Jun 28, 2016

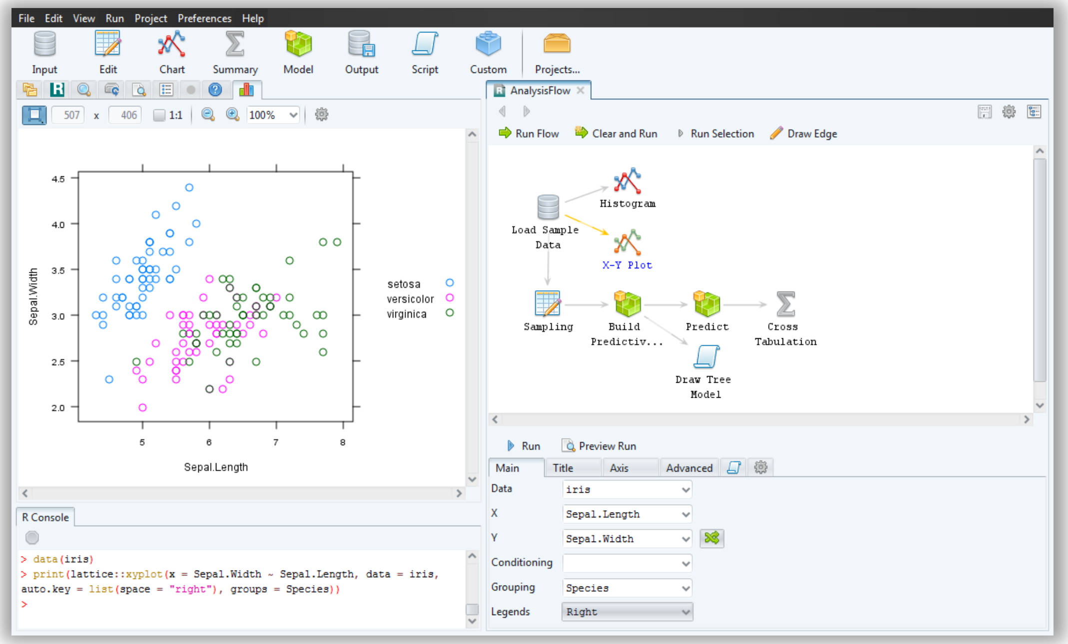
R AnalyticFlow 3

Interactive Data Analysis GUI for R

Ryota Suzuki, Tatsuhiro Nagai
Ef-prime, Inc.

R AnalyticFlow is:

- Data Analysis GUI for R
  - Desktop application written in Java
  - Works on Windows / Mac / Linux
  - Open source (LGPL)



```
> data(iris)
> print(lattice::xyplot(x = Sepal.Width ~ Sepal.Length, data = iris,
auto.key = list(space = "right"), groups = Species))
>
```

Data: iris
X: Sepal.Length
Y: Sepal.Width
Conditioning:
Grouping: Species
Legends: Right

We are:

- Ef-prime, Inc.
  - Data Analysis Consulting Company
  - Tokyo, Japan
  - Working on this project since 2007
- Tatsuhiro Nagai
  - Main Programmer
- Ryota Suzuki
  - Project Manager, UI/UX Design
  - Author of package pvclust

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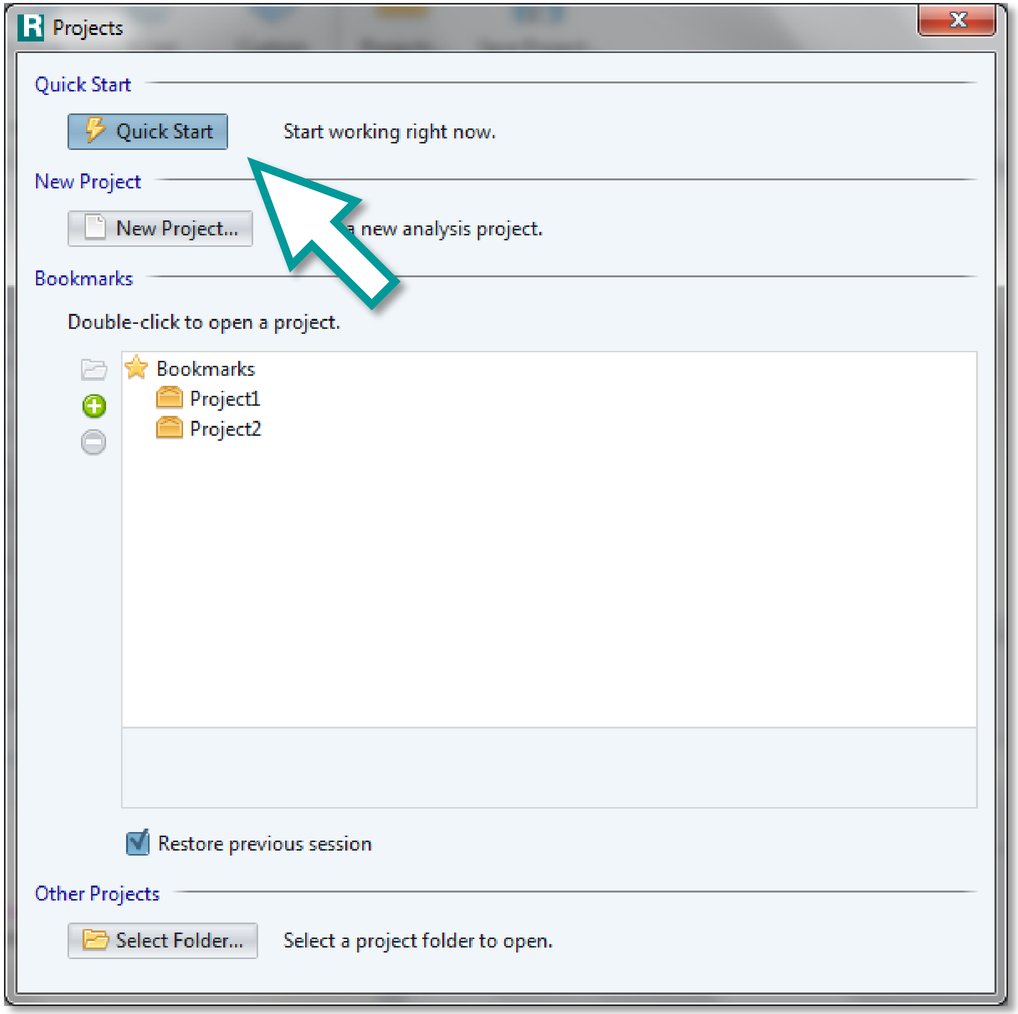
Quick Tour

Projects Dialog



Start working right now.

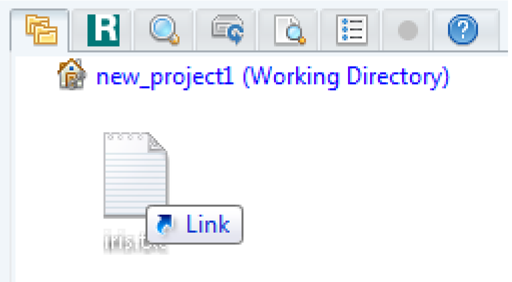
a new analysis project.

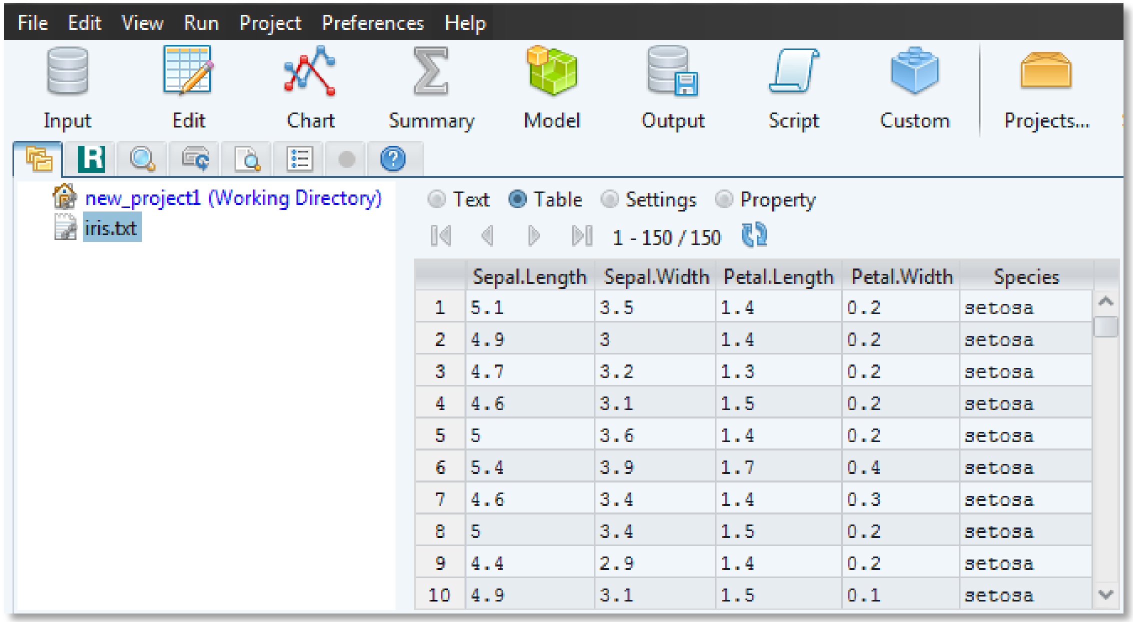
Double-click to open a project.

☑ Restore previous session

Select a project folder to open.

View Data



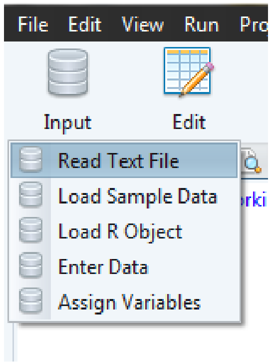


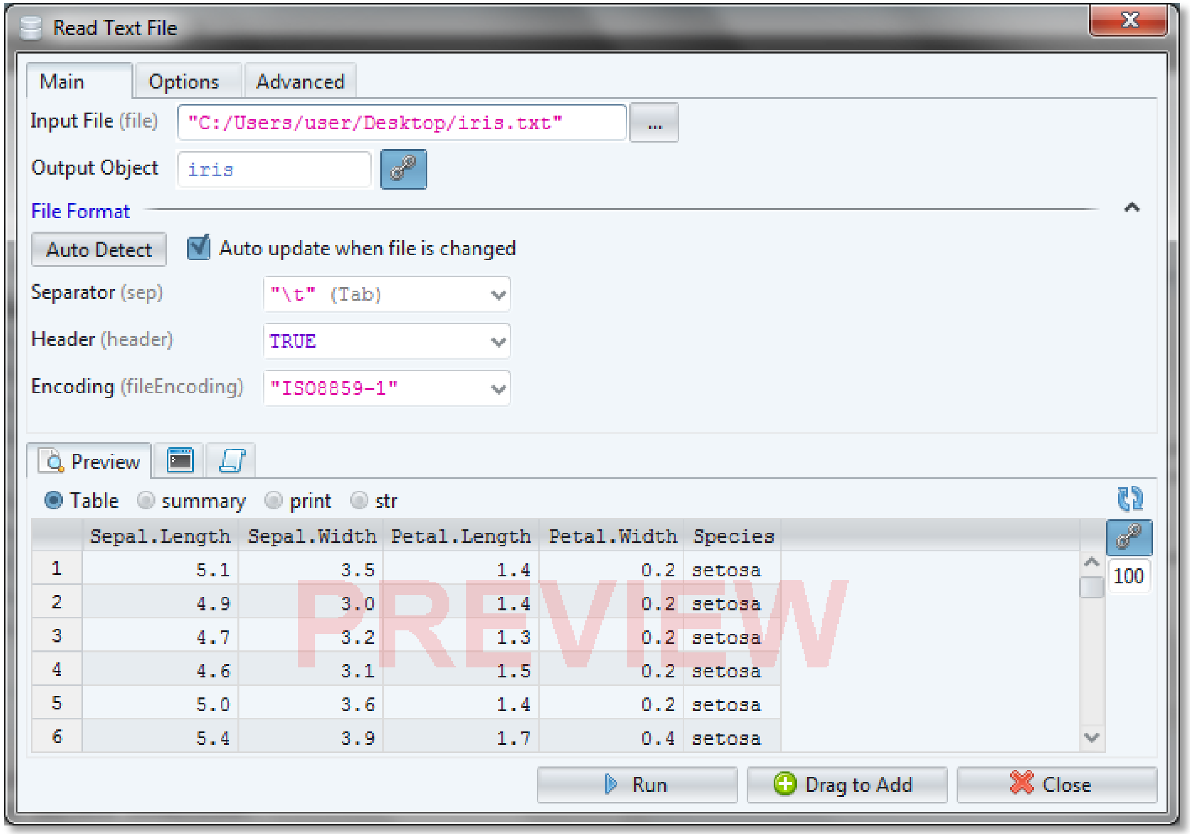
○ Text ● Table ○ Settings ○ Property

1 - 150 / 150

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.6	3.4	1.4	0.3	setosa
8	5	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa

Read Text File





Input File (file) "C:/Users/user/Desktop/iris.txt"

Output Object iris

☑ Auto update when file is changed

Separator (sep) "\t" (Tab)

Header (header) TRUE

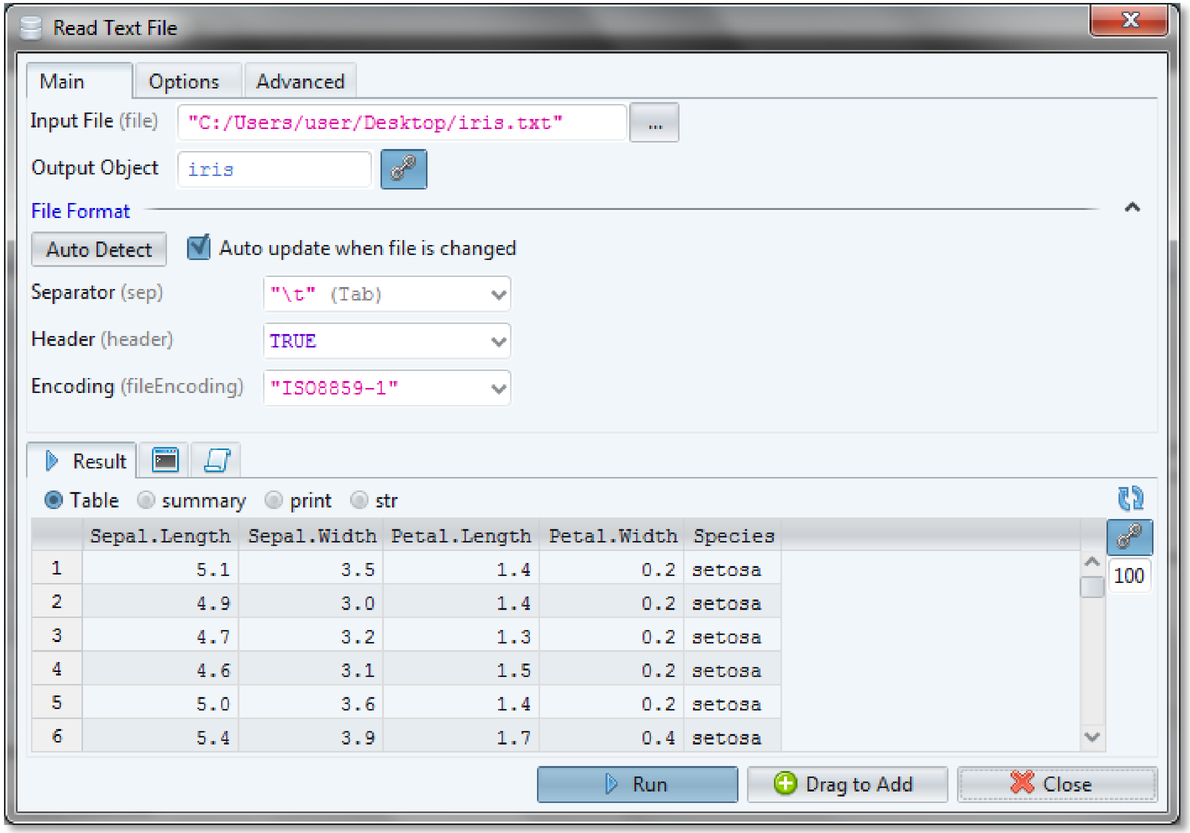
Encoding (fileEncoding) "ISO8859-1"

● Table ○ summary ○ print ○ str

100

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

Run



Input File (file) "C:/Users/user/Desktop/iris.txt"

Output Object iris

☑ Auto update when file is changed

Separator (sep) "\t" (Tab)

Header (header) TRUE

Encoding (fileEncoding) "ISO8859-1"

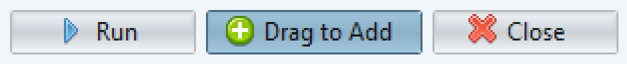
● Table ○ summary ○ print ○ str

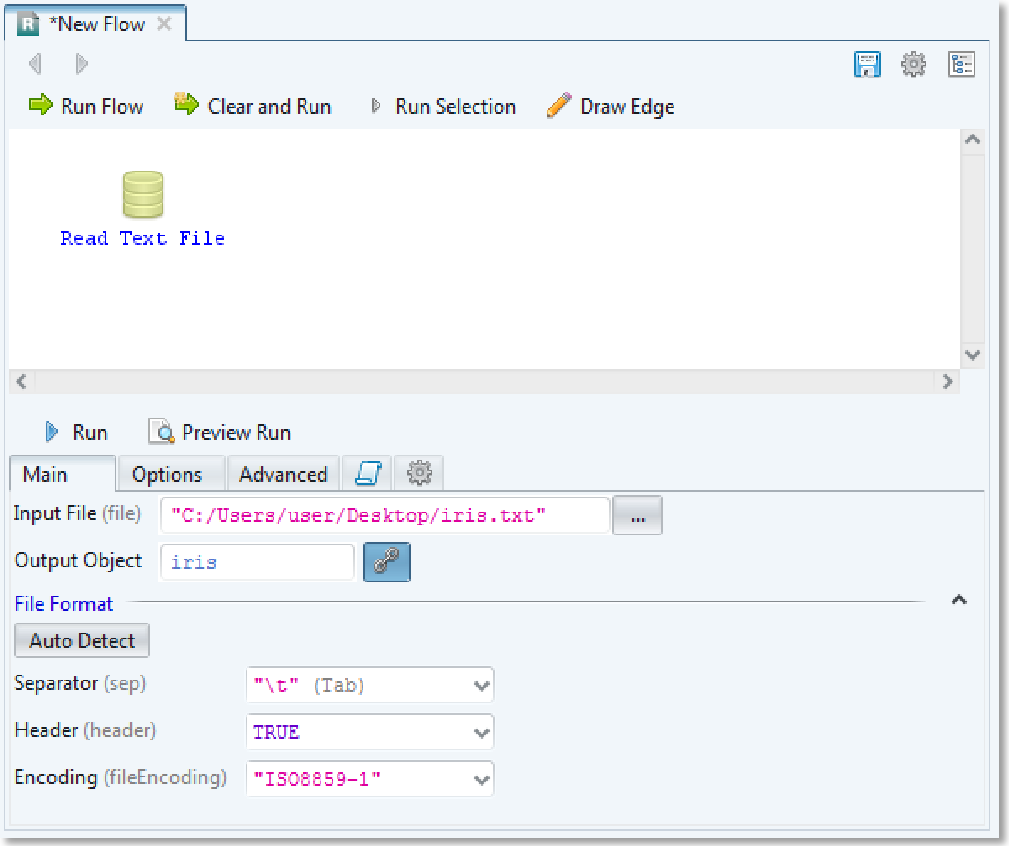
100

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

```
> iris <- read.table(file = "C:/Users/user/Desktop/iris.txt", header = TRUE,
sep = "\t", fileEncoding = "ISO8859-1", quote = "\"", stringsAsFactors =
FALSE, comment.char = "", na.strings = "")
```

Add to Workflow





Input File (file) "C:/Users/user/Desktop/iris.txt"

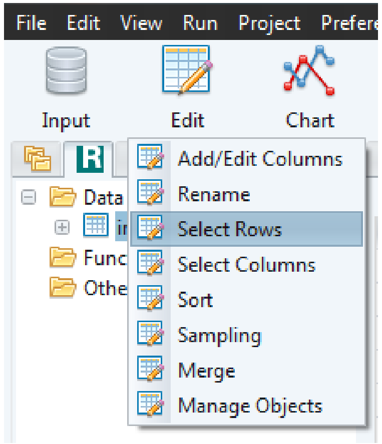
Output Object iris

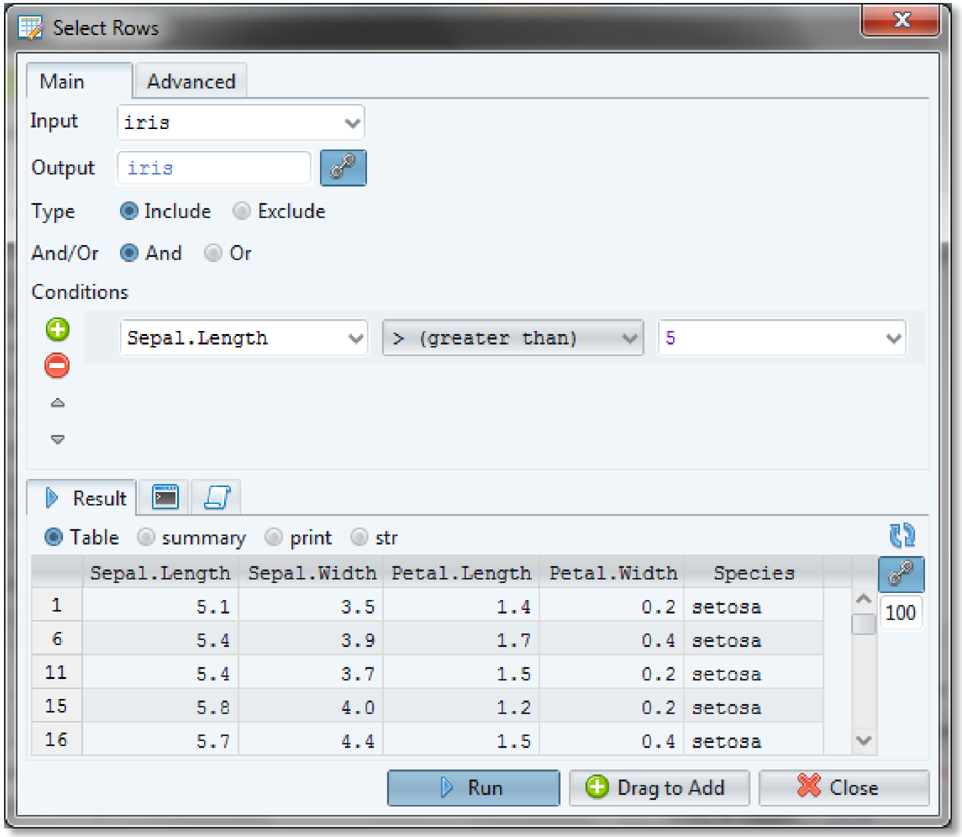
Separator (sep) "\t" (Tab)

Header (header) TRUE

Encoding (fileEncoding) "ISO8859-1"

Select Rows





Input: iris

Output: iris

Type: ● Include ○ Exclude

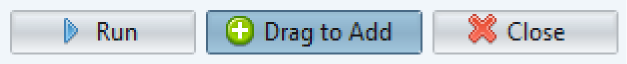
And/Or: ● And ○ Or

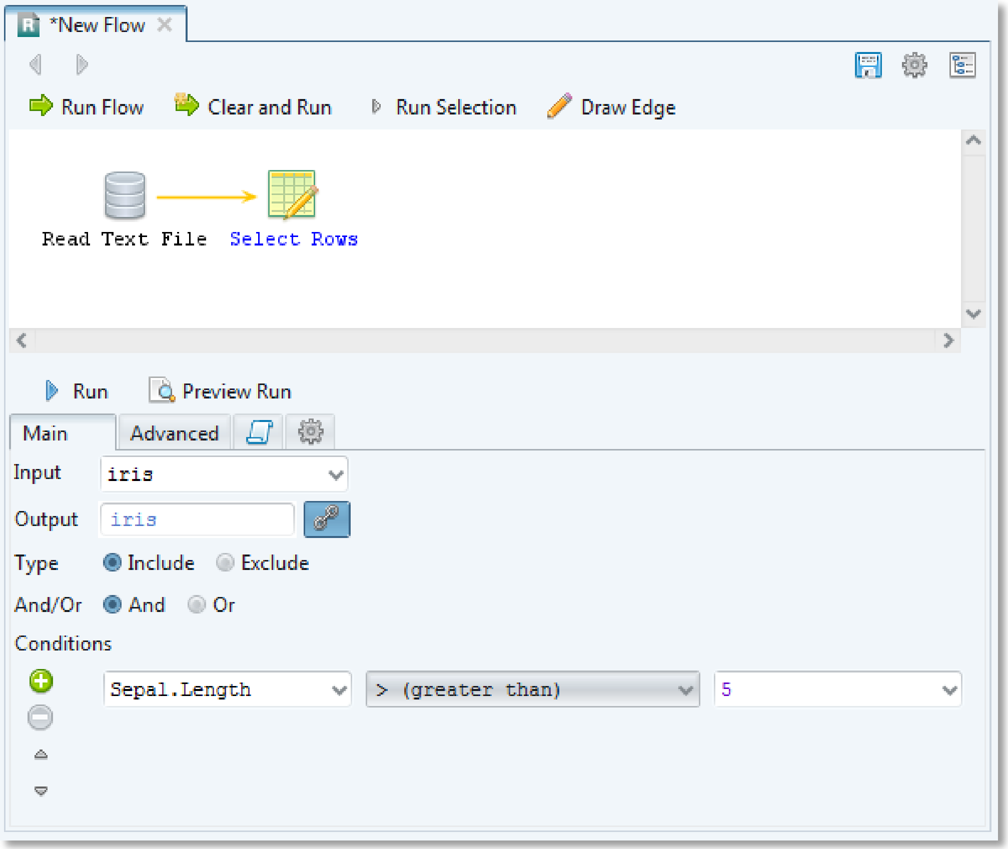
Sepal.Length > (greater than) 5

● Table ○ summary ○ print ○ str

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
11	5.4	3.7	1.5	0.2	setosa
15	5.8	4.0	1.2	0.2	setosa
16	5.7	4.4	1.5	0.4	setosa

Add to Workflow





Input: iris

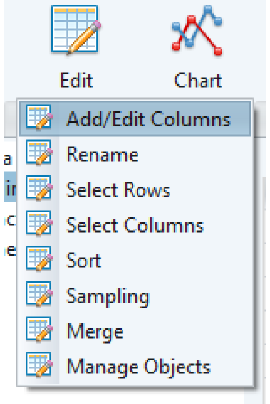
Output: iris

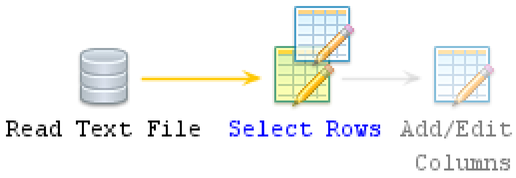
Type: ● Include ○ Exclude

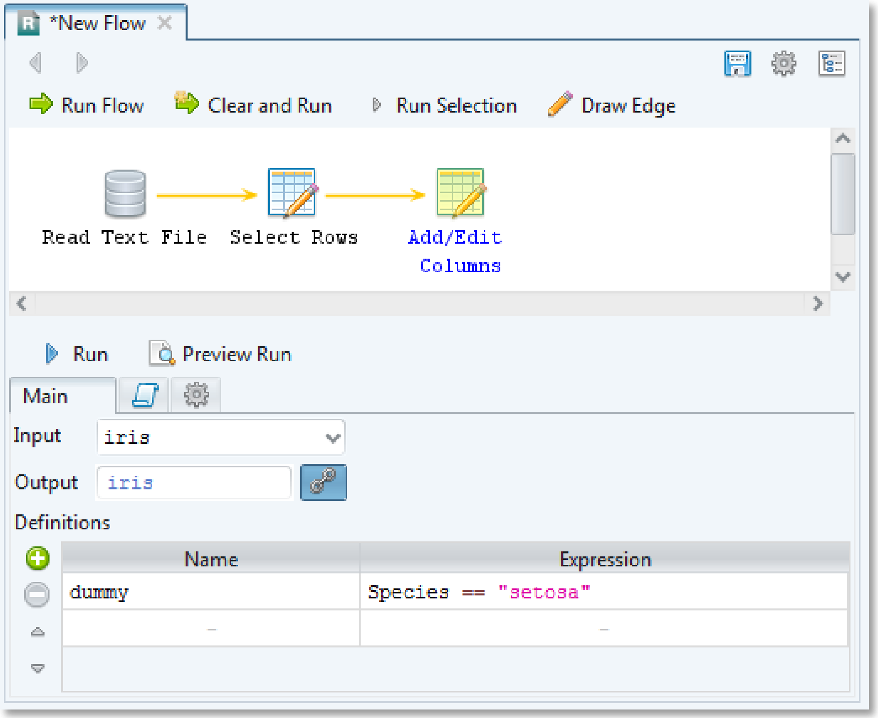
And/Or: ● And ○ Or

Conditions: Sepal.Length | > (greater than) | 5

Adding Directly







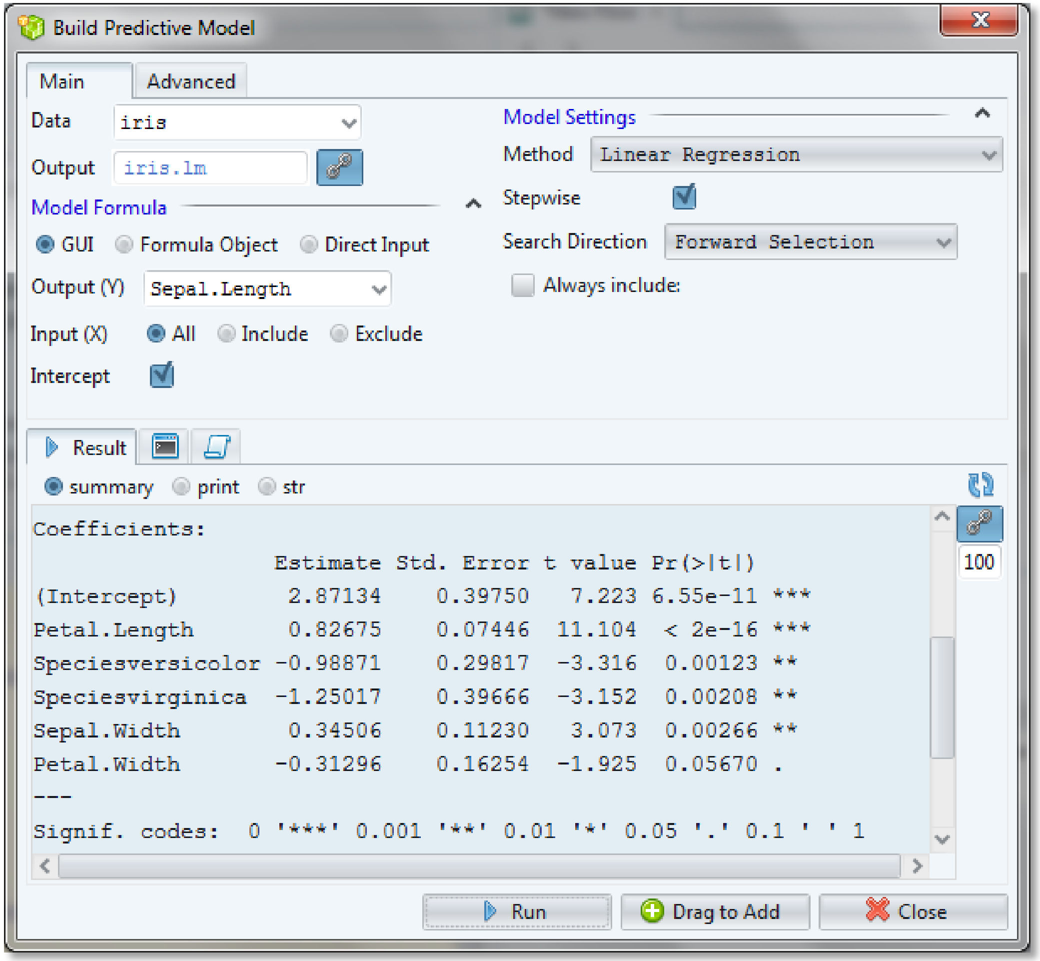
Input: iris

Output: iris

Definitions

Name	Expression
dummy	Species == "setosa"
–	–

Modeling



Data: iris

Output: iris.lm

● GUI ○ Formula Object ○ Direct Input

Output (Y): Sepal.Length

Input (X): ● All ○ Include ○ Exclude

Intercept: ☑

Method: Linear Regression

Stepwise: ☑

Search Direction: Forward Selection

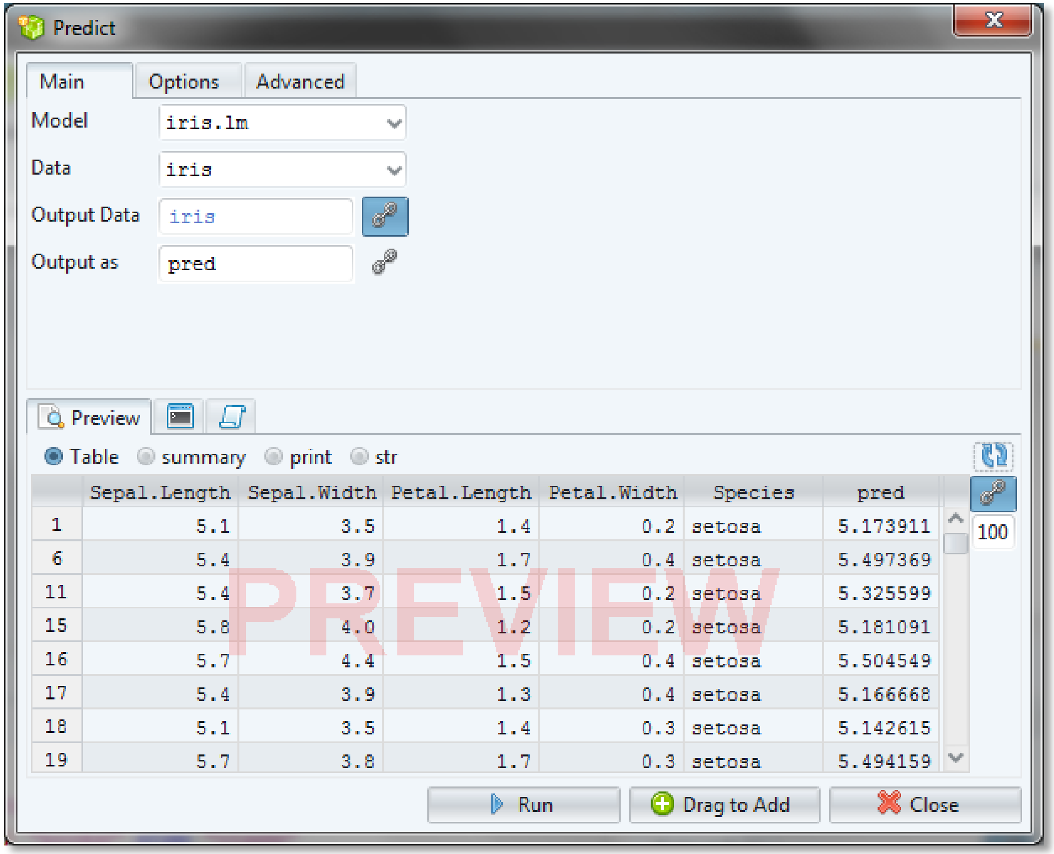
☐ Always include:

● summary ○ print ○ str

100

```
Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        2.87134    0.39750   7.223 6.55e-11 ***
Petal.Length       0.82675    0.07446  11.104  < 2e-16 ***
Speciesversicolor -0.98871    0.29817  -3.316  0.00123 **
Speciesvirginica  -1.25017    0.39666  -3.152  0.00208 **
Sepal.Width        0.34506    0.11230   3.073  0.00266 **
Petal.Width       -0.31296    0.16254  -1.925  0.05670 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Prediction



Model: iris.lm

Data: iris

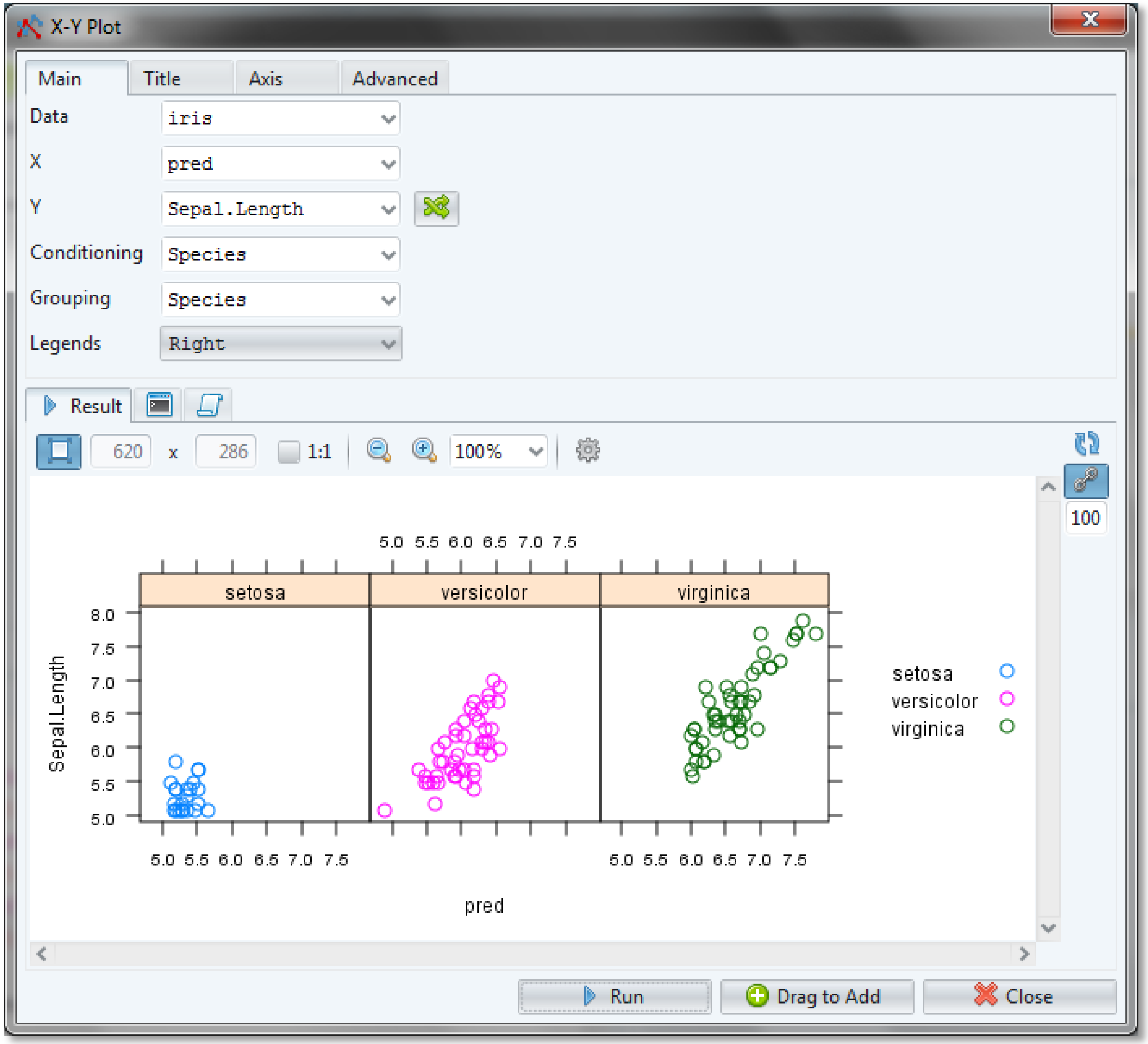
Output Data: iris

Output as: pred

● Table ○ summary ○ print ○ str

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	pred
1	5.1	3.5	1.4	0.2	setosa	5.173911
6	5.4	3.9	1.7	0.4	setosa	5.497369
11	5.4	3.7	1.5	0.2	setosa	5.325599
15	5.8	4.0	1.2	0.2	setosa	5.181091
16	5.7	4.4	1.5	0.4	setosa	5.504549
17	5.4	3.9	1.3	0.4	setosa	5.166668
18	5.1	3.5	1.4	0.3	setosa	5.142615
19	5.7	3.8	1.7	0.3	setosa	5.494159

Plot



Data iris

X pred

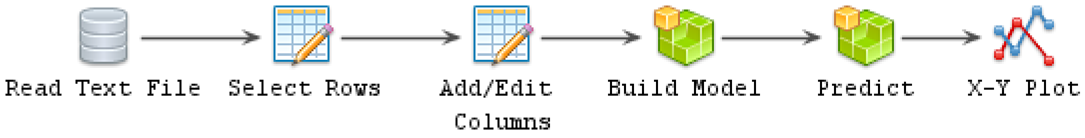
Y Sepal.Length

Conditioning Species

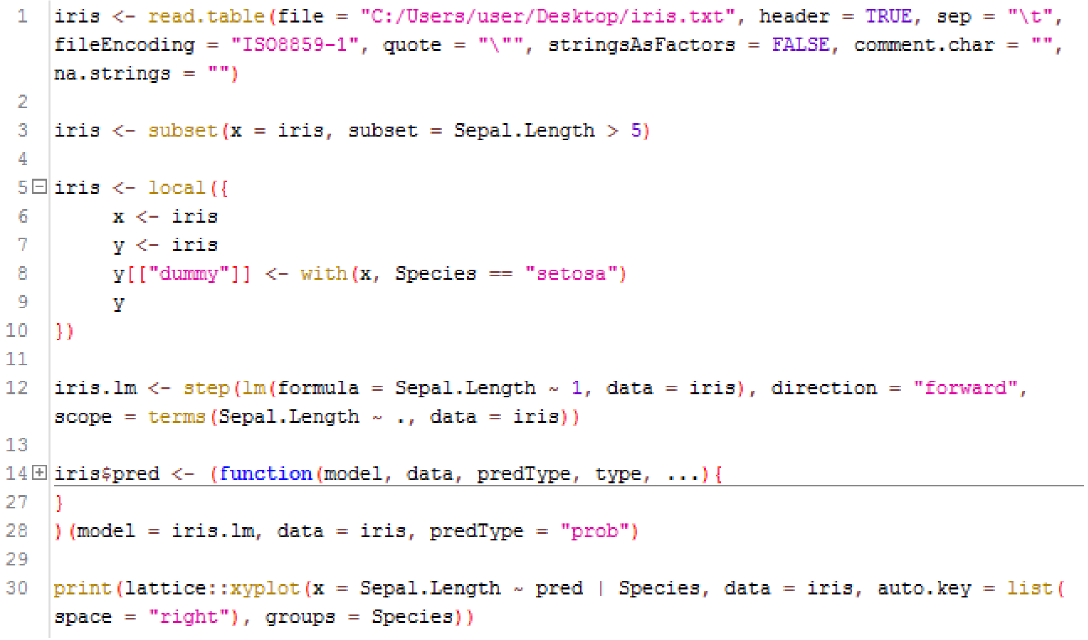
Grouping Species

Legends Right

Analysis Workflow

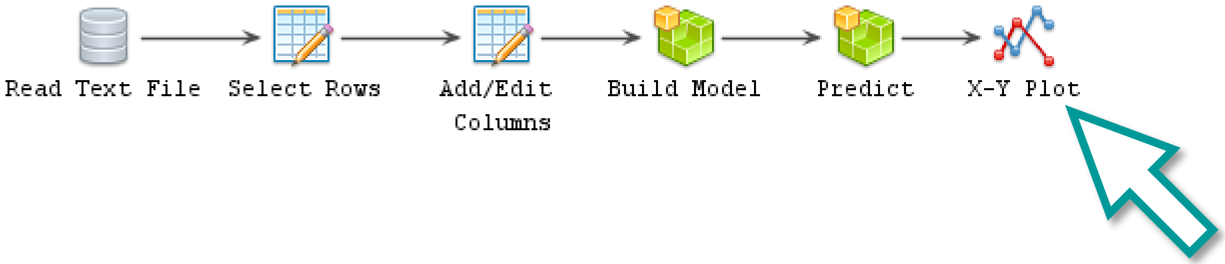


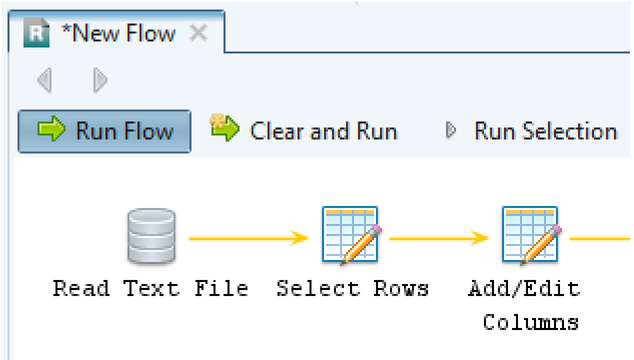
Read Text File → Select Rows → Add/Edit Columns → Build Model → Predict → X-Y Plot



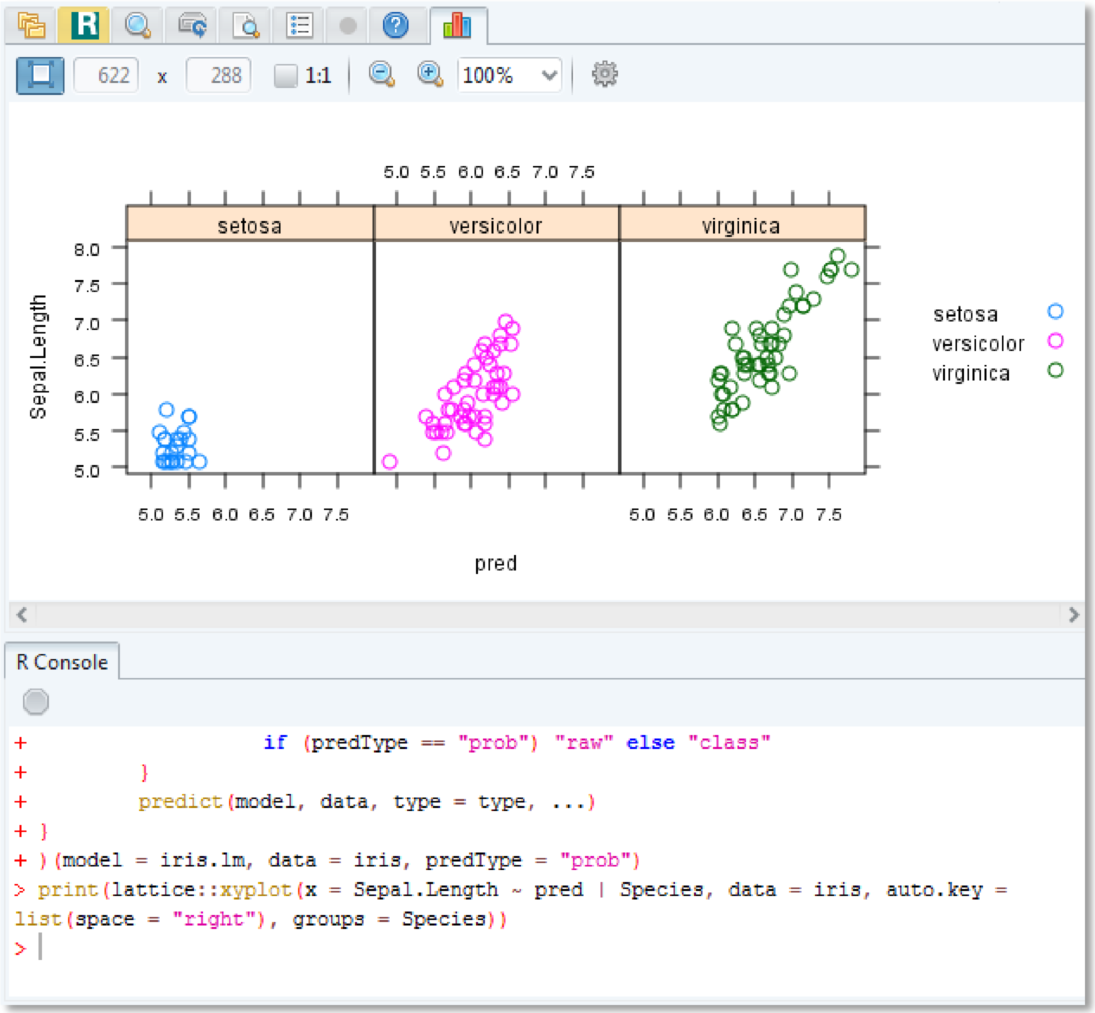
```
iris <- read.table(file = "C:/Users/user/Desktop/iris.txt", header = TRUE, sep = "\t", fileEncoding = "ISO8859-1", quote = "\"", stringsAsFactors = FALSE, comment.char = "", na.strings = "")

iris <- subset(x = iris, subset = Sepal.Length > 5)

iris <- local({
      x <- iris
      y <- iris
      y[["dummy"]] <- with(x, Species == "setosa")
      y
})

iris.lm <- step(lm(formula = Sepal.Length ~ 1, data = iris), direction = "forward", scope = terms(Sepal.Length ~ ., data = iris))

iris$pred <- (function(model, data, predType, type, ...){
}
)(model = iris.lm, data = iris, predType = "prob")

print(lattice::xyplot(x = Sepal.Length ~ pred | Species, data = iris, auto.key = list(space = "right"), groups = Species))
```

Run through the Workflow



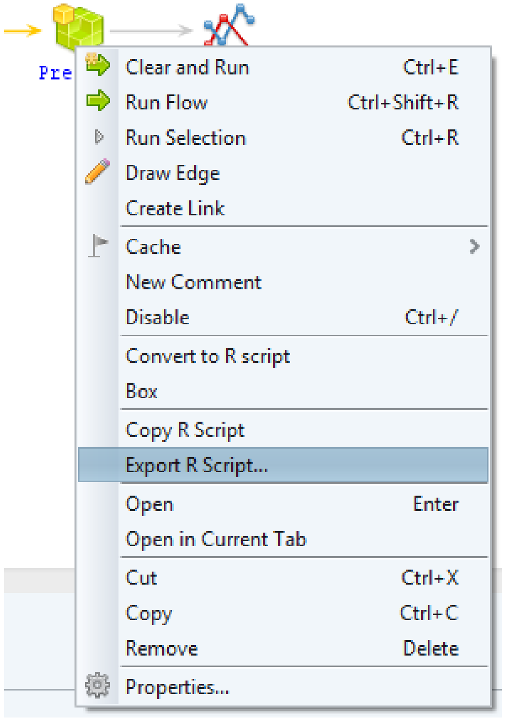


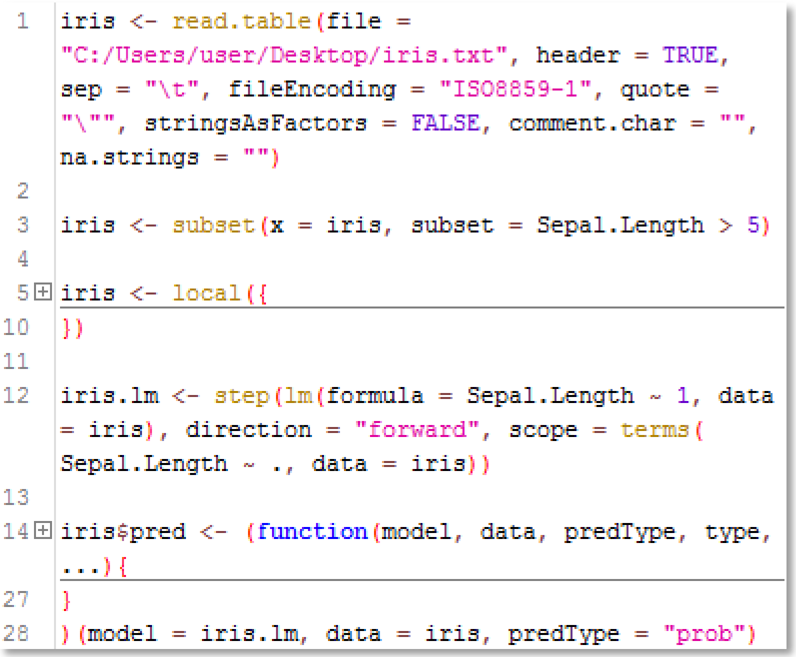
Run through the Workflow



```
+                    if (predType == "prob") "raw" else "class"
+           }
+           predict(model, data, type = type, ...)
+ }
+ )(model = iris.lm, data = iris, predType = "prob")
> print(lattice::xyplot(x = Sepal.Length ~ pred | Species, data = iris, auto.key =
list(space = "right"), groups = Species))
> |
```

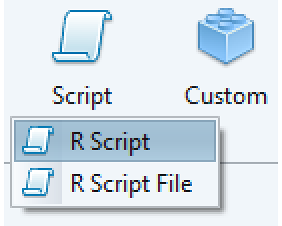
Export to R Script

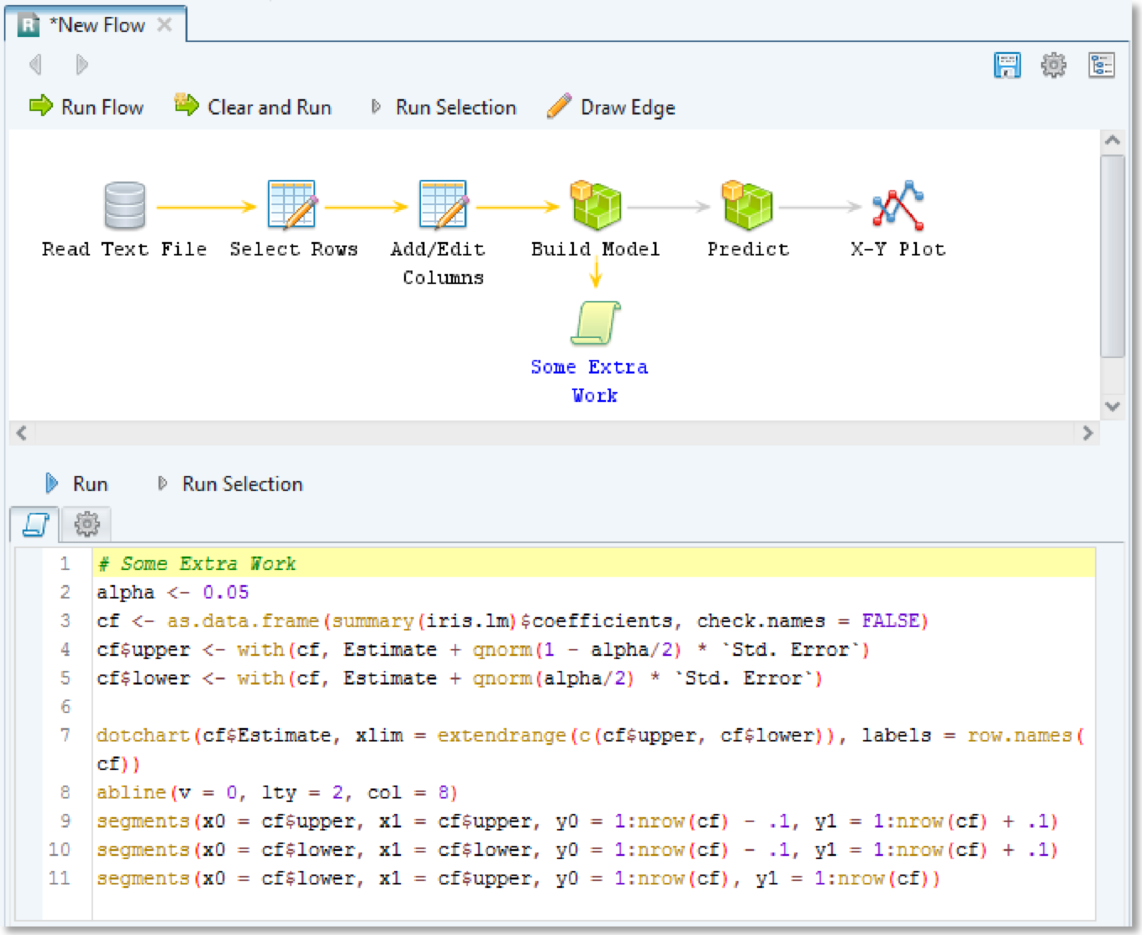




```
iris <- read.table(file = "C:/Users/user/Desktop/iris.txt", header = TRUE, sep = "\t", fileEncoding = "ISO8859-1", quote = "\"", stringsAsFactors = FALSE, comment.char = "", na.strings = "")

iris <- subset(x = iris, subset = Sepal.Length > 5)

iris <- local({
})

iris.lm <- step(lm(formula = Sepal.Length ~ 1, data = iris), direction = "forward", scope = terms(Sepal.Length ~ ., data = iris))

iris$pred <- (function(model, data, predType, type, ...){
}
)(model = iris.lm, data = iris, predType = "prob")
```

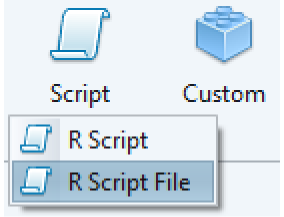
Write R Script by Hand

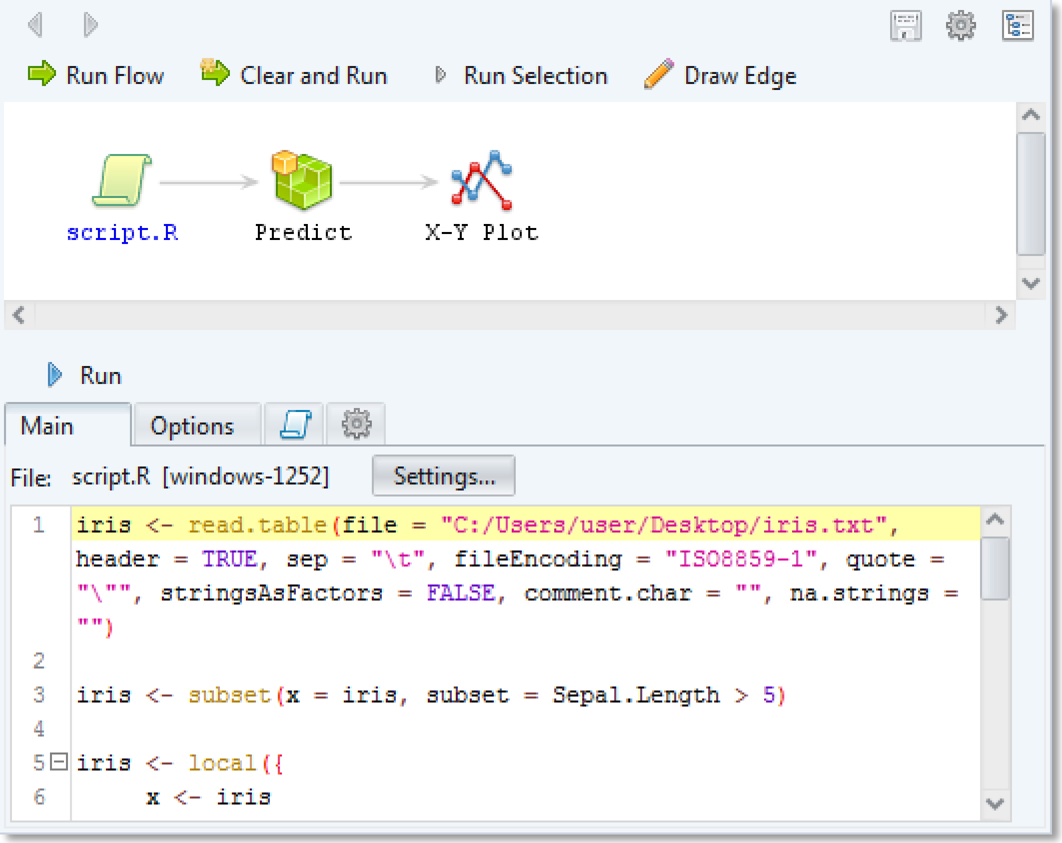




```
# Some Extra Work
alpha <- 0.05
cf <- as.data.frame(summary(iris.lm)$coefficients, check.names = FALSE)
cf$upper <- with(cf, Estimate + qnorm(1 - alpha/2) * `Std. Error`)
cf$lower <- with(cf, Estimate + qnorm(alpha/2) * `Std. Error`)

dotchart(cf$Estimate, xlim = extendrange(c(cf$upper, cf$lower)), labels = row.names(cf))
abline(v = 0, lty = 2, col = 8)
segments(x0 = cf$upper, x1 = cf$upper, y0 = 1:nrow(cf) - .1, y1 = 1:nrow(cf) + .1)
segments(x0 = cf$lower, x1 = cf$lower, y0 = 1:nrow(cf) - .1, y1 = 1:nrow(cf) + .1)
segments(x0 = cf$lower, x1 = cf$upper, y0 = 1:nrow(cf), y1 = 1:nrow(cf))
```

Insert R Script Files



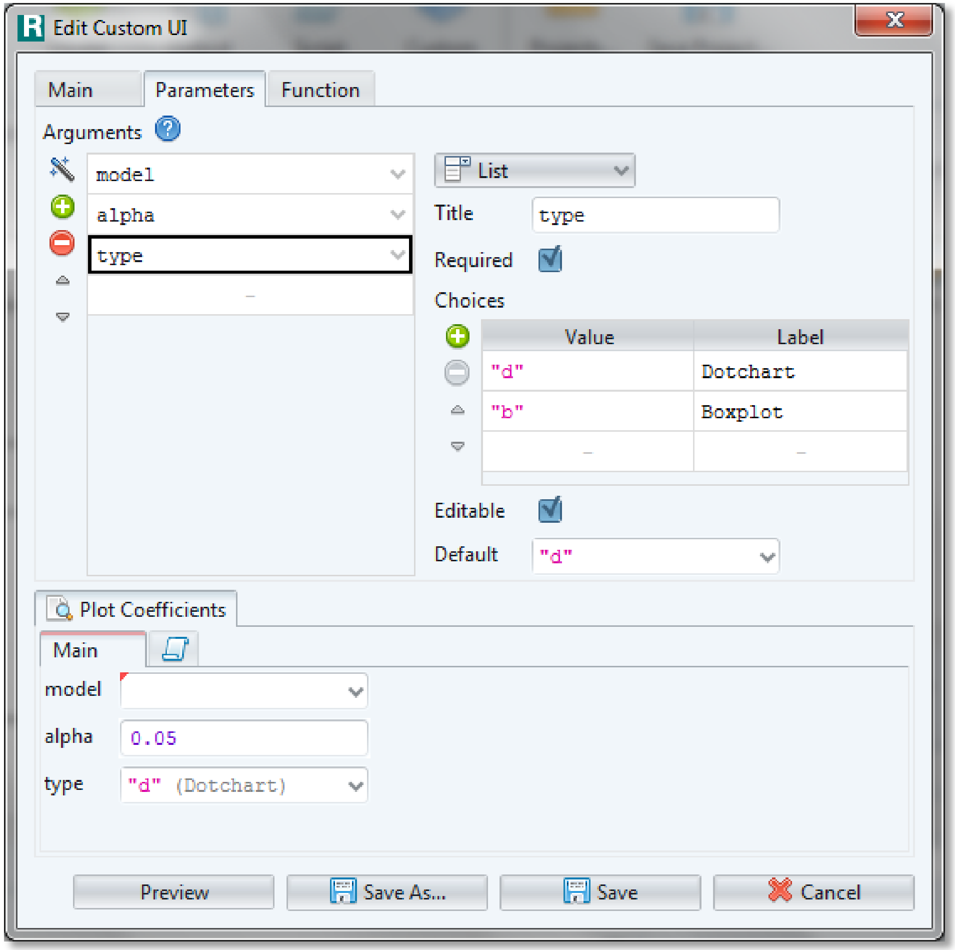


File: script.R [windows-1252]

```
iris <- read.table(file = "C:/Users/user/Desktop/iris.txt",
header = TRUE, sep = "\t", fileEncoding = "ISO8859-1", quote =
"\"", stringsAsFactors = FALSE, comment.char = "", na.strings =
"")

iris <- subset(x = iris, subset = Sepal.Length > 5)

iris <- local({
     x <- iris
```

```
> source(file = "script.R", encoding = "windows-1252", echo = FALSE)
```

Write Custom UI



Arguments

- model
- alpha
- type

List

Title: type

Required ☑

Choices

Value	Label
"d"	Dotchart
"b"	Boxplot

Editable ☑

Default: "d"

Plot Coefficients

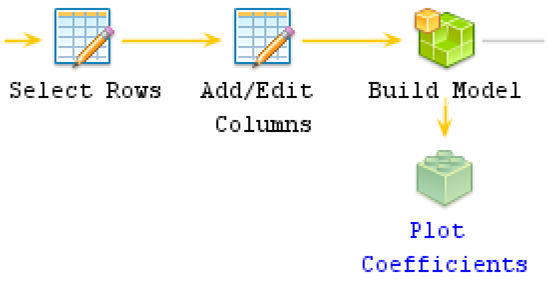
Main

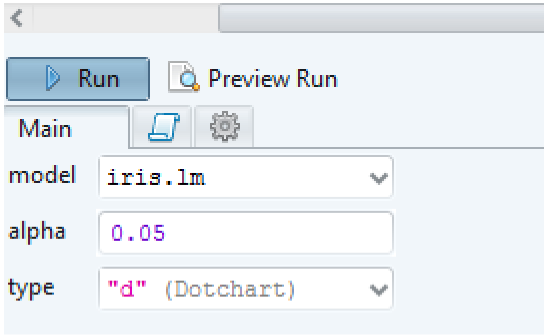
model:

alpha: 0.05

type: "d" (Dotchart)

Write Custom UI

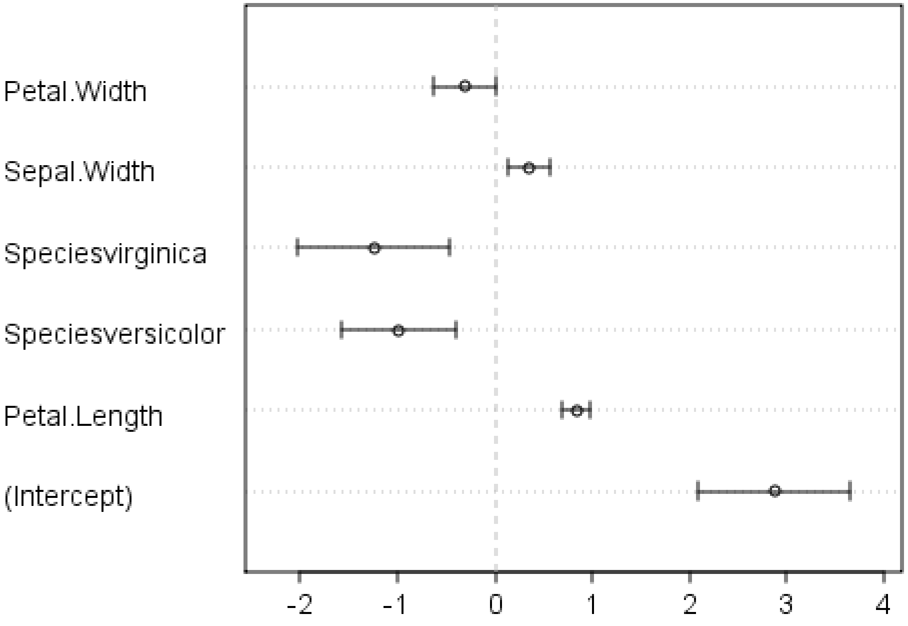




model: iris.lm

alpha: 0.05

type: "d" (Dotchart)



Benefits

- Designed for Data Analysis
  - Analyze interactively
  - Practical tools out of the box
  - More focus on data (not programming)

- Easy to Use
  - Best for R beginners
  - Great for working with non-statisticians
  - Help sharing your work visually with:
    - Your colleagues
    - Yourself several months later

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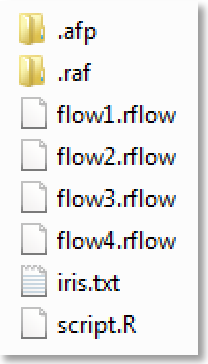
Compatibility

- Simple Project System
  - Project folder contains:
    - Data, Workflows, etc.
    - Metadata (.afp/.raf hidden-folders)



.afp
.raf
flow1.rflow
flow2.rflow
flow3.rflow
flow4.rflow
iris.txt
script.R

  - Compatible with other systems
    - You can use the same folder as an RStudio project, or use version control system together (Git, Subversion, etc.)

- Switch between R Script
  - Export workflows as R scripts
  - Insert R scripts into a workflow

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