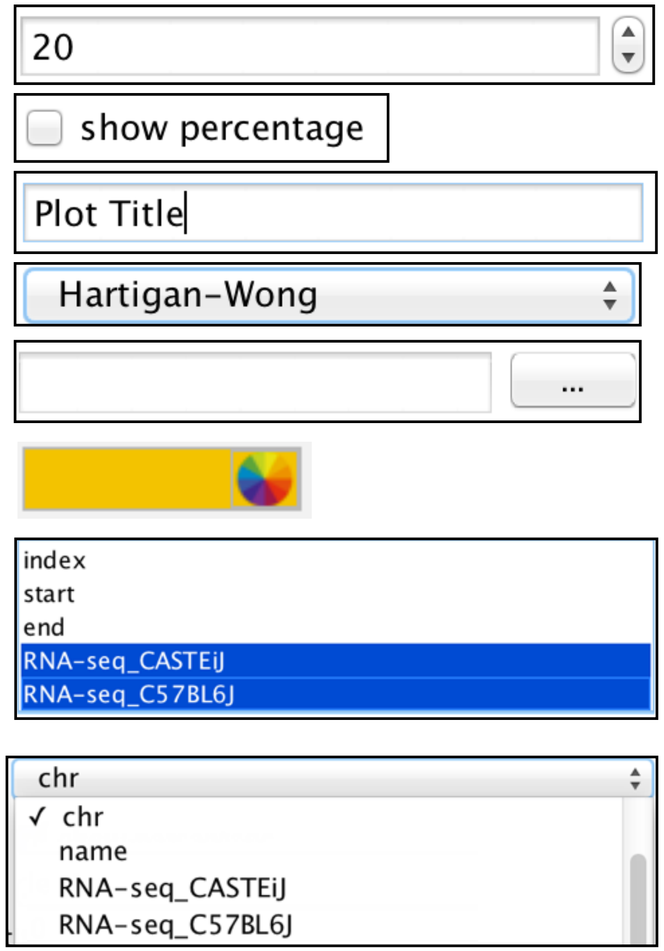


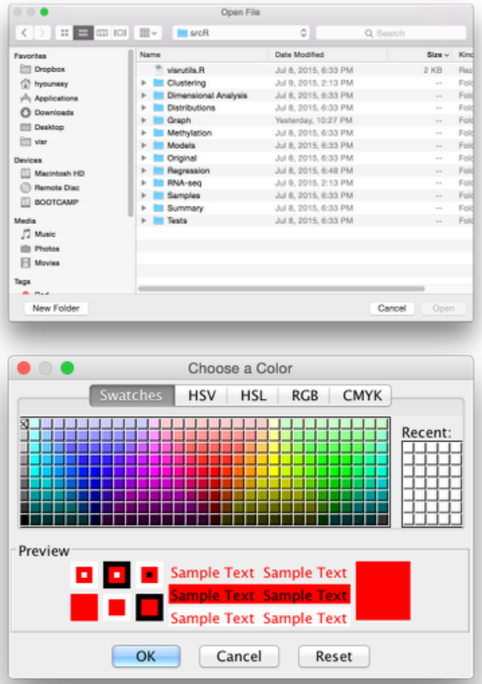
output



creating R apps: variable types

variable type
int
double
boolean
string
string with items
filename
color
range-int
range-double
column
column-numerical
multi-column
multi-column-numerical
ouput-column
output-table






```
visr.message(message, type)
```

creating R apps

- Entire app may also be coded and debugged in R (/ RStudio)
- The .json file will be generated from the R code

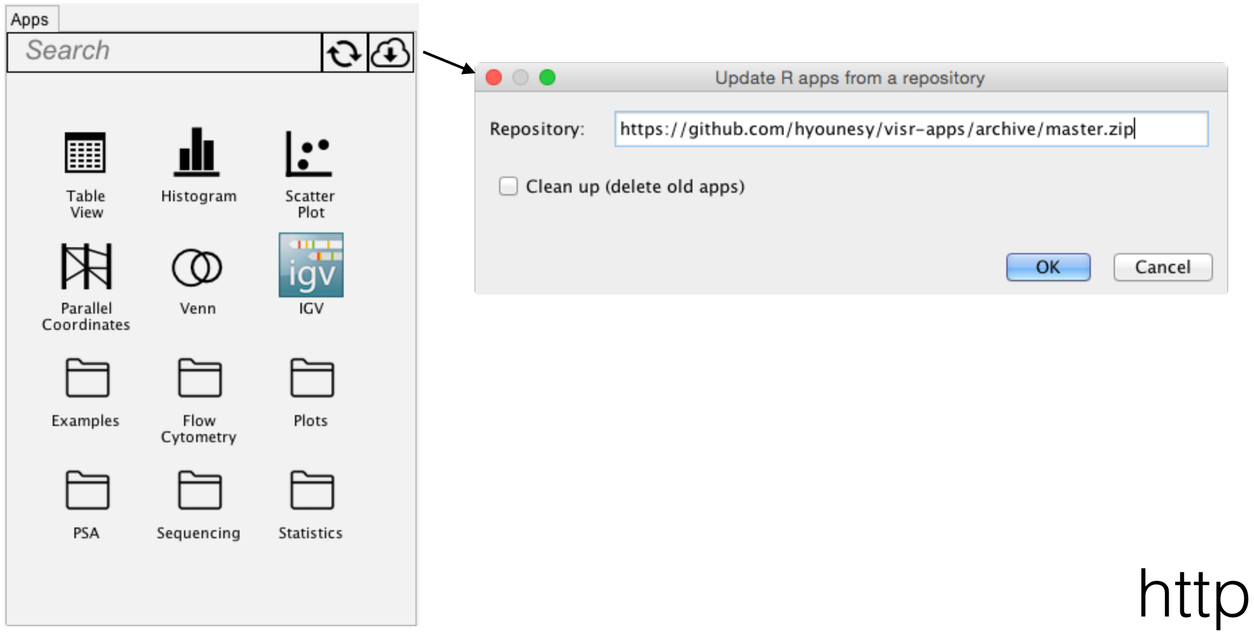
creating R apps

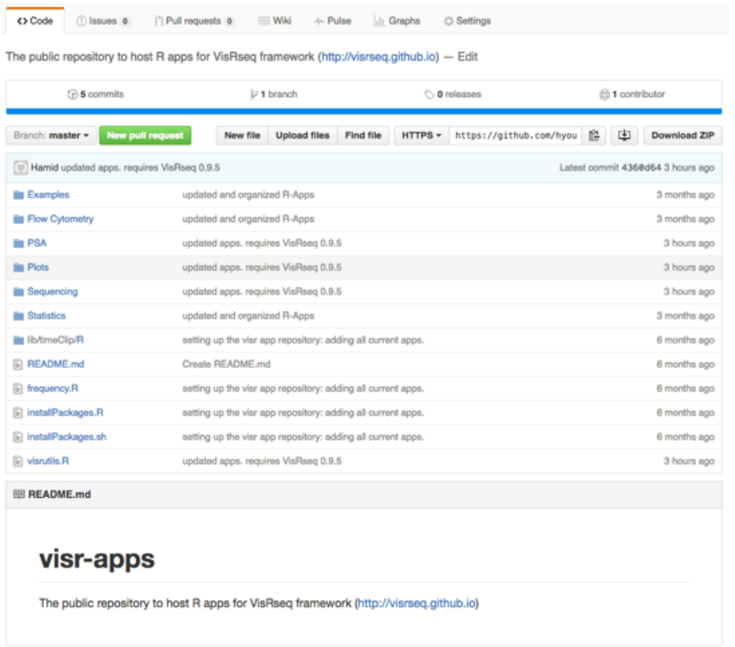
```
source("visrutils.R")

#  parameters
visr.app.start("Simple Kmeans", debugdata = iris)
visr.category("clustering parameters")
visr.param("columns", type = "multi-column-numerical",
           debugvalue = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"))
visr.param("k", default = 3)
visr.param("algorithm", items = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"))
visr.category("output")
visr.param("plot.title", default = "kmeans results")
visr.param("output.clusterid", type = "output-column")
visr.app.end(printjson=TRUE)
visr.applyParameters()

# kmeans code
cluster_data<-subset(visr.input, select = visr.param.columns)
visr.param.output.clusterid <- kmeans(cluster_data,
                                      centers = visr.param.k,
                                      algorithm = visr.param.algorithm)$cluster
plot(cluster_data, main = visr.param.plot.title,
     col = as.integer(visr.param.output.clusterid))
```

creating R apps: sharing

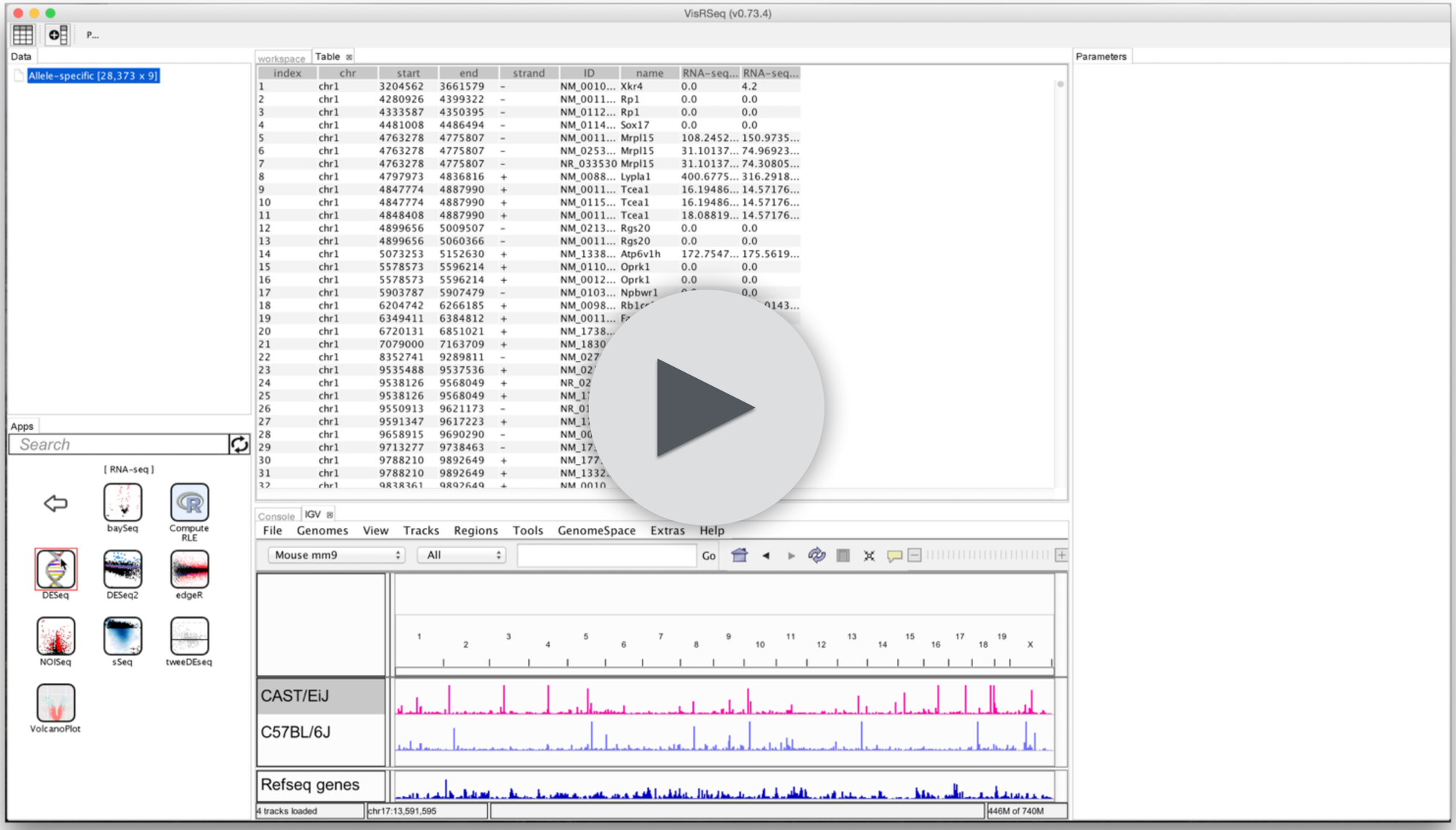




https://github.com/hyounesy/visr-apps/

Demo

Demo


VisRSeq (v0.73.4)
Data
Allele-specific [28,373 x 9]
workspace
Table
index chr start end strand ID name RNA-seq... RNA-seq...
Parameters
Apps
Search
[RNA-seq]
baySeq
Compute RLE
DESeq
DESeq2
edgeR
NOISeq
sSeq
tweeDEseq
VolcanoPlot
Console
IGV
File Genomes View Tracks Regions Tools GenomeSpace Extras Help
Mouse mm9
All
Go
CAST/EiJ
C57BL/6J
Refseq genes
4 tracks loaded
chr17:13,591,595
446M of 740M

Your assignment if you choose to accept it…

Data

- 58788 Rows
- **title:** Title of the movie.
- **year:** Year of release.
- **budget:** Total budget (if known) in US dollars
- **length:** Length in minutes.
- **mpaa:** MPAA rating.
- **rating:** Average IMDB user rating.
- **votes:** Number of IMDB users who rated this movie.
- **r1-r10:** Multiplying by ten gives percentile (to nearest 10%) of users who rated this movie a 1.
- **action, animation, comedy, drama, documentary, romance, short:** Binary variables representing if movie was classified as belonging to that genre.

Assignments

- Two categories:

  1. Data Analysis

  2. App development / improvement.

- You may participate in either or both categories.

Assignment 1: Data Analysis

- Create an infographic about the movie dataset.
- Single page PDF document or PNG image.
- Plots should be generated only using VisRseq.
- Ok to use other software (e.g. MS Word, MS Powerpoint, Photoshop, etc.) to arrange several plots and to add additional text or graphics.

Assignment 1: Data Analysis

- The submissions will be evaluated based on:
  - functionality / the amount of information content
  - clarity (i.e. ease of interpretation)
  - usability / interaction possibilities
  - interesting findings
- Describe your interesting/surprising findings in words as well.

Assignment 2: App Development

- Develop a new R-App or modify and improve an existing R-App.
- Tutorial: https://github.com/hyounesy/bioc2016.visrseq
- Goal is to enhance the current analytical power of VisRseq to allow getting more or improved results.
- App(s) may add new computational functionality (e.g. new classification method) or new plots.
- It is still in the context of movie dataset, but the app should be designed such that it can be used with any tabular data.

Assignment 2: App Development

- Submit the .R and .json files for the new or improved app.
- App(s) should be functional in the current VisRseq version.
- Include a .pdf or .md document explaining the app functionality and example output.
- If your app is selected to be included in the VisRseq framework, you will be credited in the credits section of the webpage.

Assignment Submission

- Due by Sunday, July 17th @11:59PM Beijing Time (CST).
- Results will be announced and discussed on Monday July 18th.
- Submission using a **git pull request** of:
  - directory with your full name (Firstname_Lastname)
  - containing your submissions
  - a readme.txt (or readme.md) file, specifying the category(ies) you are submitting for and any additional information about your submission.

conclusions

limitations

- Scalability: few million rows and 30-40 columns of sequencing data
- cannot run R-apps in parallel
- desktop only

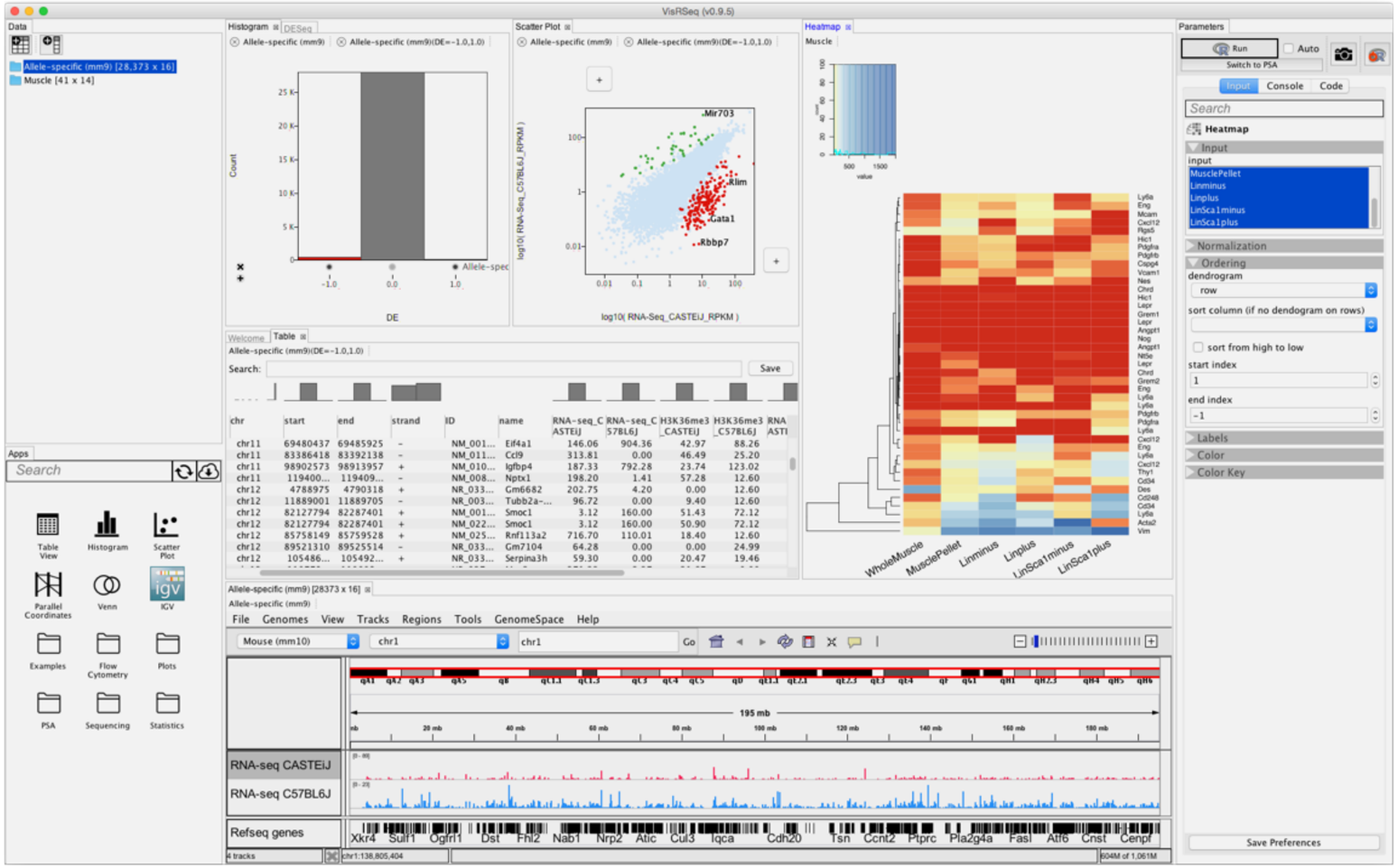
future work

- general purpose framework: Apps for other domains (e.g. Proteomics, etc.)
- workflow designer : link several apps to create “macro” apps.
- reproducibility: provenance / parameter exploration

acknowledgement

- Developers: Xu Fan, Kathy Cheng, Joseph Poper
- BC Genome Sciences Centre
- Lorincz lab, Underhill lab, Rossi lab, Mager lab

questions?



visrseq.github.io

(please email for latest version)