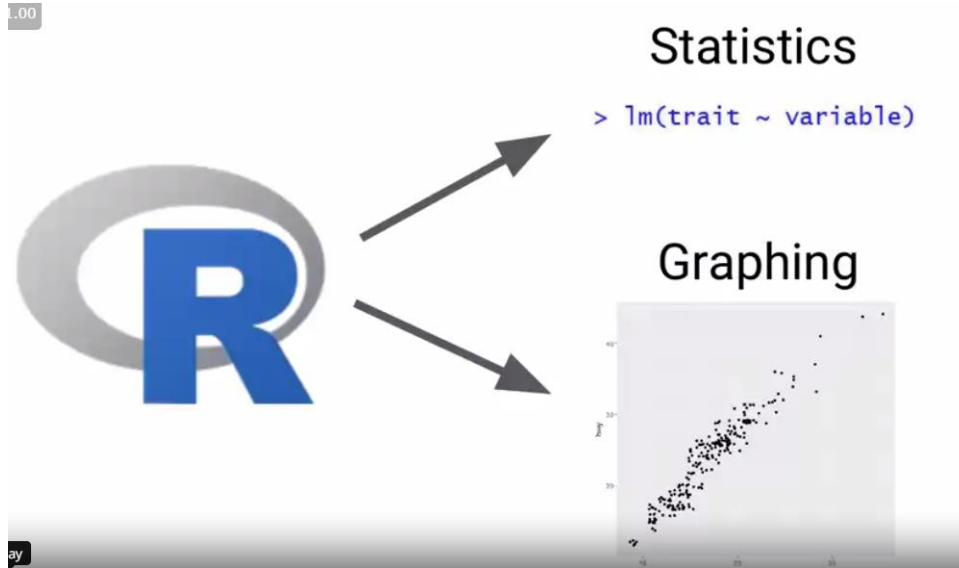


# R and RStudio

Eunbyeol Lee

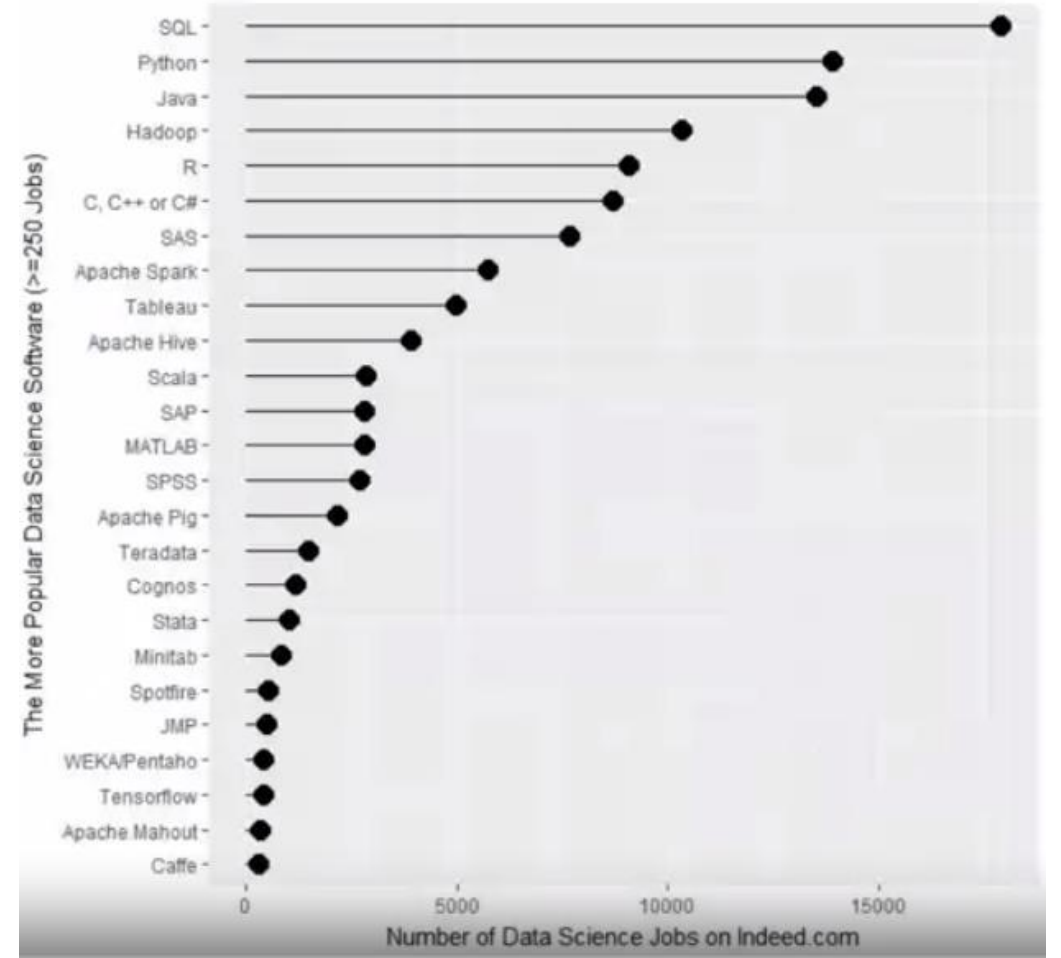
2019.11.22

# R

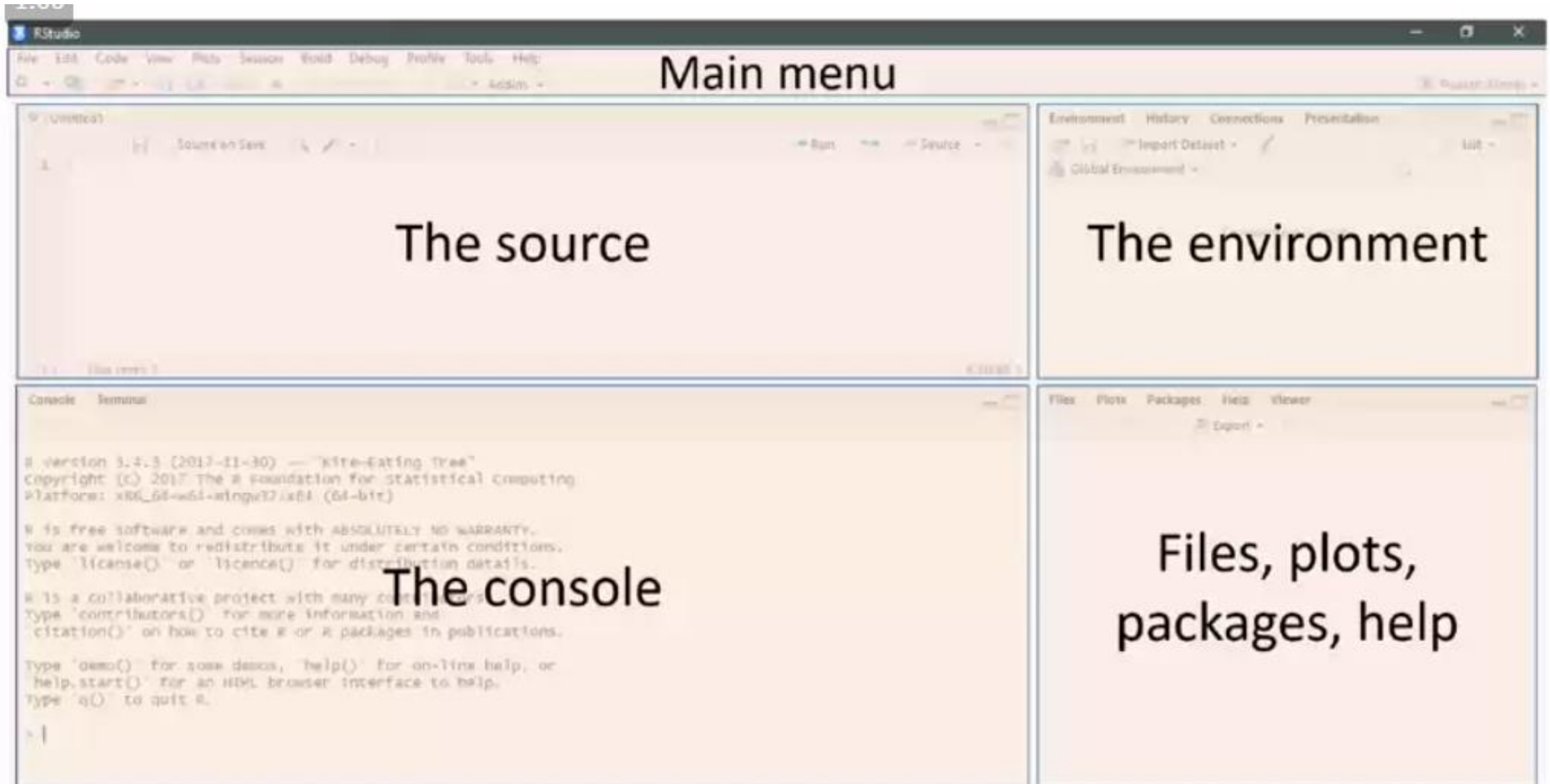


# \$

<https://cran.r-project.org/>



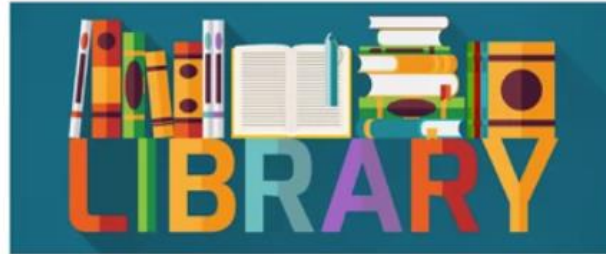
# R Studio



# R package



=



```
source("https://bioconductor.org/biocLite.R")
```

```
biocLite()
```

```
biocLite("GenomicFeatures")
```

# R package

## Step 1: Install

```
install.packages("ggplot2")
```

What packages are installed?

```
installed.packages() or library()
```

## Updating packages

```
old.packages()
```

```
update.packages()
```

```
install.packages("packagename")
```

## Step 2: Load

```
library()
```

```
library(ggplot2)
```

```
version
```

```
sessionInfo()
```

# Projects in R

