DATA SCIENCE using R

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Data Science: Introduction

- Data Science is an approach of **analysing** the past or current data and **predicting** the future outcomes with the aim of making **well-versed decisions**.

- Data science is an **inter-disciplinary field** that uses **scientific methods**, **knowledge of mathematics and statistics, algorithms, programming skills** to extract knowledge and insights from raw data.

Data Science: Introduction

Why Data Science

- Companies have been **storing their data**. Data has become the **most abundant** thing today. But, **what will we do with this data**? Let's take an example:

- Say, company which makes **mobile phones→ released their first product**→ became a **massive hit**→ its time to **come up with something new**, so as to **meet the expectations of the users**→ eagerly **waiting for next release.**

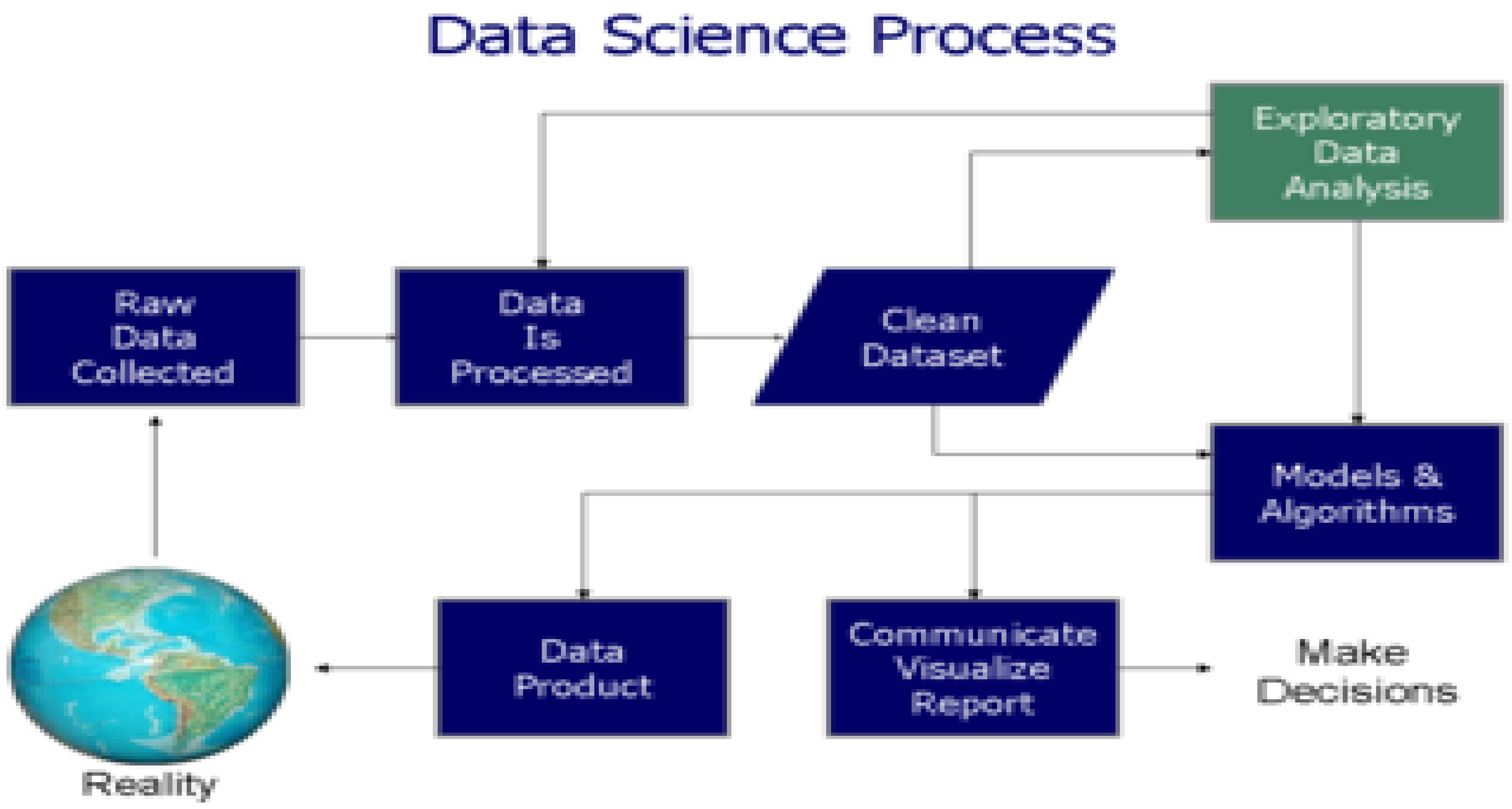
- **Here comes Data Science**→ apply various **data mining techniques** like sentiment analysis, **knowledge of mathematical and statistical methods, scientific methods, algorithms, programming skills** on user generated feedback and **pick things what users are expecting in the next release and making well-versed decisions**.

- Thus, **through Data Science we can make better decisions**, we can **reduce production cos**ts by coming out with efficient ways, and **give customers what they actually want**!

- Thus, there are **countless benefits that Data Science can result in**, and hence it has become **absolutely necessary for the company to have a Data Science Team**.

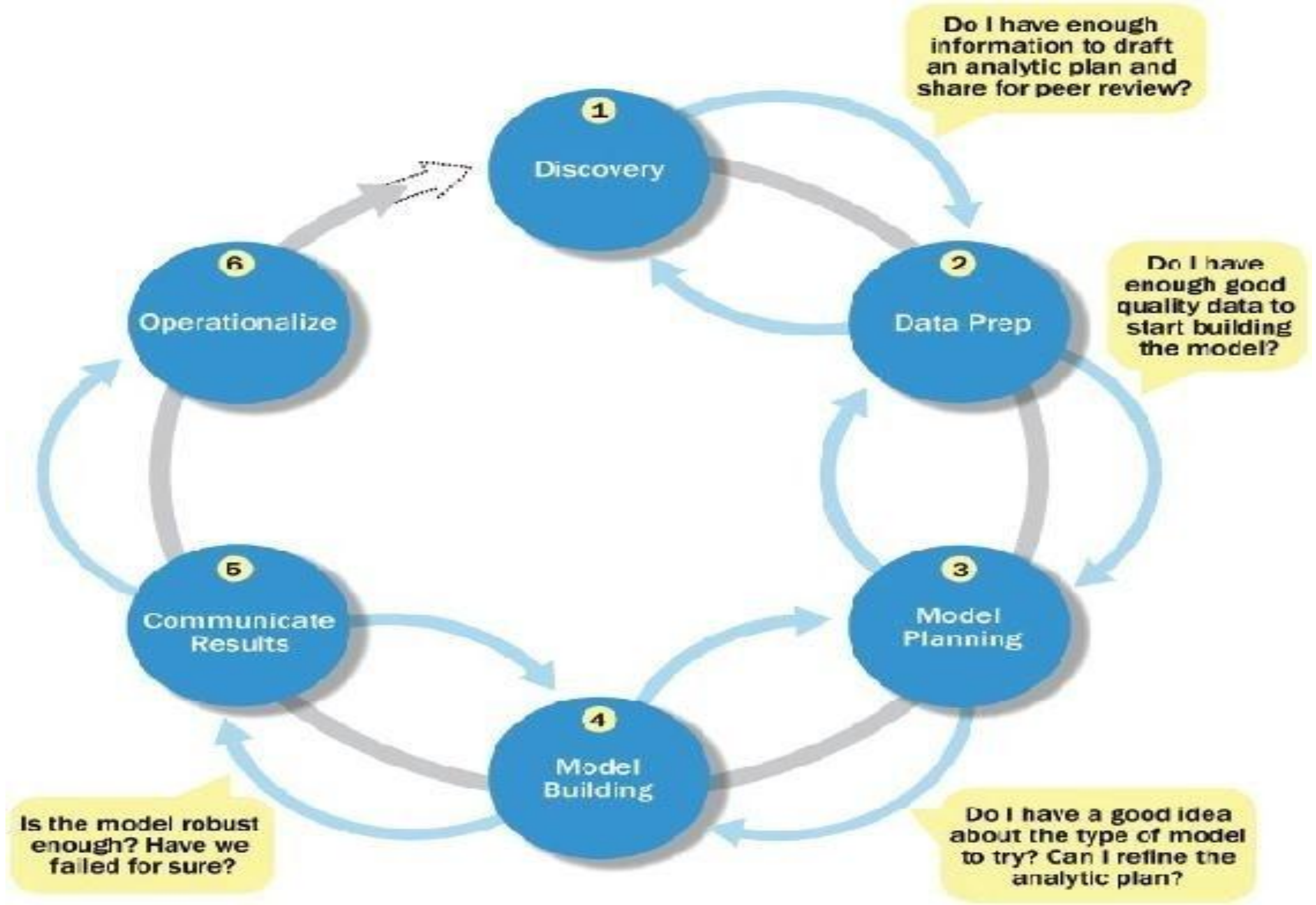
Data Science: Introduction

- **Data science – making effective decision and development of data product**



Overview of Data Analytics Lifecycle

- Data Analytics Lifecycle defines **analytics process** that takes place in **analysing the data** and **product development**.
- It mainly includes **6 phases**:



Do I have enough information to draft an analytic plan and share for peer review?
1 Discovery
2 Data Prep
Do I have enough good quality data to start building the model?
3 Model Planning
Do I have a good idea about the type of model to try? Can I refine the analytic plan?
4 Model Building
Is the model robust enough? Have we failed for sure?
5 Communicate Results
6 Operationalize

Overview of Data Analytics Lifecycle

Phase 1- Discovery:

- In Phase 1, the team learns the **business domain**, including relevant history such as whether the organization or business unit has **attempted similar projects in the past** from which they can learn.

- The team assesses the **resources available** to support the project **in terms of people, technology, time** and **data**.

- Important activities in this phase include **framing the business problem** as an **analytics challenge** that can be addressed in subsequent phases.

Phase 2- Data Preparation:

- Phase 2 requires the **presence of an analytic sandbox**, in which the team can work with data and perform analytics for the duration of the project.

- The team needs to **execute extract, load, and transform** (ELT) or **extract, transform and load** (ETL) to get data into the sandbox.

- Data should be **transformed in the ETLT process so the team can work with it and analyse it**.

- In this phase, the team also needs to **familiarize itself with the data thoroughly** and take steps to **condition the data**.

Overview of Data Analytics Lifecycle

Phase 3-Model Planning:

- Phase 3 is model planning, where the team determines the **methods, techniques** and **workflow** it intends to follow.
- The team explores the data to learn about the **relationships between variables** and subsequently **selects key variables** and the **most suitable models**.

Phase 4-Model Building:

- In Phase 4, the team **develops data sets for testing, training**.
- In addition, in this phase the team **builds and executes models** based on the work done in the model planning phase.
- The team also considers whether its **existing tools will suffice for running the models**, or if it will **need a more robust environment for executing models** and work flows (for example, fast hardware and parallel processing, if applicable).

Overview of Data Analytics Lifecycle

Phase 5-Communicate Results:

- In Phase 5, the team, in **collaboration with major stakeholders**, determines if the results of the project are a success or a failure based on the criteria developed in Phase 1.

- The team should identify **key findings, quantify the business value**, and **develop a narrative to summarize** and **convey findings to stakeholders**.

Phase 6-0perationalize:

- In Phase 6, the team **delivers final reports**, **briefings, code, and technical documents**.

- In addition, the team **may run a pilot project to implement the models in a production environment**.

Overview of Data Analytics Lifecycle: Phase 1: Discovery

- The first phase of the Data Analytics Lifecycle involves **Discovery**. This phase is focusing on the business requirements.

1. DISCOVERY:
State problem
& collect Data

- In this phase, the data science team must **learn and investigate the problem**, **develop context**(situation) and **understanding**, and **learn about the data sources needed and available** for the project. Also, the team **formulates initial hypotheses**(suggestions) that can later be tested with data. (Tasks) (Suggestions, activities, actions, ideas, predictions→ Problem Statement)

1. Learning the Business Domain

- Understanding the **domain area of the problem is essential**.
- In many cases, **data scientists will have deep computational and quantitative knowledge** that can be broadly applied across many disciplines. These data scientists have **deep knowledge of the methods, techniques**, and **ways for applying heuristics to a variety of business and conceptual problems**. Others in this area may have deep knowledge of a domain area, coupled with quantitative expertise.
- At this early stage in the process, the **team needs to make an assessment and formulates initial hypotheses**. The earlier the team can make this assessment the better, helps to identify the resources needed for the project team and ensures the team in the right direction in development of project.

Overview of Data Analytics Lifecycle: Phase 1: Discovery

2. Resources

- As part of the discovery phase, the **team needs to assess the resources available to support the project**. Resources include **technology, tools, systems, data**, and **people**.
- In addition, **try to evaluate the level of analytical sophistication**(skills) within the organization and **gaps** that may exist related to tools, technology, and skills.
- In addition to the skills and computing resources, it is advisable to take inventory of the **types of data** available to the team for the project. The team will need to determine whether it must collect additional data, purchase it from outside sources, or transform existing data.
- Ensure the project team has the **right mix of domain experts, customers, analytic talent**, and project management to be effective. In addition**, evaluate how much time is needed** and if the team has the right breadth and depth of skills.

3. Framing the Problem

- Framing the problem well is critical to the **success of the project**.
- Framing is the process of **stating the analytics problem to be solved**. Essentially, the team needs to **clearly articulate the current situation and its main challenges**. As part of this activity, it is important to **identify the main objectives of the project**, **identify what needs to be achieved in business terms**, and identify what needs to be done to meet the needs.
- At this point, it is a best practice to **write down the problem statement** and **share it with the key stakeholders**.
- Perhaps equally important is to **establish failure criteria**. Most people doing projects **prefer only to think of the success criteria** and what the conditions will look like when the participants are successful.

Overview of Data Analytics Lifecycle Phase 1: Discovery

4. Identifying Key Stakeholders

- Another important step is to identify the **key stakeholders** and their interests in the project.
- The team can identify **anyone who will benefit from the project** or **will be significantly impacted by the project**.
- When interviewing stakeholders, **learn about the domain area** and any **relevant history from similar analytics projects**. For example, the team may identify the results each **stakeholder wants from the project** and the criteria it will use to judge the success of the project.
- **Depending on the number of stakeholders and participants**, the team may consider **outlining the type of activity** and **participation expected from each stakeholder and participant**.

5. Interviewing the Analytics Sponsor

- The team should plan to **collaborate with the stakeholders to clarify and frame the analytics problem**. At the outset, project sponsors may have a predetermined solution that may not necessarily realize the desired outcome. In these cases, the team must use its knowledge and expertise to identify the true underlying problem and appropriate solution.
- When interviewing the main stakeholders, **the team needs to take time to thoroughly interview the project sponsor**, who tends to be the one funding the project or providing the high-level requirements. **It is critical to thoroughly understand the sponsor's perspective to guide the team in getting started on the project.**

Overview of Data Analytics Lifecycle Phase 1: Discovery

6. Developing Initial Hypotheses(IH)

- **Developing a set of IHs** is a key facet of the discovery phase. This step involves **forming ideas that the team can test with data**. (suggestions, actions, activities ideas)

- This process involves **gathering and assessing hypotheses from stakeholders** and **domain experts** who may have their **own perspective on what the problem is**, **what the solution should be**, and **how to arrive at a solution**. These stakeholders would know the domain area well and can offer **suggestions on ideas** to test as the team formulates hypotheses during this phase.

- These suggestions on ideas will also give the team opportunities to expand the project to address the most important interests of the stakeholders.

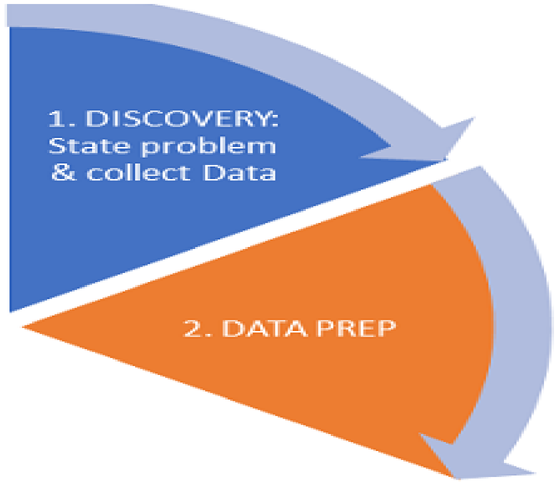
Overview of Data Analytics Lifecycle Phase 1: Discovery

7. Identifying Potential Data Sources

- As part of the discovery phase, identify the **kinds of data the team will need to solve the problem**. Consider the **volume, type, and time span of the data** needed to test the hypotheses.
- The team should perform five main activities during this step of the discovery phase:
- **Identify data sources:** Make a **list of datasets currently available** and those that can be purchased to test the initial hypotheses outlined in this phase.
- **Capture aggregate data sources:** It enables the team to gain a quick overview of the data and **perform further exploration on specific areas**. (combine dataset related to same domin)
- **Review the raw data:** Begin **understanding the interdependencies among the data attributes**, and become familiar with the **content of the data, its quality**, and **its limitations**.
- **Evaluate the data structures and tools needed:** The **data type and structure dictate which tools the team can use to analyze the data, which technologies may be good candidates for the project.** (How data is stored, in what structure→ with this team needs to identify what tool can be used, what technology map reduce, parallel computing can be used)
- **Scope the sort of data infrastructure needed for this type of problem**: In addition to the tools needed, the **data influences the kind of infrastructure that's required, such as disk storage and network capacity**.

Overview of Data Analytics Lifecycle: Phase 2: Data Preparation

- The second phase of the Data Analytics Lifecycle involves **data preparation**, which includes **explore**, **pre-process** and **condition data** prior to modelling and analysis. ((Understanding, transforming and conditioning)



- **Exploring** (Insights) the data is done by **preparing an analytics sandbox**. The team needs to **learn about the data** and **become familiar** with it. Understanding the data in detail is **critical to the success of the project**. The team also must decide how to **condition** and **transform data** to get it into a format to facilitate subsequent analysis.

- Many tend to **jump into Phase 3 or Phase 4** to begin rapidly developing models and algorithms without spending the time to prepare the data for modelling. Consequently, teams come to **realize the data they are working with does not allow them to execute the models they want**, and they end up back in Phase 2 anyway. (May not get accurate result, may be difficult to analyse, model may not work properly on unconditioned data)

Overview of Data Analytics Lifecycle: Phase 2: Data Preparation

1. **Preparing the Analytic Sandbox**

- The **first sub phase of data preparation requires the team to obtain an analytic sandbox** (also commonly referred to as a workspace), in which the **team can explore the data** without interfering with **live production databases**. (A workspace in which data assets are gathered from multiple sources and technologies for analysis. Often, this workspace is created by using a sampling of the dataset rather than the entire dataset.)

- Consider an **example in which the team needs to work with a company's financial data.** The **team should access a copy of the financial data from the analytic sandbox rather than interacting with the production version of the organization's main database**, because that will be tightly controlled and needed for financial reporting. (Company will put the data into sandbox from where data science team can explore)

- When developing the analytic sandbox, it is a **best practice to collect all kinds of data there**, including everything from **summary-level aggregated data**, **structured data**, **raw data feeds**, and **unstructured text data from call logs or web logs**, depending on the kind of analysis the team plans to undertake.

Overview of Data Analytics Lifecycle: Phase 2: Data Preparation

2. Performing ETLT

- In ETL, users perform **extract, transform, load processes** to extract data from a data store, perform data transformations, and load the data back into the data store.
- However, the **analytic sandbox approach differs slightly; it advocates (ELT) extract, load, and then transform**. In this case, the **data is extracted in its raw form** and **loaded into the data store**, where analysts can choose to **transform the data into a new state or leave it in its original, raw condition.** The reason for this approach is that there is **significant value in preserving the raw data** and including it in the sandbox before any transformations take place.
- For instance, consider an analysis for fraud detection on credit card usage. Many times, outliers in this data population can represent higher-risk transactions that may be indicative of fraudulent credit card activity. Using ETL, these outliers may be inadvertently filtered out and cleaned before being loaded into the data store.

3. Learning About the Data

- A critical aspect of a data science project is to **become familiar with the data itself**.

Some of the activities in this step are

- **Clarifies the data** that the data science team has access to at the start of the project
- **Highlights gaps by identifying datasets within an organization that the team may find useful but may not be accessible to the team today**. As a consequence, this activity can trigger a **project to begin building relationships with the data owners and finding ways to share data in appropriate ways**.
- **Identifies datasets outside the organization that may be useful to obtain through open APIs, data sharing, or purchasing data** to supplement already existing datasets

Overview of Data Analytics Lifecycle: Phase 2: Data Preparation

4. Data Conditioning

- Data conditioning refers to the **process of cleaning data, normalizing datasets**, and performing **transformations on the data**.
- A critical step within the Data Analytics Lifecycle, data conditioning can involve many complex steps to **join or merge data sets** or otherwise get datasets into a state that enables analysis in further phases.
- However, it is also **important to involve the data scientist in this step** because many decisions are made in the data conditioning phase that affect subsequent analysis. Because teams begin forming ideas in this phase about which data to keep and which data to transform or discard, it is important to involve multiple team members in these decisions.

- **Additional questions and considerations**
  - ➢ What are the **data sources**?
  - ➢ What are the **target fields** (for example, columns of the tables)?
  - ➢ How **consistent are the contents** and files? data contains missing or inconsistent values.
  - ➢ Assess the **consistency of the data types**. For instance, if the team expects certain data to be numeric, confirm it is numeric or if it is a mixture of alphanumeric strings and text.
  - ➢ Review the **content of data columns or other inputs**, and check to **ensure they make sense**. For instance, if the project involves analyzing income levels, preview the data to confirm that the income values are positive.
  - ➢ Look for any evidence of **systematic error**. Examples include **data feeds from sensors or other data sources causes invalid, incorrect, or missing data values.**

Overview of Data Analytics Lifecycle: Phase 2: Data Preparation

5. Common Tools for the Data Preparation Phase

Several tools are commonly used for this phase:

- **Hadoop** can perform massively parallel ingest and custom analysis for web traffic parsing, GPS location analytics, genomic analysis, and combining of massive unstructured data feeds from multiple sources.

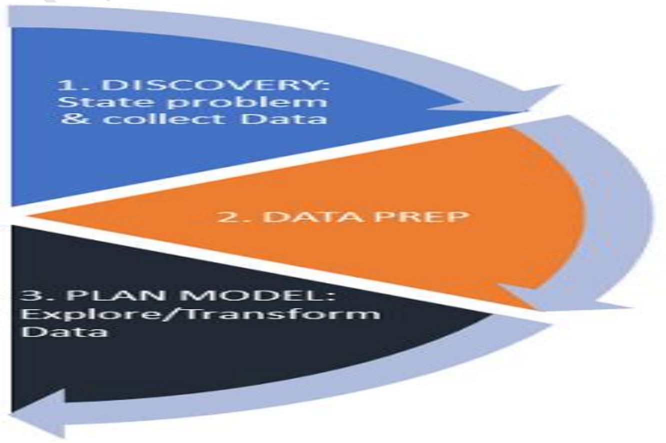
- **Alpine Miner** provides a graphical user interface (GUI) for creating analytic work flows, including data manipulations and a series of analytic events such as staged data-mining techniques (for example, first select the top 100 customers, and then run descriptive statistics and clustering) on Postgres SQL and other Big Data sources.

- **Open Refine** (formerly called Google Refine) is "a free, open source, powerful tool for working with messy data. It is a popular GUI-based tool for performing data transformations, and it's one of the most robust free tools currently available.

- Similar to Open Refine, **Data Wrangler** is an interactive tool for data cleaning and transformation. In addition, data transformation outputs can be put into Java or Python. The advantage of this feature is that a subset of the data can be manipulated in Wrangler via its GUI, and then the same operations can be written out as Java or Python code to be executed against the full, larger dataset offline in a local analytic sandbox.

Overview of Data Analytics Lifecycle:Phase 3: Model Planning

- In Phase 3, the **data science team identifies candidate models to apply to the data for clustering, classifying**, or finding relationships in the data depending on the goal of the project. (Clustering Techniques→ K-Means, Mean-Shift, Density-Based Spatial, Expectation–Maximization, Agglomerative Hierarchical , Classification Technique→Logistic Regression, Naïve Bayes, Stochastic Gradient Descent, K-Nearest Neighbours, Decision Tree, Random Forest, Support Vector Machine)


1. DISCOVERY: State problem & collect Data
2. DATA PREP
3. PLAN MODEL: Explore/Transform Data

- Some of the activities to consider in this phase include the following:

  ➢ **Assess the structure of the datasets (textual data, data base→ structured data, semi structured data).** The structure of the data sets is one factor that **dictates the tools and analytical techniques** for the next phase. Depending on whether the team plans to **analyze textual data or transactional data**, for example, **different tools and approaches are required**.

  ➢ **Ensure that the analytical techniques enable the team to meet the business objectives (problem statement set in phase-1)** and accept or reject the working hypotheses.

  ➢ **Determine if the situation warrants a single model or a series of techniques** as part of a larger analytic workflow. (if analysis need to be taken stage by stage→ first clustering technique→ within each cluster→ Mean Shift clustering technique)

Overview of Data Analytics Lifecycle:Phase 3: Model Planning

1. Data Exploration and Variable Selection

- In Phase 3, the objective of the data exploration is to **understand the relationships among the variables** to inform selection of the variables and methods and to understand the problem domain. (Diabetic patient information→ list of symptoms, blood level and weakness)

- Data science team needs to consider the **inputs and data that will be needed**, and then it must **examine whether these inputs are actually correlated with the outcomes that the team plans to predict or analyze**. (diabetic symptoms→ thirsty, weakness, low blood level→ predicting diabetic or not)

- The key to this approach is to aim for capturing the **most essential predictors and variables rather than considering every possible variable that people think may influence the outcome** (Consider only key variables rather than thinking every variable effects the prediction→ simply iterates the process)

- **Approaching the problem in this manner requires iterations** and testing to identify the most essential variables for the intended analyses. The team should plan to test a range of variables to include in the model and **then focus on the most important and influential variables**.

Overview of Data Analytics Lifecycle:Phase 3: Model Planning

2. Model Selection

- In the model selection subphase, the team's main goal is to choose an **analytical technique**, or a short **list of candidate techniques**, based on the end goal of the project. (Finding out list of techniques applicable for the set objectives and finding out most suitable technique)
- In this case, a **model simply refers to an abstraction from reality**, attempts to **construct models** that **emulate real-world situation** or with live data with a set of rules and conditions.
- In the case of **machine learning and data mining**, these **rules and conditions are grouped into several general sets of techniques**, such as **classification, association rules, and clustering**. (For eg: analyzing and predicting sales of stationary items at different places→ uses clustering technique to divide the zones→ apply association rule and decision tree techniques to identify % of people who purchase note book will also purchase pen, Thus depending upon the project identifies set of techniques and tools needed)
- An additional consideration in this area for **dealing with Big Data** involves determining if the team will be **using techniques that are best suited for structured data, unstructured data**, or a hybrid approach. For instance, the team can leverage Map Reduce to analyse unstructured data. (Structured data but selected Text Analytic technique→ then not suitable)
- The team can **move to the model building phase once it has a good idea about the type of model** to try and the team has gained enough knowledge to refine the analytics plan.

Overview of Data Analytics Lifecycle:Phase 3: Model Planning

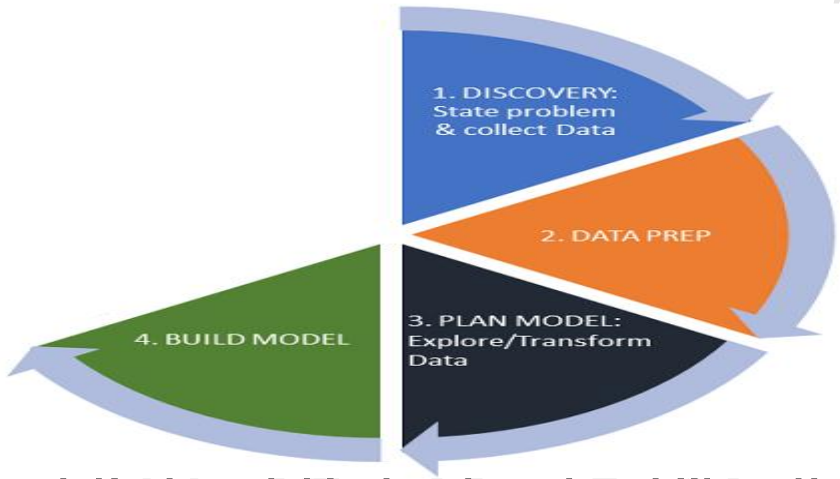
3. Common Tools for the Model Planning Phase

Many tools are available to assist in this phase. (many tools available where a data science team can plan for tools and techniques in this phase to build the model)

- **R has a complete set of modelling capabilities** (has rich set of built in functions for K-Means clustering, Decision Tree, Naïve Baisy, Logistic regression etc→ for structured data) and provides a good environment **for building interpretive models** with high-quality code. ln addition, **it has the ability to interface with databases via an ODBC connection** and to **performing statistical tests and analytics on Big Data**.
- **SQL Analysis services** can perform in-database analytics of common **data mining functions**, involved **aggregations**, and basic **predictive models**. (support aggregate built in functions, predictive built in functions→ Structured data)
- **SAS/ACCESS** (Statistical Analysis System→ programming Language) provides integration between **SAS** and the **analytics sandbox** (Support built in function to integrate with Analytic Sandbox, analyse and predict→web, social media, and marketing analytics→ support built in functions to analyse data of any type(structured, files, unstructured))

Overview of Data Analytics Lifecycle:Phase 4: Model Building

- In Phase 4, the **data science team needs to develop data sets for training, testing purposes**. These data sets enable the data scientist to **develop the analytical model** and **train it** ("training data"), **while holding aside some of the data** ("hold-out data" or "test data") for testi


1. DISCOVERY: State problem & collect Data
2. DATA PREP
3. PLAN MODEL: Explore/Transform Data
4. BUILD MODEL

- In the **model building phase, an analytical model is developed and fit on the training data and evaluated against the test data**.

- The phases of **model planning and model building can overlap** quite a bit, and in practice one **can iterate back and forth** between the two phases for a while before settling on a final model.

- During this phase, **users build and run models** from analytical software packages such as R or SAS, **assess the validity of the model and its results**. For instance, determine if the model accounts for most of the data and has robust predictive power. At this point, refine the models to optimize the results.

Overview of Data Analytics Lifecycle:Phase 4: Model Building

- It is **vital to record the results and logic of the model during this phase**. In addition, one must take care to **record any operating assumptions** that were made in the modeling process regarding the data or the context.

- Questions to consider whether developed models are suitable to a specific situation and ensure the models being developed ultimately meet the objectives outlined in Phase 1.
  - ✓ Does the model **appear valid** and **accurate** on the test data?
  - ✓ Does the model output/behavior **make sense** to the domain experts? (Output is sensible output what domain expert expecting → purchasing notebook→90% purchases pen)
  - ✓ Do the **parameter values** of the fitted model make sense in the context of the domain?
  - ✓ Is the model **sufficiently accurate to meet the goal**?
  - ✓ Does the **model avoid intolerable mistakes**? Depending on context, false positives may be more serious or less serious than false negatives.(True positive→ False Positive)
  - ✓ Is a **different form of the model required to address the business problem**?

- Once the **data science team can evaluate either if the model is sufficiently robust to solve the problem or if the team has failed, it can move to the next phase in the Data Analytics Lifecycle**.

Overview of Data Analytics Lifecycle:Phase 4: Model Building

- **Common Tools for the Model Building Phase**

  There are **many tools available to assist in this phase**, focused primarily on statistical analysis or data mining software.

  Common tools in this space include, but are not limited to, the following:

- **Commercial Tools:**

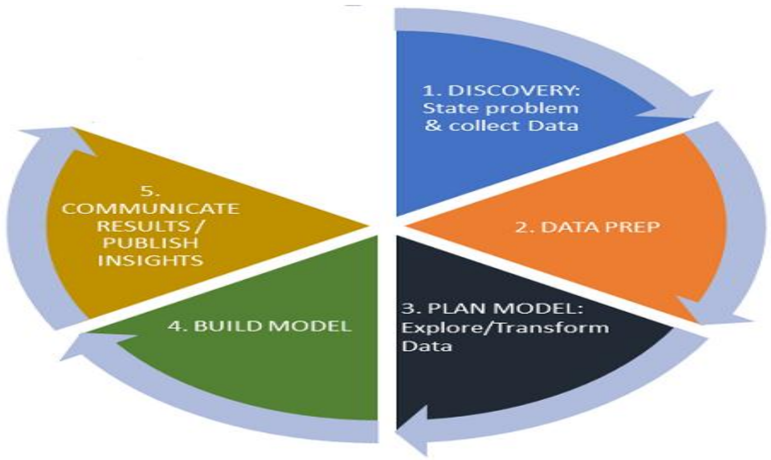
  - **SAS Enterprise Miner** (Programming language with built in functions) allows **users to run predictive and descriptive models** based on large volumes of data from across the enterprise. It is built for enterprise-level computing and analytics.
  - **SPSS Modeler** (provided by IBM and now called IBM SPSS Modeler) **offers methods to explore and analyze data** through a **GUI**.
  - **Matlab** provides a **high-level language** for performing a variety of **data analytics**, algorithms, and **data exploration**.
  - **Alpine Miner** provides a **GUI front end for users** to develop analytic workflows and **interact with Big Data tools** and platforms on the back end.
  - **STATISTICA** and **Mathematica** are also popular and well-regarded **data mining** and **analytics tools**.

Overview of Data Analytics Lifecycle:Phase 4: Model Building

- **Free or Open Source tools:**
  - **R** and **PL/R,** R is both a language and an environment for doing **statistics and generating graphs**. It thinks of **data as matrices, lists and vectors. PL/R is a procedural language** (writing database procedures and Triggers (calling automatically when some incident happens) using R) for PostgreSQL with R. Using this approach means that R commands can be executed in database.
  - **Octave , a free software programming language** for computational **modeling**, has some of the functionality of **Matlab**. Because it is freely available. Octave is used in major universities when teaching machine learning.
  - **WEKA is a free data mining software package** with an analytic workbench. The functions created in WEKA can be executed within Java code.
  - **Python is a programming language that provides toolkits for machine learning and analysis**, such as scikit-learn, **numpy, scipy, panda**s, and related **data visualization using matplotlib**.

Overview of Data Analytics Lifecycle:Phase 5: Communicate Results

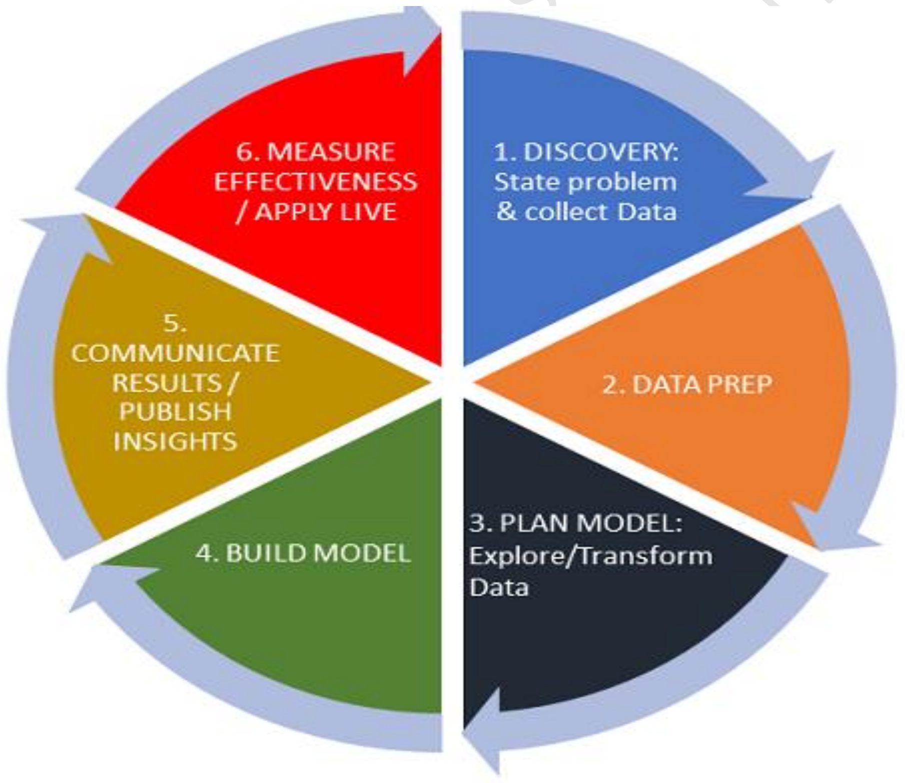
- After executing the model, the team needs to **compare the outcomes of the modeling to the criteria established for success and failure.**


1. DISCOVERY: State problem & collect Data
2. DATA PREP
3. PLAN MODEL: Explore/Transform Data
4. BUILD MODEL
5. COMMUNICATE RESULTS / PUBLISH INSIGHTS

- In Phase 5, the team **communicate the findings and outcomes to the various team members and stakeholders**, taking into account caveats (cautions), assumptions and any limitations of the results.
- During this step, **assess the results and identify which data points may have been surprising** and which were in line with the hypotheses that were developed in Phase 1.
- This is the **phase to underscore the business benefits** of the work and begin making the case to implement the logic into a **live production environment.**
- As a result of this phase, the **team will have documented the key findings and major insights derived from the analysis.** The deliverable of this phase will be the most visible portion of the process to the outside stakeholders and sponsors

Overview of Data Analytics Lifecycle:Phase 6: Operationalize

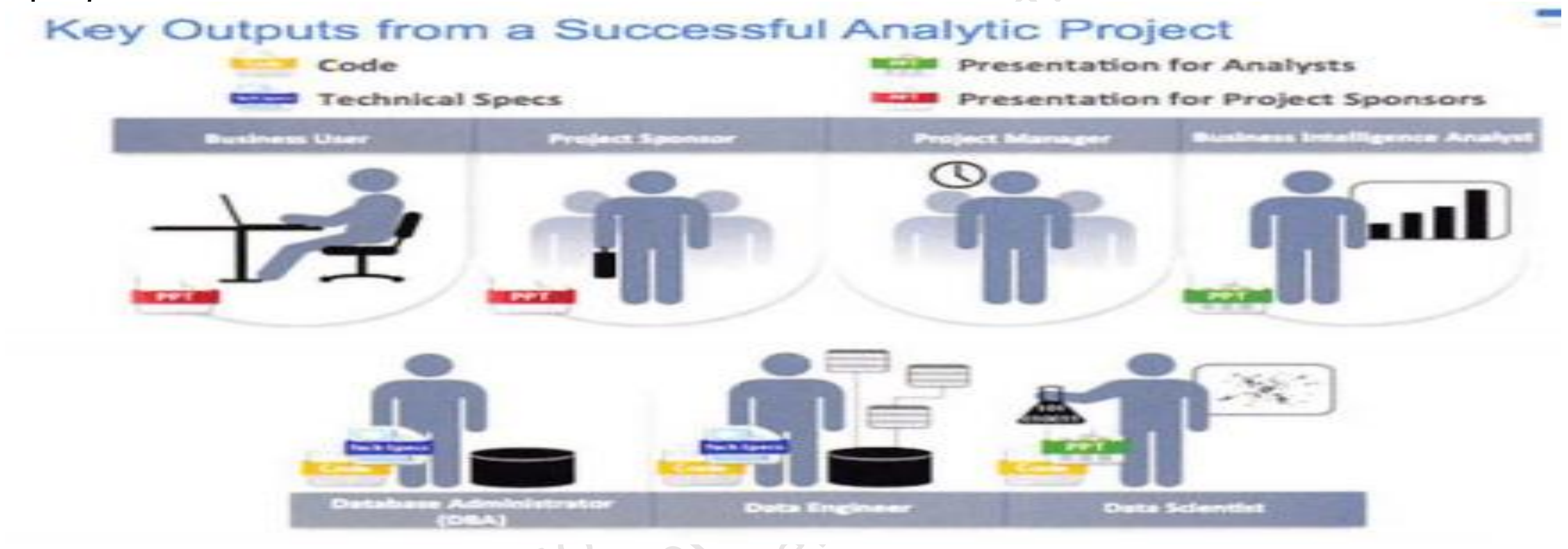
- In the final phase, the team c**ommunicates the benefits of the project more broadly and sets up a pilot** (Preliminary) **project** to deploy the work in a **controlled way before broadening the work to a full enterprise** or ecosystem of users.


1. DISCOVERY: State problem & collect Data
2. DATA PREP
3. PLAN MODEL: Explore/Transform Data
4. BUILD MODEL
5. COMMUNICATE RESULTS / PUBLISH INSIGHTS
6. MEASURE EFFECTIVENESS / APPLY LIVE

- This approach enables the team to learn about the **performance** and related **constraints** of the model in a production environment on a small scale and make **adjustments before a full deployment**.

Key outputs from a successful analytics project

- Figure portrays the **key outputs for each of the main stakeholders** of an analytics project and what they **usually expect** at the conclusion of a project.


Key Outputs from a Successful Analytic Project
Code
Technical Specs
Presentation for Analysts
Presentation for Project Sponsors
Business User
Project Sponsor
Project Manager
Business Intelligence Analyst
PPT
Tech Specs
Database Administrator (DBA)
Data Engineer
Data Scientist

- ➢ **Business User** typically tries to **determine the benefits** and implications of the findings to the business.

- ➢ **Project Sponsor** typically asks questions related to the **business impact of the project, the risks and return on investment** (ROI), and the way the project can be evangelized within the organization (and beyond).

- ➢ **Project Manager** needs to determine **if the project was completed on time and within budget and how well the goals were met**.

Key outputs from a successful analytics project

- **Business Intelligence Analyst** needs to know if the **reports and dashboards he manages will be impacted and need to change**.

- **Data Engineer and Database Administrator** (DBA) typically need to **share their code from the analytics project and create a technical document** on how to implement it. (Must give technical document related to data and database code)

- **Data Scientist** needs to **share the code and explain the model to her peers, managers, and other stakeholders**.

UNIT-2

Data Types in R

- R Programming has 5 data types:
  - **Character**
  - **Numerical**
  - **Integer**
  - **Logical**
  - **Complex.**
- **Character Data Type:** Character data type stores **letter or a combination of letters** enclosed within the quotes. Eg: ‘a’, “good”, ’65’, etc.
- **Numerical Data Type:** Numeric data types stores **digits and decimal numbers**. Eg: 23.2, 44, etc.
- **Integer Data Type:** Integer data type stores **integer number**, numbers that do not contain decimal values. They are mentioned with the letter ‘L’ towards the end so that the programming language stores it as an integer. Eg: 2L, 67L, etc.
- **Logical Data Type:** Logical data type stores **boolean values True or False**.
- **Complex Data Type:** Complex data type stores complex numbers, **a combination of real and imaginary numerical values**. Eg: 4+7i.

Data Structures/Data Objects/Data Types

- R programming supports **6 types of data objects**.
  - **Vector**
  - **List**
  - **Data Frame**
  - **Matrix**
  - **Array**
  - **Factor**
- In programming languages like C, C++ and Java, variables are declared as data type; however, in R the variables are not declared as some data type. Variable are treated like a data objects. They are particular instance of particular class.
- Objects are nothing but a data structure having few attributes and methods which are applied to its attributes. (Just like in Python). For eg: Matrix class includes set of attributes and set of methods to be applied on these attributes like dim( ), length( ), attributes( )

Data Structures/Data Objects/Data Types

- matrix1<- matrix(0, nrow = 5, ncol = 5)

- print(matrix1)

```
     [,1] [,2] [,3] [,4] [,5]
[1,]    0    0    0    0    0
[2,]    0    0    0    0    0
[3,]    0    0    0    0    0
[4,]    0    0    0    0    0
[5,]    0    0    0    0    0
```

- rownames(matrix1)<-c("R1","R2","R3","R4","R5")

- colnames(matrix1)<-c("C1","C2","C3","C4","C5")

- print(matrix1)

```
   C1 C2 C3 C4 C5
R1  0  0  0  0  0
R2  0  0  0  0  0
R3  0  0  0  0  0
R4  0  0  0  0  0
R5  0  0  0  0  0
```

- dim(matrix1)

```
[1] 5 5
```

- length(matrix1)

```
[1] 25
```

- attributes(matrix1)

```
$dim
[1] 5 5
$dimnames
$dimnames[[1]]
[1] "R1" "R2" "R3" "R4" "R5"
$dimnames[[2]]
[1] "C1" "C2" "C3" "C4" "C5"
```

Data Structures/Data Objects/Data Types

Vectors

- **Vectors** are one of the basic R programming data objects containing **sequence of data elements of the same data type**.
- Members in a vector are officially called **components**.
- Vectors are generally created using the **c( ) function**.
- **Creating Vector**

```
V1<-c(10,20,30)

V2<-c('a','b','c')
```

- **Printing vector**

```
V1

V2
```

Data Structures/Data Objects/Data Types

Vectors

```
V1<-c(10,20,30)  #Creating Vector
V1  #Pinting Vector
V2<-c('a','b','c')
V2
V3<-c(10.5,20.5,30.5)
V3
V4<-c("Raju","Sanju","Manju")
V4
V5=c(50,60,70,0)
V5
print(V1)
V1*2
V1+2
V1/2
V1/3
V1=V1*2
V1
V1%%2
class(V1)
class(V2)
class(V3)
class(V4)
```

Data Structures/Data Objects/Data Types

Vectors

```
xm <- mean(V1)
xm
str(V1)
V6<-c(1:200)
V6
V61 <- c(0:10, 50)
V61
str(V61)
V7<-seq(1, 3, by=0.2)
V7
V71<-seq(1, 20, by=2)
V71
V8<-LETTERS[1:5]
V8
V1
V1[3]
V1[c(1, 3)]
V1[2:3]
V1[-1]
V1[-2]
V1[6]
V1[2] <- 0;        # modify 2nd element
V1
```

Data Structures/Data Objects/Data Types

Vectors

```
V8=c(10,-2,20,-4)
V8
V8[V8<0] <- 5
V8
length(V1)
V1=c(V1,40,50,60)    #The function c() can also be used to add elements to a vector.
V1
V9 <- c(0.5, NA, 0.7) # R supports missing data in vectors. They are represented as NA (Not Available) and can be used for all the vector types
V9
anyNA(V9) #anyNA() returns TRUE if the vector contains any missing values # The function is.na() indicates the elements of the vectors that represent missing data.
V10=c(1,'a')
V10
dim(V1)  #returns NULL because an atomic vector doesn't have a dimension.
V11 <- cbind(1, 2, 3, 4, 5)      #We can create a true vector with cbind()
class(V11)
dim(V11)      #This returns the dimension (number of LInes first, the number of Columns).
```

Data Structures/Data Objects/Data Types

Lists

- Lists are one of the basic R programming data objects containing **data elements of different data types like number, character, strings.** It can also contain **vectors, matrices, a nested list itself inside it as elements.**

- List can be created using the **list() function**.

```
L1=list(10,'a',20.5,"Raju")    #Creating List
L1         #Printing List
L2=list(11,'b',30.5,"Sanju",L1)
L2
typeof(L1)
length(L1)
L1[c(1:2)]    # index using integer vector Indexing with [ ] will give us sublist not the content inside the component.
L1[-2]       # using negative integer to exclude second component
```

Data Structures/Data Objects/Data Types

Lists

```
L3 <- list("a" = 2.5, "b" = TRUE, "c" = 1:3)  # can give tag names, However, tags are optional.

L3

L4 <- list("Name" = "John", "Age" = 20, "Branch" = "CS")

L4

L4["Age"]          # However, this approach will allow us to access only a single component at a time.

L4$Age           # an alternative approach.

L4[["Name"]] <- "Clair"  # We can change components of a list through reassignment

L4

L4[["Married"]] <- FALSE  # Adding new components is easy. We simply assign values using new tags and it will pop into action.

L4

L4[["Age"]] <- NULL  # We can delete a component by assigning NULL to it.

str(L4)

L1[1]
```

Data Structures/Data Objects/Data Types

Lists

```
L2

L2[1]

L2[5]

L2[[5]][2]

L5=list()    # creating empty list

L5=c(10,'a')  #adding elements to the list

names(L4)

L5

L6 <- list(c(1, 2), c(3, 4))

L6

L7 <- list(3, c(1, 2), "lists are amazing!")

L7

L1

L8=list(L1,50,'b',"Red")

L8
```

Data Structures/Data Objects/Data Types

Lists

- Lists can be extremely useful inside functions. Because the functions in R are able to return only a single object, we can “staple” together lots of different kinds of results into a single object that a function can return.

- A list does not print to the console like a vector. Instead, each element of the list starts on a new line.

- Elements are indexed by double brackets. If the elements of a list are named, they can be referenced by the $ notation (i.e. xlist$data).

Data Structures/Data Objects/Data Types

Matrix

- Matrix is a **two dimensional data structure** in R programming.
- Same as vector, the components in a matrix must be of the same **basic type**.
- Matrix can be **created using the matrix() function**.
- Dimension of the matrix can be defined by passing appropriate value for arguments **nrow** and **ncol**.

```
M1<-matrix(data=7,nrow=3,ncol=3)

M1

M2<-matrix(data=(1:9),nrow=3,ncol=3,byrow=F)

M2
```

- We can see that the matrix is filled **column-wise**. This can be **reversed to row-wise filling by passing TRUE to the argument byrow**.

```
M3<-matrix(data=(1:9),nrow=3,ncol=3,byrow=T)

M3
```

- byrow=TRUE signifies that the matrix should be filled by rows. byrow=FALSE indicates that the matrix should be filled by columns (the default).

Data Structures/Data Objects/Data Types

Matrix

- In all cases, however, a matrix is stored in **column-major order internally**.

- **Providing value for both dimension is not necessary**. If one of the dimension is provided, the other is inferred from length of the data.

```
M4<-matrix(data=(1:9),nrow=3)

M4
```

- It is possible to **name the rows and columns of matrix during creation by passing a 2 element list to the argument dimnames**.

```
M5 <- matrix(1:9, nrow = 3, ncol=3,byrow=F,dimnames = list(c("R1","R2","R3"), c("C1","C2","C3")))

M5
```

- These **row names and column names can be accessed or changed** with two helpful functions **colnames()** and **rownames().**

```
rownames(M5)

colnames(M5)
```

Data Structures/Data Objects/Data Types

Matrix

- It is also **possible to change row names and column names**

```
rownames(M5) <- c("ROW1","ROW2","ROW3")

colnames(M5) <- c("COL1","COL2","COL3")

M5

rownames(M5)

colnames(M5)

attributes(M1)

dim(M1)
```

- Another way of creating a matrix is by using functions **cbind() and rbind()**

```
M6<-cbind(c(1,2,3),c(4,5,6))
M6
M7<-rbind(c(1,2,3),c(4,5,6))
M7
```

Data Structures/Data Objects/Data Types

Matrix

- Finally, we can also **create a matrix from a vector by setting its dimension using dim().** Matrices can also be created directly from vectors by adding a dimension attribute.

```
M8 <- c(1,2,3,4,5,6)
M8
class(M8)
dim(M8) <- c(2,3)
M8
class(M8)
```

- We can **access elements of a matrix using the square bracket**

```
M8[2,3]
M8[c(1,2),c(2,3)]
M8[c(1,2),c(1,3)]
M8[c(2),c(2,3)]
```

Data Structures/Data Objects/Data Types
Matrix

- select elements greater than 5

```
M8
M8[M8>4]
M2
M2[2,] #2nd row of a matrix
M2[,3] #3rd column of a matrix
```

- select even elements

```
M8[M8%%2 == 0]
```

- We can combine assignment operator with the above learned methods for accessing elements of a matrix to modify it.

```
M8[2,2] <- 10;
M8
```

- modify elements less than 5.

```
M8[M8<5] <- 0
M8
```

- A common operation with matrix is to transpose it. This can be done with the function t().

```
t(M8)
```

Data Structures/Data Objects/Data Types

Matrix

We can add row or column using rbind() and cbind() function respectively. Similarly, it can be removed through reassignment.

```
M9<-rbind(c(10, 20, 30),c(40, 50,60),c(70,80,90))
M9
M9<-cbind(M9, c(1, 2, 3))
M9
M9<-rbind(M9,c(1,2,3,4))
M9
```

- In all cases, however, a matrix is stored in column-major order internally

```
M10<-rbind(c(10, 20, 30),c(40, 50,60))

M10
     [,1] [,2] [,3]
[1,]   10   20   30
[2,]   40   50   60
```

- Dimension of matrix can be modified as well, using the dim() function.

```
dim(M10) <- c(3,2);

M10
     [,1] [,2]
[1,]   10   50
[2,]   40   30
[3,]   20   60
```

Data Structures/Data Objects/Data Types

Matrix

- We can perform **mathematical operations on matrices**

  M1

  M2

  M1+M2

  M1-M2

  M1*M2

  M1%*%M2

  M1/M2

  M1%%M2

Data Structures/Data Objects/Data Types

Data Frames

- Data Frame is a type of data object in R. It is two dimensional object where each column is of one data type i.e, different column in the frame is of different data type.
- It is a special case of a list.
- DataFrame can be created using the data.frame() function.

```
num1<- c(1,2,3,4)
char1<-c('a','b','c','d')
real1<-c(10.5,20.5,30.5,40.5)
str1 <- c("Red", "White", "Green","Black")
logical1<- c(TRUE,TRUE,TRUE,FALSE)
F1<-data.frame(num1,char1,real1,str1,logical1)
F1
```

Output

```
 num1  char1   real1   str1   logical1
   1     a      10.5    Red     TRUE
   2     b      20.5    White   TRUE
   3     c      30.5    Green   TRUE
   4     d      40.5    Black   FALSE
```

Data Structures/Data Objects/Data Types

Frames

- Following are the characteristics of a data frame.
  - The **column names should be non-empty**.
  - The **row names should be unique**.
  - The **data stored in a data frame can be of numeric, factor or character type**.
  - Each **column should contain same number of data items**.

- We can print the data frame using print()

  print(F1)
- Get the structure of the data frame.

  str(F1)
- We can print the names of the data frame using names()

  names(F1)
- We can print attributes of the data frame using attributes()

  attributes(F1)

Output

```
$names
[1] "num1"    "char1"    "real1"    "str1"     "logical1"
$class
[1] "data.frame"
$row.names
[1] 1 2 3 4
```

Data Structures/Data Objects/Data Types

Frames

- We can **print** class of the data frame using **class() function**

```
class(F1)
```

- We can access the class of **each column in the data frame** using **sapply() function**

```
sapply(F1, class)
```

- We can access **number of rows and number of columns** in the data frame using **nrow()** and **ncol() function.**

```
nrow(F1)
ncol(F1)
```

- Data frames can be **accessed like a matrix** by providing index for row and column.

```
F1

F1[2,3]

F1[2,]

F1[,3]

F1[2:4]
```

- We can **access specific column** with in the data frame

```
F1["str1"]

F1$str1
```

Data Structures/Data Objects/Data Types

Frames

- We can **modifying the content of a Data Frame** in R

```
F1[2,3]<-100.5
F1
F1[2,"str1"]<-"Yellow"
F1
```

- We can give **row names to the data frame using rownames()** or **row.names()**

```
F1
names<-c("A","B","C","D")
rownames(F1)<-names
F1
```

- We can give **column names to the data frame using names().**

```
F1
names(F1)<-c("E","F","G","H","I")
F1
```

Data Structures/Data Objects/Data Types

Frames

- Data Frame has been **widely used in the reading comma-separated files (CSV), text files**. Their use is **not only limited to reading the data, but you can also use them for machine learning problems**, especially when dealing with numerical data. Data Frames can be **useful for understanding the data, data wrangling, plotting and visualizing**.

- A data frame is a very important data type in R. It's pretty much the *de facto* data structure for most tabular data and what **we use for statistics**.

- Note that for data frames, there is a separate function for setting the row names, the **row.names() function**. Also, data frames do not have column names, they just have names (like lists). So to set the column names of a data frame just use the **names() function**.

Object	Set column names	Set row names
data frame	names()	row.names()
matrix	colnames()	rownames()

Data Structures/Data Objects/Data Types

Matrix vs Data frame in R

- A data structure is a particular way of organizing data in a computer so that it can be used effectively. The idea is to reduce the space and time complexities of different tasks.
- The two most important data structures in R are Matrix and Data frame, they look the same but different in nature.

Matrix in R

- It’s a **homogeneous collection of data sets** which is arranged in a two dimensional rectangular organisation. It’s a m*n array with similar data type. It is created using a vector input. It has a fixed number of rows and columns. We can perform many arithmetic operations on R matrix like – addition, subtraction, multiplication, and divisions.

DataFrames in R

- It is used for **storing data tables**. It can contain **multiple data types in multiple columns called fields**. It is a **list of vector of equal length**. It is a generalized form of a matrix. It is like a table in excel sheets. It has column and row names. The name of rows are unique with no empty columns. The **data stored must be numeric, character or factor type.** Data Frames are **heterogeneous**.

Matrix vs Dataframe in R

Collection of data sets arranged in a two dimensional rectangular organisation.	Stores data tables that contains multiple data types in multiple column called fields.
It’s m*n array with similar data type.	It is a list of vector of equal length. It is a generalized form of matrix.
It has fixed number of rows and columns.	It has variable number of rows and columns.
The data stored in columns can be only of same data type.	The data stored must be numeric, character or factor type.
Matrix is homogeneous.	DataFrames is heterogeneous.

Data Structures/Data Objects/Data Types

Factors

- Factor is a type of data object in R that takes only **predefined, finite number of values** (categorical data).
- For example, a **data field** such as **marital status** may contain only values from the set { **Single, Married, Separated, Divorced, , Widowed** } . **Performance field** may contain the values from the set { **Excellent", "Good", "Average", "Poor** }
- These predefined, distinct values are called **Levels**. They can be **strings** or **integers**.
- They are extremely useful in **data analytics** for statistical modelling.
- A Factor can be created using the function **factor()**. Levels of a factor are inferred from the data if not provided.

```
FT1 <- factor(c("Single", "Married", "Married", "Single"));

FT1

FT2 <- factor(c("Single", "Married", "Married", "Single", "Divorced"),levels = c("Single", "Married", "Divorced"));

FT2
```

Data Structures/Data Objects/Data Types

Factors

- Factors are closely related with vectors. In fact, factors are stored as integer vectors. This is clearly seen from its structure.
- We can access structure of a factor using str() function

```
str(FT2)
```

Output

```
Factor w/ 3 levels "Single","Married",..: 1 2 2 1 3
```

```
FT2 <- factor(c("Single", "Married", "Married", "Single", "Divorced"),levels = c("Married", "Single","Divorced"));
FT2
str(FT2)
```

Output

```
Factor w/ 3 levels "Married","Single",..: 2 1 1 2 3
```

- Number of level defined in the factor can be accessed using nlevel() function

```
nlevels(FT2)
```

Data Structures/Data Objects/Data Types

Factors

For Eg: A variable gender with 20 "male" entries and 30 "female" entries

```
gender <- c(rep("male",20), rep("female", 30))  #rep() is a replicate function creates a vector with 20  Male entries and 30 Female entries

gender

gender <- factor(gender, order = TRUE,levels = c("male","female"))

gender

str(gender)

gender[1]>gender[21]

gender[21]>gender[1]

gender <- c(rep("male",20), rep("female", 30))

gender

gender <- factor(gender, order = FALSE,levels = c("male","female"))

gender

str(gender)

gender[1]>gender[21]

gender[21]>gender[1]
```

Importing and Exporting Data in R

- **Exporting data is writing** data from **R** to **.txt** (tab-separated values) and **.csv** (comma-separated values) file formats.
- It’s also possible to write csv files using the functions write.csv() and write.csv2().
- write.csv() uses “.” for the decimal point and a comma (“,”) for the separator.

```
my_data<-c(10.5,20.5,30.5,40.5)
getwd()
write.csv(my_data, file = "my_data.csv")
```

- write.csv2() uses a comma (“,”) for the decimal point and a semicolon (“;”) for the separator.

```
write.csv2(my_data, file = "my_data1.csv")
```

- The R base function write.table() can be used to export a data frame or a matrix to a file.

```
x<-matrix(data=c(10.5,20.5,30.5,40.5,50.5,60.5,70.5,80.5,90.5),nrow=3,ncol=3)
write.table(x, "my_data2", append = FALSE, sep =" ", dec = ";",row.names=TRUE, col.names=TRUE)
write.table(x, "my_data2", append = FALSE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
write.table(x, "my_data2", append = TRUE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
write.table(x, "my_data2", append = FALSE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
```

Importing and Exporting Data in R

- The R base function write.table() can be used to export a data frame or a matrix to a file.

```
x<-matrix(data=c(10.5,20.5,30.5,40.5,50.5,60.5,70.5,80.5,90.5),nrow=3,ncol=3)
write.table(x, "my_data2", append = FALSE, sep =" ", dec = ";",row.names=TRUE, col.names=TRUE)
write.table(x, "my_data2", append = FALSE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
write.table(x, "my_data2", append = TRUE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
write.table(x, "my_data2", append = FALSE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
```

Syntax:

```
write.table(x, file, append = FALSE, sep = " ", dec = ".", row.names = TRUE, col.names = TRUE)
```

- x: a matrix or a data frame to be written.
- file: a character specifying the name of the result file.
- sep: the field separator string, e.g., sep = "\t" (for tab-separated value).
- dec: the string to be used as decimal separator. Default is "."
- row.names: either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
- col.names: either a logical value indicating whether the column names of x are to be written along with x, or a character vector of column names to be written. If col.names = NA and row.names = TRUE a blank column name is added, which is the convention used for CSV files to be read by spreadsheets.

Importing and Exporting Data in R

- **R base functions for importing data from .txt** (tab-separated values) and **.csv** (comma-separated values) file formats

  read.csv(): for reading "comma separated value" files (".csv").

  read.csv2(): variant used in countries that use a comma "," as decimal point and a semicolon ";" as field separators.

  read.delim(): for reading *"tab-separated value"* files (".txt"). By default, point (".") is used as decimal points.

  read.delim2(): for reading *"tab-separated value"* files (".txt"). By default, comma (",") is used as decimal points.

  read.table() is a general function that can be used to read a file in table format
- The R base function **read.table**() is a general function that can be used to read a file in table format. The data will be imported as a data frame.

- # Read tabular data into R
  read.table(file, header = FALSE, sep = "", dec = ".")
- # Read "comma separated value" files (".csv")
  read.csv(file, header = TRUE, sep = ",", dec = ".", ...)
- # Or use read.csv2: variant used in countries that # use a comma as decimal point and a semicolon as field separator.
  read.csv2(file, header = TRUE, sep = ";", dec = ",", ...)
- # Read TAB delimited files read.delim(file, header = TRUE, sep = "\t", dec = ".", **...**)
  read.delim2(file, header = TRUE, sep = "\t", dec = ",", ...)

Importing and Exporting Data in R

file: the path to the file containing the data to be imported into R.

sep: the field separator character. “\t” is used for tab-delimited file.

header: logical value. If TRUE, **read.table()** assumes that your file has a header row, so row 1 is the name of each column. If that’s not the case, you can add the argument **header = FALSE**.

dec: the character used in the file for decimal points.

Importing and Exporting Data in R

- my_data<-c(10.5,20.5,30.5,40.5)
- getwd()
- write.csv(my_data, file = "my_data.csv")
- write.csv2(my_data, file = "my_data1.csv")
- x<-matrix(data=c(10.5,20.5,30.5,40.5,50.5,60.5,70.5,80.5,90.5),nrow=3,ncol=3)
- write.table(x, "my_data2", append = FALSE, sep =" ", dec = ";",row.names=TRUE, col.names=TRUE)
- write.table(x, "my_data2", append = FALSE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
- write.table(x, "my_data2", append = TRUE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
- write.table(x, "my_data2", append = FALSE, sep =" ", dec = ".",row.names=TRUE, col.names=TRUE)
- a<-read.table("my_data2")
- a
- b<-read.csv("my_data.csv", header=TRUE, sep =",", dec=".")
- b
- c<-read.csv2("my_data1.csv", header=TRUE, sep=";", dec=",")
- c
- read.delim("my_data2")
- read.delim("my_data2", header=TRUE, sep="\t", dec=".")
- read.delim2("my_data2")
- write.table(x, "my_data2", append = FALSE, sep =" ", dec = ";",row.names=TRUE, col.names=TRUE)
- read.delim2("my_data2", header=TRUE, sep="\t", dec=";")

Contingency Table

- **Contingency table**, also known as a **cross tabulation** or **crosstab or frequency distribution table** is a type of table in a **matrix format** that describes the **relationships between two or more categorical variables**.

- The contingency table below shows the favourite leisure activities for 50 adults - 20 men and 30 women.

Favourite Leisure Activity / **Sex**	**Dance**	**Sports**	**TV**
Men	**2**	**10**	**8**
Women	**16**	**6**	**8**
Total	**18**	**16**	**16**

- Contingency table is used to **analyse** and **record the relationship between two or more categorical variables**.

- They are heavily used in **survey research**, **business intelligence**, **engineering and scientific research**.

- This Contingency table displays relationship among two different categorical variables that may be dependent or contingent on one another.

Contingency Table

- Download iris data set using the following link

  https://www.kaggle.com/uciml/iris

```
dat <- iris
head(dat)
```

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

Descriptive Statistics

str(dat)

```
'data.frame':    150 obs. of  5 variables:

$ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...

$ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...

$ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...

$ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...

$ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

Contingency Table

- The dataset iris has only one qualitative variable **Sepal.Length**, so we create a new qualitative variable just to create Contingency Table.
- Create the new qualitative variable **size** which corresponds to *“small”,* if the length of the petal is smaller than the median of all flowers, *“big”* otherwise

```
dat$size <- ifelse(dat$Sepal.Length<median(dat$Sepal.Length),"small","big")
dat$size
```

OUTPUT

```
"small" "small" "small" "small" "small" "small" "small“ …
```

- The occurrences by **size** can be found using the function **table( )**

```
table(dat$size)
```

OUTPUT

```
big     small
77      73
```

Contingency Table

- We can create a contingency table of the two variables Species and size using the table() function

```
table(dat$Species, dat$size)
```

OUTPUT

```
           big small
setosa       1    49
versicolor  29    21
virginica   47     3
```

Descriptive Statistics

- Descriptive statistics is a **branch of statistics aiming at summarizing, describing and presenting a dataset**.
- Descriptive statistics is often the **first step and an important part in any statistical analysis**.
- It allows to check the **quality of the data** and it helps to “understand” the data by having a **clear overview of it**.

```
dat <- iris
head(dat)
```

	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

Descriptive Statistics

- The **structure of the dataset can be accessed using the function str( ).**

```
str(dat)
```

OUTPUT

```
'data.frame':    150 obs. of  5 variables:

$ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...

$ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...

$ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...

$ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...

$ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

- The iris dataset contains **150 observations (records)** and **5 variables (Columns)**, representing the **length** and **width of the sepal** and **petal** and the **species of 150 flowers**. **Length and width of the sepal and petal are numeric variables** and the **species is a factor with 3 levels: (setosa, versicolor, virginica)**

Descriptive Statistics

- **Minimum** and **Maximum** value can be found using **min( )** and **max( )** functions:

```
min(dat$Sepal.Length)
        4.3
max(dat$Sepal.Length)
        7.9
```

- Alternatively the **range( )** function can be used to find **Minimum** and **Maximum** value.

```
rng <- range(dat$Sepal.Length)
        4.3     7.9
```

- The minimum value can be accessed using **rng[1]** and the maximum value can be accessed using **rng[2]**
- The **range can then be easily computed, by subtracting the minimum from the maximum** value

```
max(dat$Sepal.Length) - min(dat$Sepal.Length)
                3.6
```

Descriptive Statistics

- There is no **default function to compute the range**. However, we can create our **own function in R to compute the range**

```
range2 <- function(x)
  {
    range <- max(x) - min(x)
    return(range)
  }
range2(dat$Sepal.Length)
```

```
3.6
```

- The **Mean value** can be computed using **mean( )** function:

```
mean(dat$Sepal.Length)
```

```
5.843333
```

if there is at least one missing value in the dataset, use **mean(dat$Sepal.Length, na.rm = TRUE)** to compute the mean with the NA excluded.

- The Median can be computed using **median( )** function:

```
median(dat$Sepal.Length)
```

or

with the **quantile()** function:

```
quantile(dat$Sepal.Length, 0.5)
```

```
5.8
```

First and Third Quartile: Example (Just for the Reference)

- The **lower half of a data set is the set of all values that are to the left of the median value** when the data has been put into increasing order.
- The **upper half of a data set is the set of all values that are to the right of the median value** when the data has been put into increasing order.
- The **first quartile, denoted by Q1 , is the median of the lower half of the data set**. This means that about **25% of the numbers in the data set lie below Q1** and about 75% lie above Q1 .
- The **third quartile, denoted by Q3 , is the median of the upper half of the data set**. This means that about **75% of the numbers in the data set lie below Q3** and about 25% lie above Q3 .

Example: Find the first and third quartiles of the data set {3, 7, 8, 5, 12, 14, 21, 13, 18}.

First, we write data in increasing order: **3, 5, 7, 8, 12, 13, 14, 18, 21.**

$$\underbrace{3,\ 5,\ 7,\ 8,}_{\text{“lower half”}}\ \underset{\text{median}}{\textcircled{12}}\ \underbrace{13,\ 14,\ 18,\ 21}_{\text{“upper half”}}$$

The **median is 12.**

Therefore, **the lower half of the data is: {3, 5, 7, 8}.**

The **first quartile, Q1, is the median of {3, 5, 7, 8}.**

Since there is an even number of values, we need the mean of the middle two values to find the first quartile:

$$Q_1 = \frac{5+7}{2} = \frac{12}{2} = 6$$

- Similarly, **the upper half of the data is: {13, 14, 18, 21}, so**

$$Q_3 = \frac{14+18}{2} = \frac{32}{2} = 16$$

Descriptive Statistics

First and Third Quartile

- As the median, the **First** and **Third Quartiles** can be computed using **quantile( )** function and by setting the **second argument to 0.25 or 0.75**

```
quantile(dat$Sepal.Length, 0.25)     # Calculate Median for the First Quartile i.e, 25% of data (Sepal.Length) in the dataset is less than 5.1
25%
5.1
quantile(dat$Sepal.Length, 0.75)     # Calculate Median for the Third Quartile i.e, 75% of data (Sepal.Length) in the dataset is less than 6.4
75%
6.4
```

Interquartile Range

- The interquartile range, the difference between the first and third quartile can be computed with the IQR() function:

```
IQR(dat$Sepal.Length)
1.3
```

Descriptive Statistics

Standard Deviation and Variance

- The **Standard Deviation** and the **Variance** can be computed with the **sd( )** and **var( )** functions:

```
sd(dat$Sepal.Length)        # standard deviation
           0.8280661
var(dat$Sepal.Length)       # variance
           0.6856935
```

- To compute the **standard deviation** or **variance** of **multiple variables at the same time**, we can use **lapply()** function with the appropriate statistics as second argument:

```
lapply(dat[, 1:4], sd)   # The command dat[, 1:4] selects the variables 1 to 4
   $Sepal.Length
     0.8280661
  $Sepal.Width
     0.4358663
  $Petal.Length
     1.765298
  $Petal.Width
     0.7622377
```

Descriptive Statistics

Coefficient of Variation

- The coefficient of variation can be found by computing manually, which is the **standard deviation divided by the mean**.

```
sd(dat$Sepal.Length) / mean(dat$Sepal.Length)
```

```
0.1417113
```

Dirty Data

- The figure shows **few accounts with account holder age less than 10 are unusual**.
- However, the left side of the graph shows a huge spike of customers **who are zero years old** or **have negative ages**. This is likely to be **evidence of missing data**.
- One possible explanation is that the null age values could have been replaced by **0** or **negative values during the data input**.
- Therefore, **data cleansing needs to be performed over the accounts with abnormal age values**.
- **Analysts should take a closer look at the records to decide if the missing data should be eliminated** or if an **appropriate age value can be determined** using other available information for each of the accounts.
- In R, the is **. na ( ) function provides tests for missing values**.

For Eg: create a vector x where the fourth value is not available (NA). The is . na (} function returns TRUE at each NA value and FALSE otherwise.

```
X<- c(l, 2, 3, NA, 4)
is.na(x)
FALSE FALSE FALSE TRUE FALSE
```

Dirty Data

- Some arithmetic functions, such as **mean ( )** , applied to **data containing missing values can yield an NA result**.

```
mean(x)
 NA
```

- To prevent this, set the **na. rm** parameter to TRUE to remove the missing value during the function's execution.

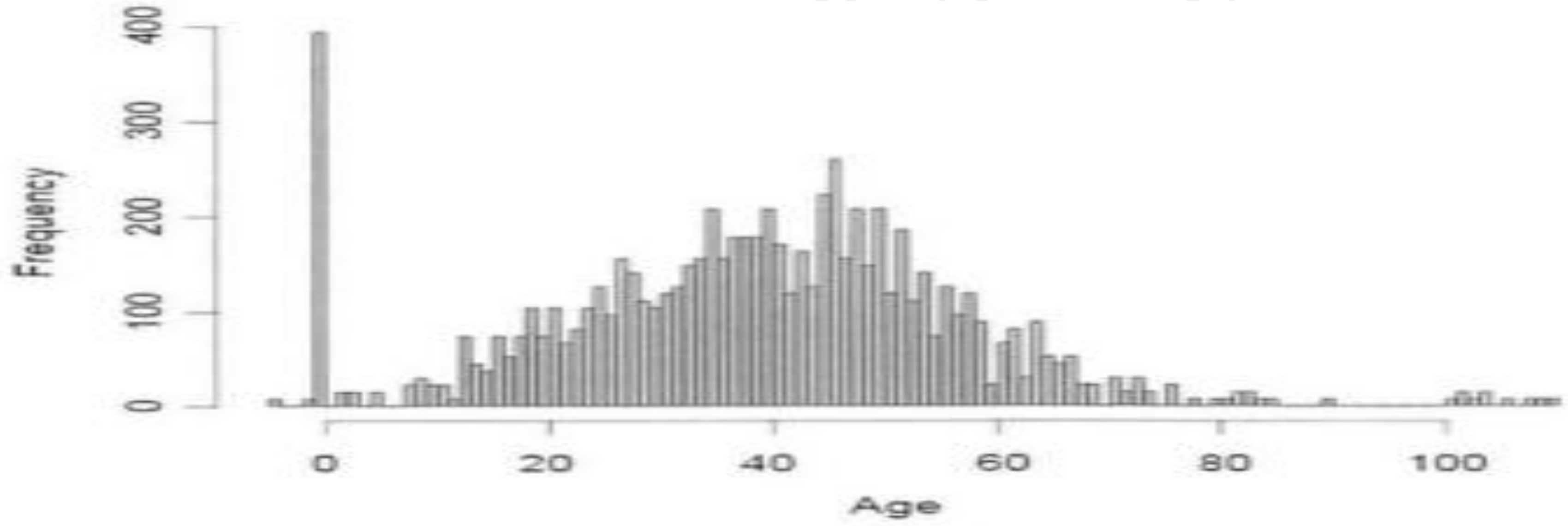
```
mean(x, na.rm=TRUE)
     2. 5
```

- The **na. exclude () function returns the object with incomplete cases removed**.
- **DF <- data.frame(x = c(l, 2, 3), y = c(10, 20, NA))**
- **DF**
- **X   y**
  1 10
  2   20
  3   NA
- **DFl <- na.exclude(DF)**
- **DFl**
  X   y
  1 10
  2 20

Dirty Data

- Analysts should look for **anomalies**, **verify the data** with domain knowledge, and **decide the most appropriate approach to clean the data.**

- Consider a scenario in which a **bank is conducting data analyses of its account holders to gauge customer retention**. Below figure shows the **age distribution of the account holders**.



- If the age data is in a vector called age, the graph can be created with the following R script:

```
hist(age, breaks=l00 , main= "Age Distribution of Account Holders ",xlab="Age", ylab="Frequency", col="gray" )
```

Descriptive Statistics

- We can compute the **minimum, 1st Quartile, Median, Mean, 3rd Quartile and the Maximum for all numeric variables** of a dataset at once using summary():

```
summary(dat)
Sepal.Length      Sepal.Width     Petal.Length     Petal.Width
 Min.   :4.300    Min.   :2.000   Min.   :1.000    Min.   :0.100
1st Qu.:5.100    1st Qu.:2.800   1st Qu.:1.600    1st Qu.:0.300
Median :5.800    Median :3.000   Median :4.350    Median :1.300
Mean   :5.843    Mean   :3.057   Mean   :3.758    Mean   :1.199
3rd Qu.:6.400    3rd Qu.:3.300   3rd Qu.:5.100    3rd Qu.:1.800
Max.   :7.900    Max.   :4.400   Max.   :6.900    Max.   :2.500
Species
setosa    :50
versicolor:50
virginica :50
```

Exploratory Data Analysis

- So far, discussed **generating descriptive statistics**.
- Functions such as **summary () can help analysts easily get an idea of the magnitude and range of the data**, but other aspects such as **linear relationships and distributions are more difficult to see from descriptive stat**istics.
- For example, the following code shows a **summary view of a data frame "iris"** with five columns Sepal.Length, Sepal.Width, Petal.Length, Petal.Width and Species. The **output shows the summary of all these five variables, but it's not clear what the relationship may be between these five variables.**

For example: summary(dat)

```
Sepal.Length        Sepal.Width      Petal.Length     Petal.Width
 Min.   :4.300      Min.   :2.000    Min.   :1.000    Min.   :0.100
1st Qu.:5.100      1st Qu.:2.800    1st Qu.:1.600    1st Qu.:0.300
Median :5.800      Median :3.000    Median :4.350    Median :1.300
Mean   :5.843      Mean   :3.057    Mean   :3.758    Mean   :1.199
3rd Qu.:6.400      3rd Qu.:3.300    3rd Qu.:5.100    3rd Qu.:1.800
Max.   :7.900      Max.   :4.400    Max.   :6.900    Max.   :2.500
Species
setosa    :50
versicolor:50
virginica :50
```

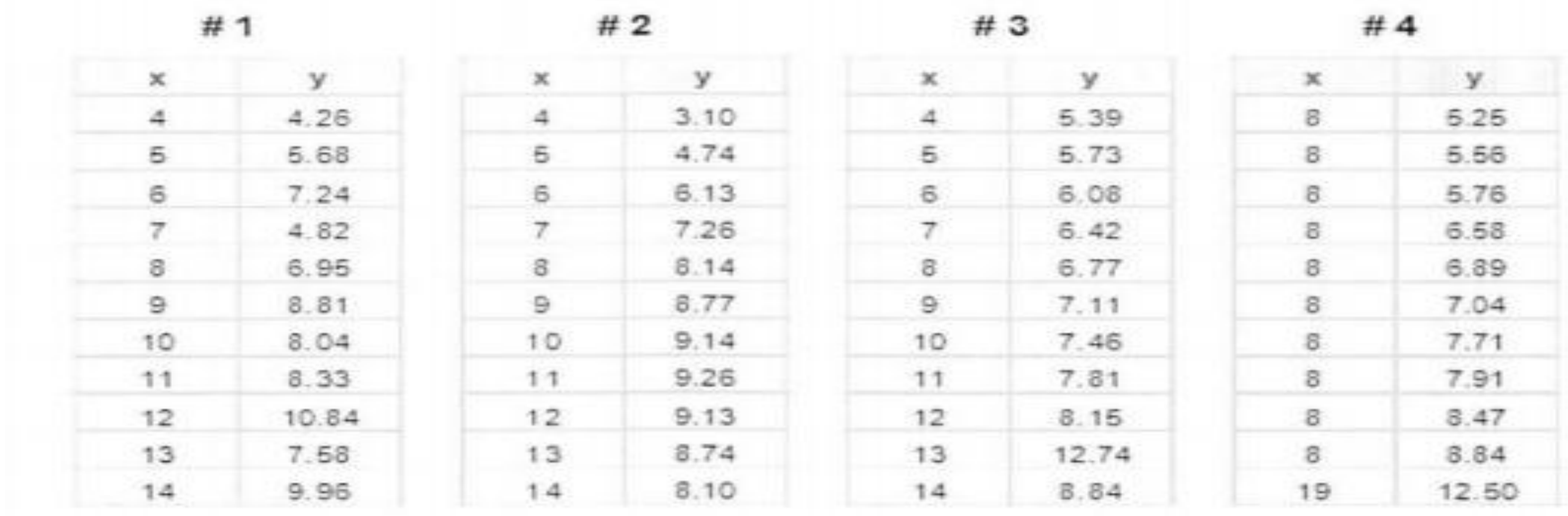
Exploratory Data Analysis

- A **useful way to detect patterns and anomalies in the data is through the exploratory data analysis with visualization**.
- **Visualization gives a succinct, holistic view of the data** that may be difficult to grasp from the numbers and summaries alone.
- **Visualization** easily depicts the **relationship between two variables**.
- **Exploratory data analysis is a data analysis approach** to reveal the important **characteristics of a dataset, mainly through visualization.**

Exploratory Data Analysis

Visualization Before Analysis

- To illustrate the **importance of visualizing data, consider Anscombe's quartet**. Anscom be's quartet **consists of four datasets**, as shown below. It was constructed by **statistician Francis Anscombe to demonstrate the importance of graphs in statistical analyses**.

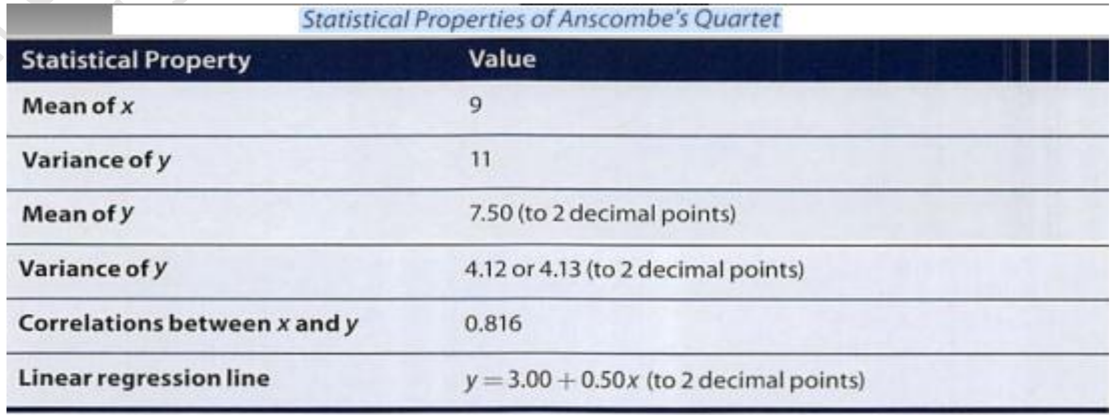


# 1		# 2		# 3		# 4	
x	y	x	y	x	y	x	y
4	4.26	4	3.10	4	5.39	8	6.25
5	5.68	5	4.74	5	5.73	8	5.56
6	7.24	6	6.13	6	6.08	8	5.76
7	4.82	7	7.26	7	6.42	8	6.58
8	6.95	8	8.14	8	6.77	8	6.89
9	8.81	9	8.77	9	7.11	8	7.04
10	8.04	10	9.14	10	7.46	8	7.71
11	8.33	11	9.26	11	7.81	8	7.91
12	10.84	12	9.13	12	8.15	8	8.47
13	7.58	13	8.74	13	12.74	8	8.84
14	9.96	14	8.10	14	8.84	19	12.50

Anscombe's quartet

- **The four data sets in Anscom be's quartet have nearly identical statistical properties, as shown in above Table.**

- **Statistical Properties of Anscombe's Quartet**



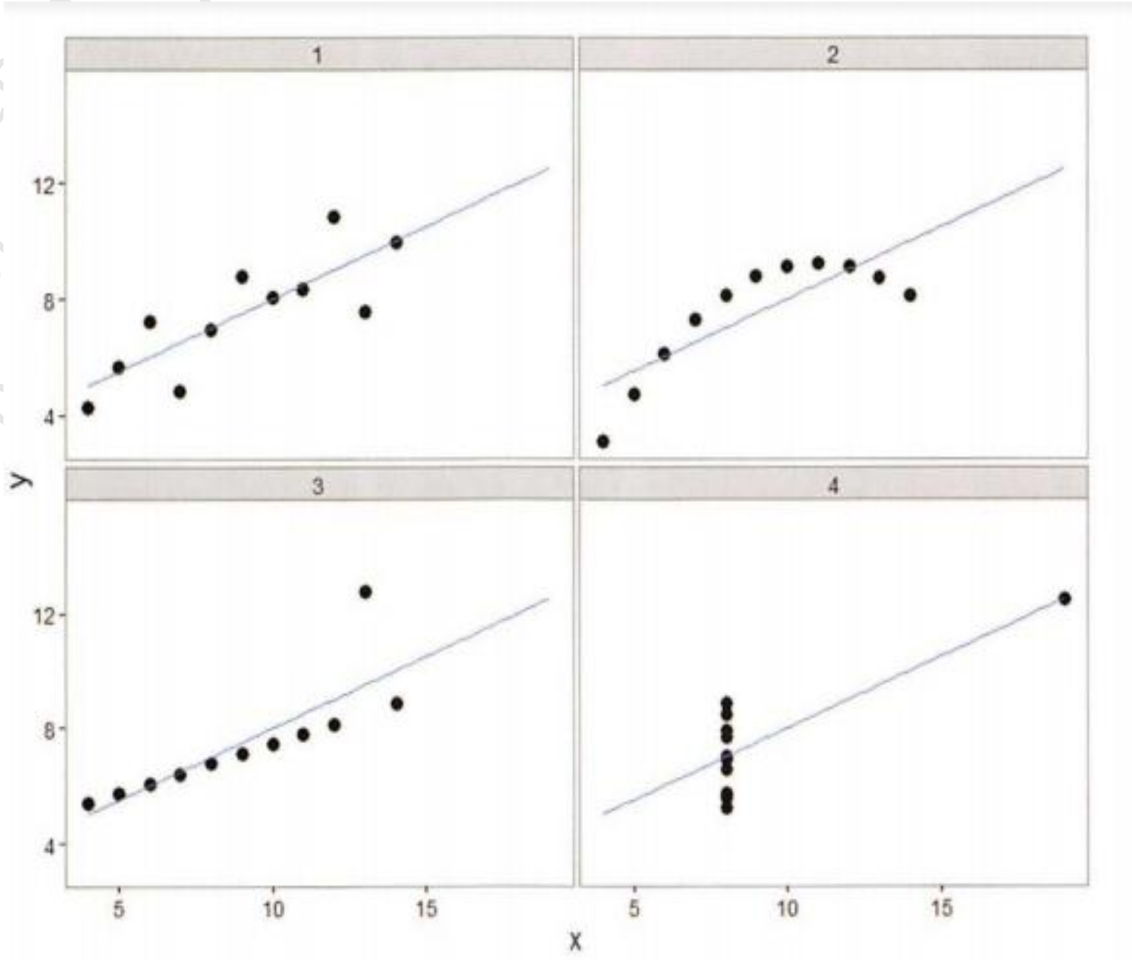
Statistical Properties of Anscombe's Quartet

Statistical Property	Value
Mean of *x*	9
Variance of *y*	11
Mean of *y*	7.50 (to 2 decimal points)
Variance of *y*	4.12 or 4.13 (to 2 decimal points)
Correlations between *x* and *y*	0.816
Linear regression line	$y = 3.00 + 0.50x$ (to 2 decimal points)

Exploratory Data Analysis

- Based on the **nearly identical statistical properties across each dataset, one might conclude that these four datasets are quite similar**.
- However, the **scatterplots as shown in below figure tell a different story**. Each **dataset is plotted as a scatterplot**, and the fitted lines are the result of **applying linear regression models**.
- The estimated **regression line fits Dataset 1 reasonably well**.
- **Dataset 2 is definitely nonlinear**.
- **Dataset 3 exhibits a linear trend, with one apparent outlier at x = 13**.
- For **Dataset 4, the regression line fits the dataset quite well.**

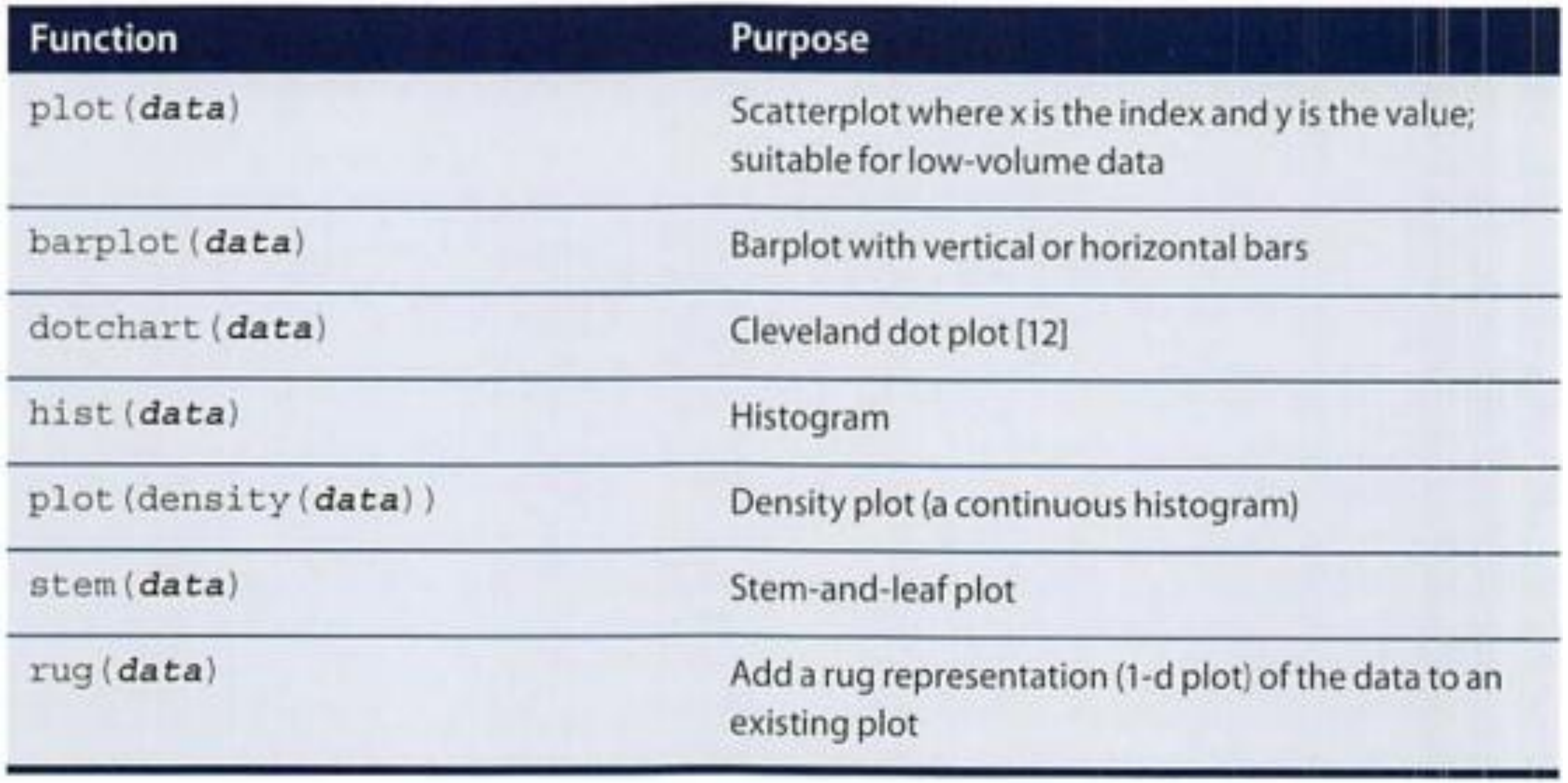
  However, with only points at two x values.



Exploratory Data Analysis: Visualizing a Single Variable

- R has **many functions available to examine a distributions of a single variable**. Some of these functions are listed in below table

Example Functions for Visualizing a Single Variable



Function	Purpose
`plot(`***`data`***`)`	Scatterplot where x is the index and y is the value; suitable for low-volume data
`barplot(`***`data`***`)`	Barplot with vertical or horizontal bars
`dotchart(`***`data`***`)`	Cleveland dot plot [12]
`hist(`***`data`***`)`	Histogram
`plot(density(`***`data`***`))`	Density plot (a continuous histogram)
`stem(`***`data`***`)`	Stem-and-leaf plot
`rug(`***`data`***`)`	Add a rug representation (1-d plot) of the data to an existing plot

Exploratory Data Analysis: Visualizing a Single Variable

- **Quantitative Variables - Variables whose values result from counting or measuring something.**

Examples: height, weight, number of items sold to a shopper, Sepal.Length, Sepal.Width, Petal.Length, Petal.Width

- **Qualitative Variables - Variables that are not measurement variables.** A **qualitative variable**, also called a **categorical variable**, is a variable that **isn't numerical**. It describes **data that fits into categories.**

For example: A qualitative variable **size** corresponds to *"**small**"*, if the length of the petal is smaller than the median of all flowers, "***big***" otherwise

```
dat$size <- ifelse(dat$Sepal.Length<median(dat$Sepal.Length),"small","big")

dat$size
```

OUTPUT

```
"small" "small" "small" "small" "small" "small" "small“ …
```

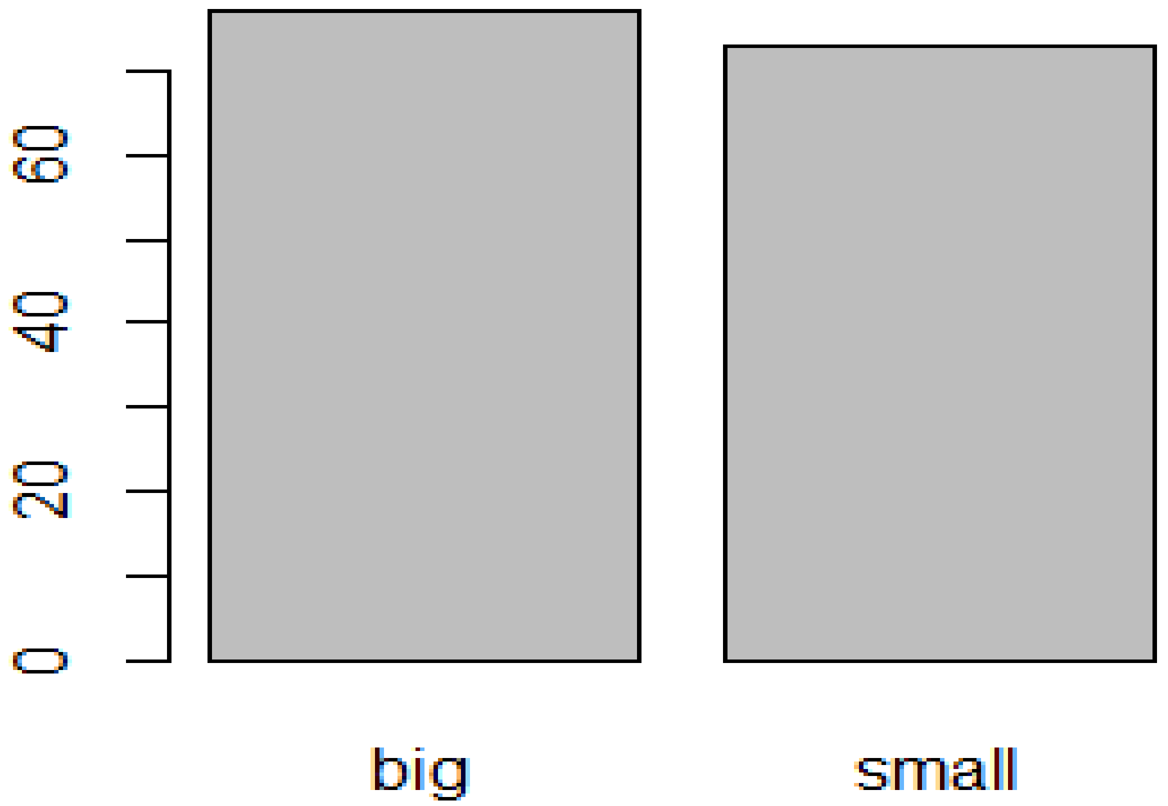
Example 2: hair color, religion, political party, profession

Exploratory Data Analysis: Visualizing a Single Variable Barplot

- A **Barplot** is a **tool to visualize the distribution of a qualitative variable. Barplots can only be done on qualitative variables**.
- Now. we can draw a Barplot on the qualitative variable **size**

```
table(dat$size)
    big    small
     77     73

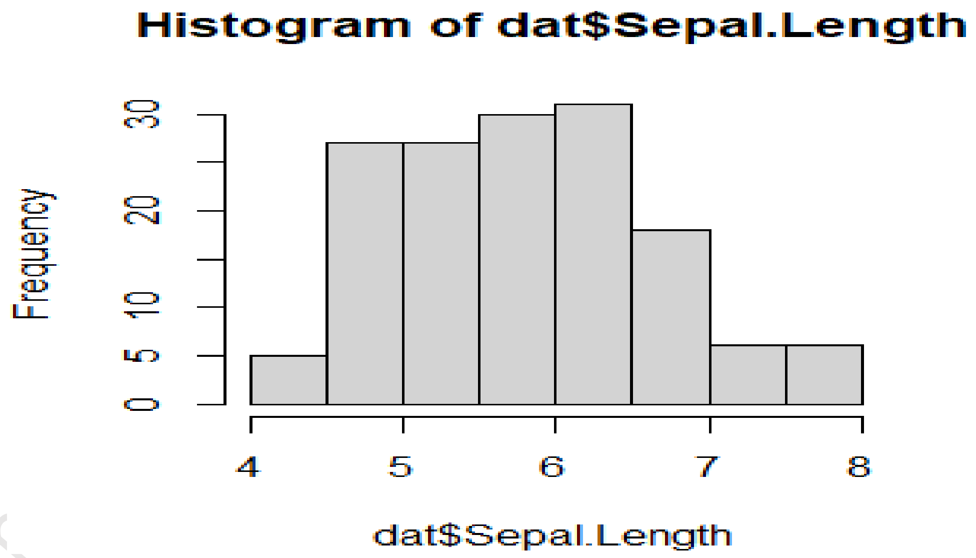
barplot(table(dat$size))
```



Exploratory Data Analysis: Visualizing a Single Variable Histogram

- A Histogram gives an idea about the **distribution of a quantitative variable**.
- The idea is to break the range of values into intervals and count how many observations fall into each interval.
- Histograms are a bit similar to Barplots, but Histograms are used for quantitative variables whereas Barplots are used for qualitative variables.
- To draw a histogram in R, use hist():

hist(dat$Sepal.Length)

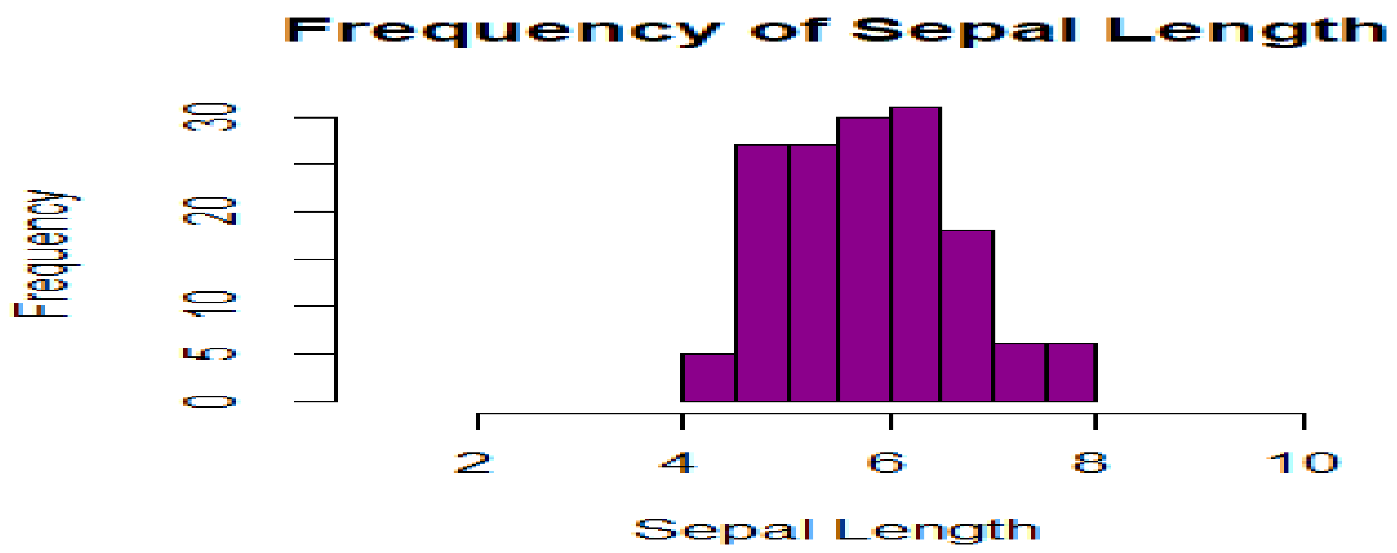


- We can see above that there are 8 cells with equally spaced breaks. In this case, the height of a cell is equal to the number of observation falling in that cell.

Exploratory Data Analysis: Visualizing a Single Variable Histogram

- We can **pass in additional parameters to control the way our plot looks**. Read about them in the help section **?hist**.
- Some of the **frequently used** ones are, **main to give the title**, **xlab and ylab to provide labels for the axes**, **xlim and ylim to provide range of the axes**, **col to define color** etc.
- Additionally, with the argument **freq=FALSE** we can get the probability distribution instead of the frequency.

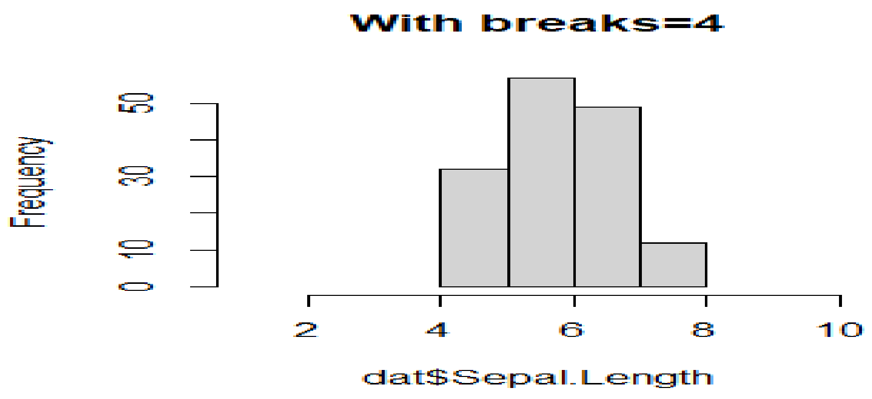
```
hist(dat$Sepal.Length, main="Frequency of Sepal Length", xlab="Sepal Length", xlim=c(1,10),col="darkmagenta", freq=TRUE)
```



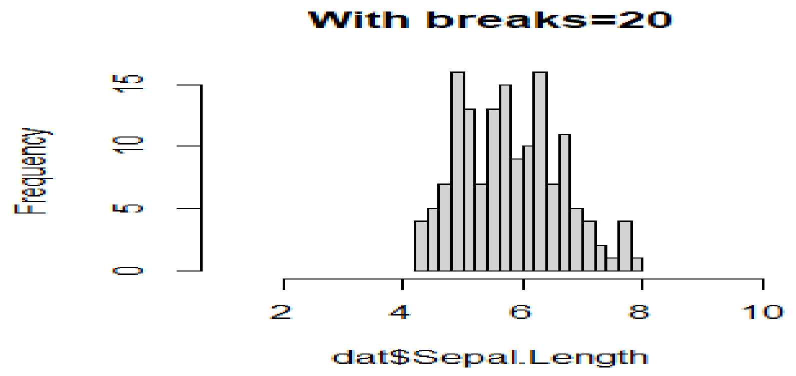
Exploratory Data Analysis: Visualizing a Single Variable Histogram

- **Histogram with different breaks**
- With the **breaks argument, we can specify the number of cells we want in the histogram**. However, **this number is just a suggestion**.
- **R calculates the best number of cells, keeping this suggestion in n** data with different number of cells.

hist(dat$Sepal.Length, breaks=4, main="With breaks=4",xlim=c(1,10))



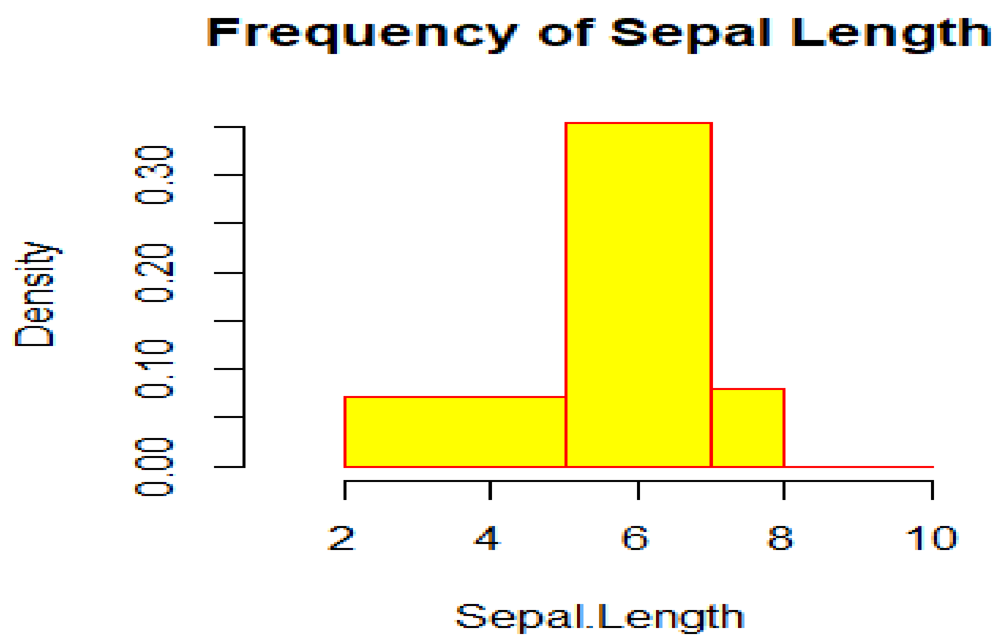
hist(dat$Sepal.Length, breaks=20, main="With breaks=20",xlim=c(1,10))



Exploratory Data Analysis: Visualizing a Single Variable Histogram

- **Histogram with non-uniform width**

```
hist(dat$Sepal.Length,main="Frequency of Sepal Length", xlab="Sepal.Length", xlim=c(1,10), col="yellow",border="red",
breaks=c(2,5,7,8,9,10))
```



- https://www.datamentor.io/r-programming/box-plot/

First and Third Quartile: Example (Just for the Reference)

- The **lower half of a data set is the set of all values that are to the left of the median value** when the data has been put into increasing order.
- The **upper half of a data set is the set of all values that are to the right of the median value** when the data has been put into increasing order.
- The **first quartile, denoted by Q1 , is the median of the lower half of the data set**. This means that about **25% of the numbers in the data set lie below Q1** and about 75% lie above Q1 .
- The **third quartile, denoted by Q3 , is the median of the upper half of the data set**. This means that about **75% of the numbers in the data set lie below Q3** and about 25% lie above Q3 .

Example: Find the first and third quartiles of the data set {3, 7, 8, 5, 12, 14, 21, 13, 18}.

First, we write data in increasing order: **3, 5, 7, 8, 12, 13, 14, 18, 21.**

$$\underbrace{3,\ 5,\ 7,\ 8,}_{\text{“lower half”}}\ \underset{\text{median}}{\boxed{12},}\ \underbrace{13,\ 14,\ 18,\ 21}_{\text{“upper half”}}$$

The **median is 12.**

Therefore, **the lower half of the data is: {3, 5, 7, 8}.**

The **first quartile, Q1, is the median of {3, 5, 7, 8}.**

Since there is an even number of values, we need the mean of the middle two values to find the first quartile:

$$Q_1 = \frac{5+7}{2} = \frac{12}{2} = 6$$

- Similarly, **the upper half of the data is: {13, 14, 18, 21}, so**

$$Q_3 = \frac{14+18}{2} = \frac{32}{2} = 16$$

Exploratory Data Analysis: Visualizing a Single Variable Boxplot

- In R, boxplot is created using the **boxplot() function**.
- The **boxplot() function takes in any number of numeric vectors, drawing a boxplot for each vector**.
- We can also pass in a **list** (or **data frame**) with **numeric vectors** as its components.
- Let us use the built-in dataset **airquality** which has "**Daily air quality measurements in New York, May to September 1973**."

str(airquality)

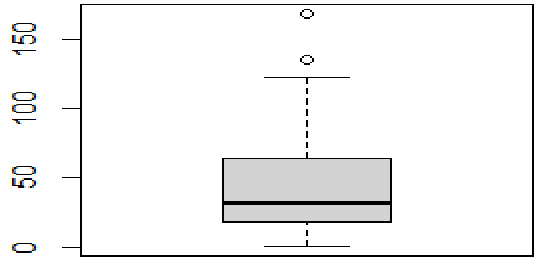
```
'data.frame':	153 obs. of  6 variables:
 $ Ozone  : int  41 36 12 18 NA 28 23 19 8 NA ...
 $ Solar.R: int  190 118 149 313 NA NA 299 99 19 194 ...
 $ Wind   : num  7.4 8 12.6 11.5 14.3 14.9 8.6 13.8 20.1 8.6 ...
 $ Temp   : int  67 72 74 62 56 66 65 59 61 69 ...
 $ Month  : int  5 5 5 5 5 5 5 5 5 5 ...
 $ Day    : int  1 2 3 4 5 6 7 8 9 10 ...
```

Exploratory Data Analysis: Visualizing a Single Variable

Boxp

- Let us create a boxplot for the ozone readings.

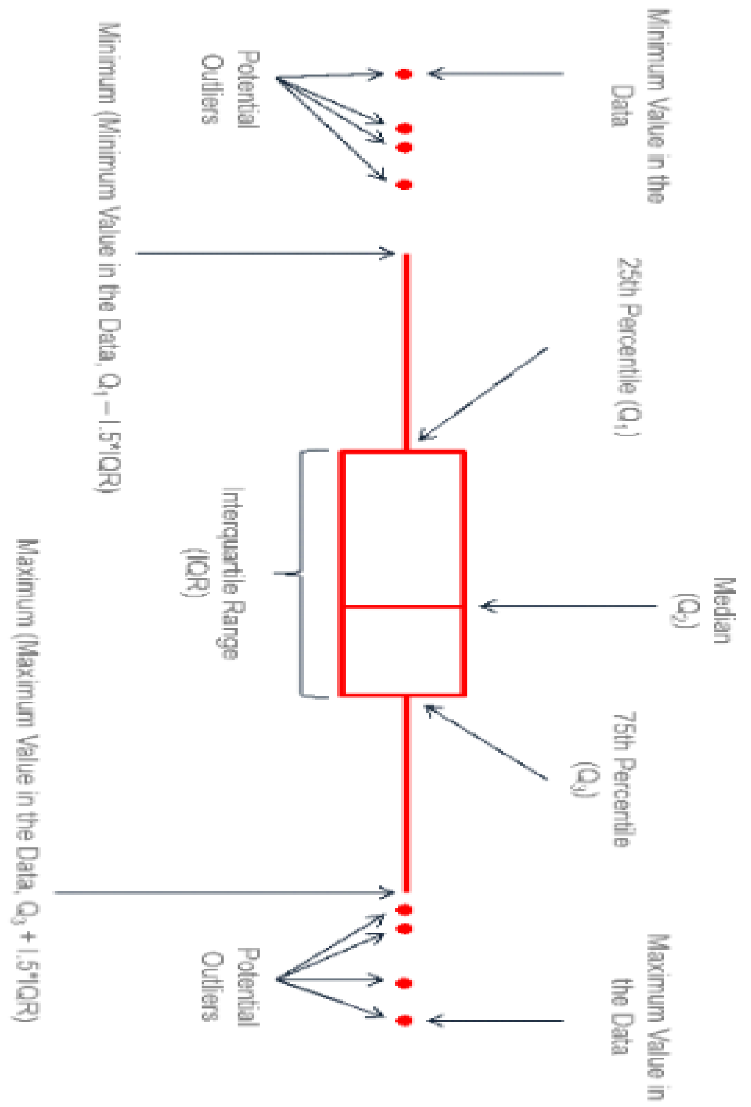
boxplot(airquality$Ozone)



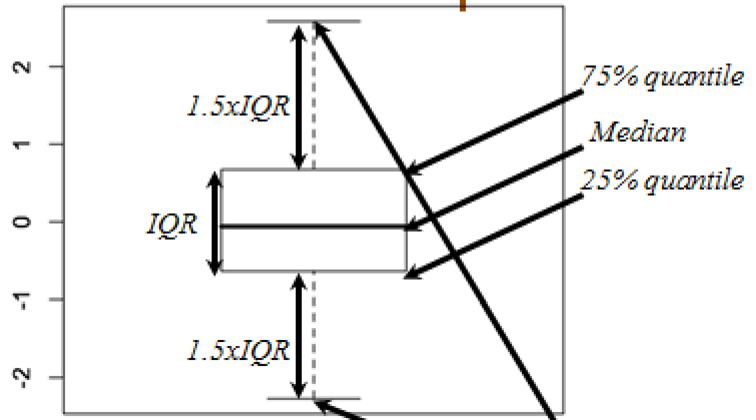
A boxplot gives a nice **summary of one or more numeric variables**.

- The line that divides the box into 2 parts represents the **median of the data**.
- The ends of the box shows the upper (Q3) and lower (Q1) quartiles.
- The difference between Quartiles 1 and 3 is called the **interquartile range (IQR)**
- The extreme line shows **Q3+1.5xIQR to Q1-1.5xIQR (the highest and lowest value excluding outliers).**
- Dots beyond the extreme line shows potential outliers.

Exploratory Data Analysis: Visualizing a Single Variable

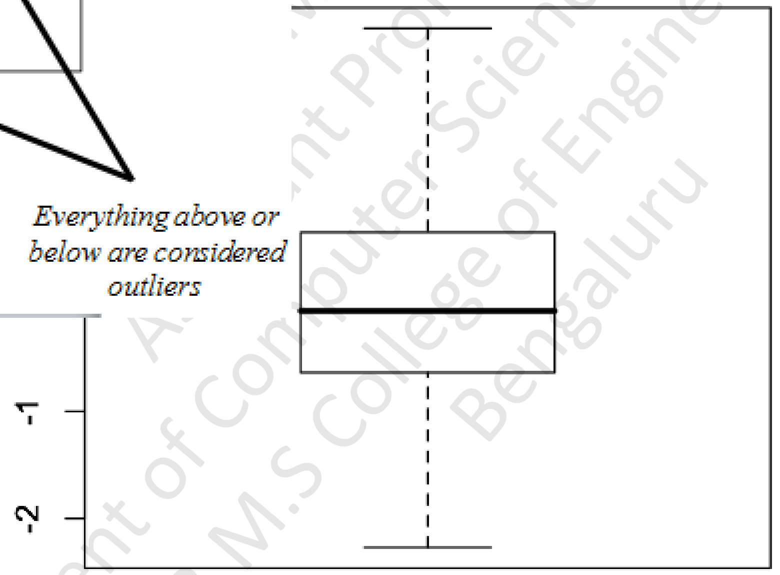

Minimum Value in the Data
Potential Outliers
Minimum (Minimum Value in the Data, $Q_1 - 1.5*IQR$)
25th Percentile (Q_1)
Interquartile Range (IQR)
Median (Q_2)
75th Percentile (Q_3)
Maximum (Maximum Value in the Data, $Q_3 + 1.5*IQR$)
Potential Outliers
Maximum Value in the Data

boxplot

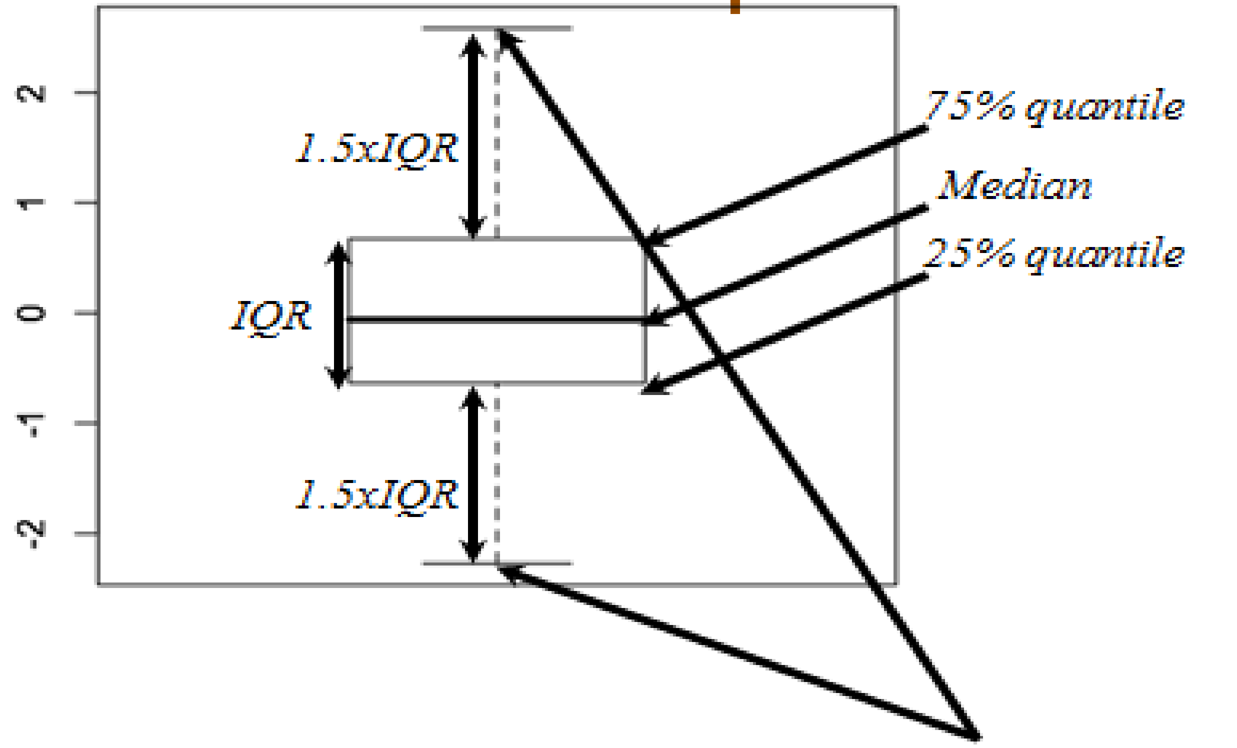


IQR (interquantile range)= 75% quantile -25% quantile

Everything above or below are considered outliers



boxplot

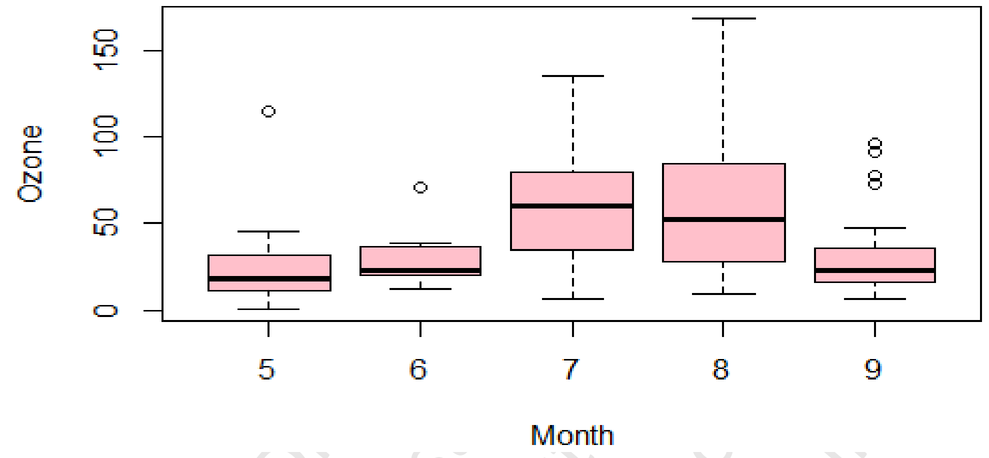


IQR (interquantile range)= 75% quantile -25% quantile

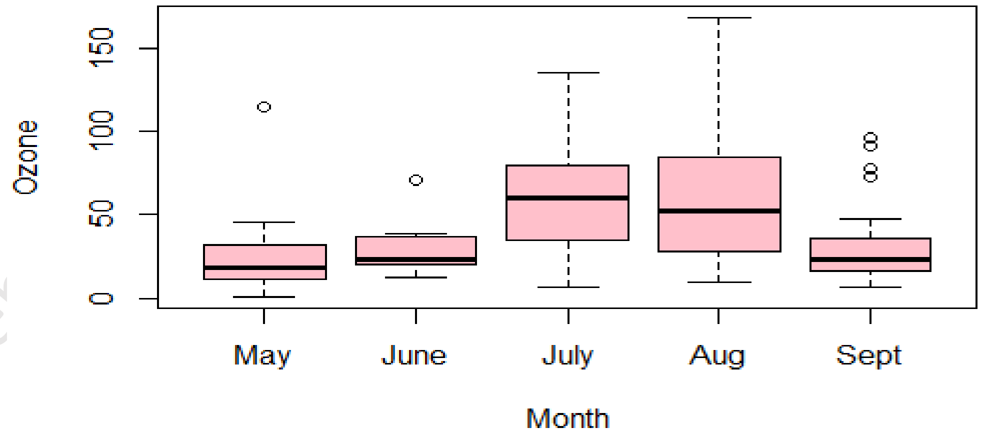
Everything above or below are considered outliers

Exploratory Data Analysis: Visualizing a Single Variable Boxplot

- **boxplot(Ozone~Month,data=airquality,col="pink")**

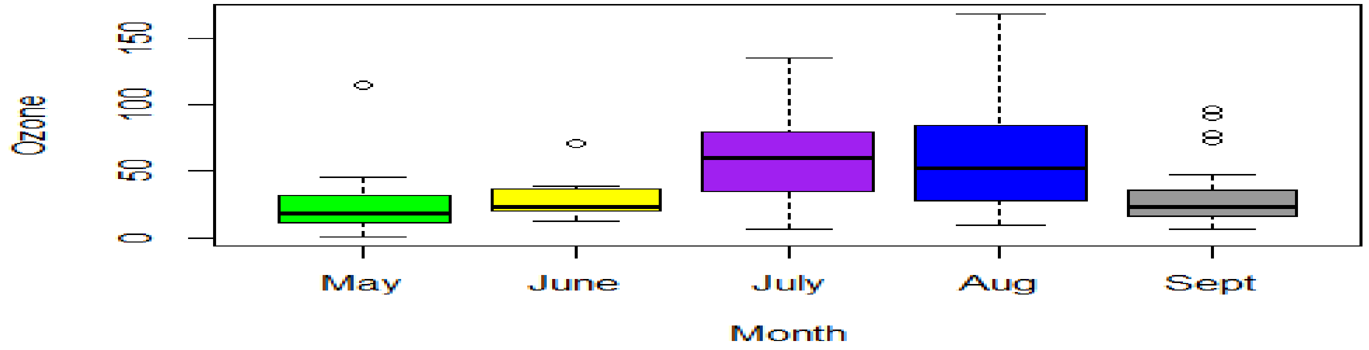


- **boxplot(Ozone~Month,data=airquality,col="pink",names = c("May","June","July","Aug","Sept"))**
- names are the group labels which will be printed under each boxplot.



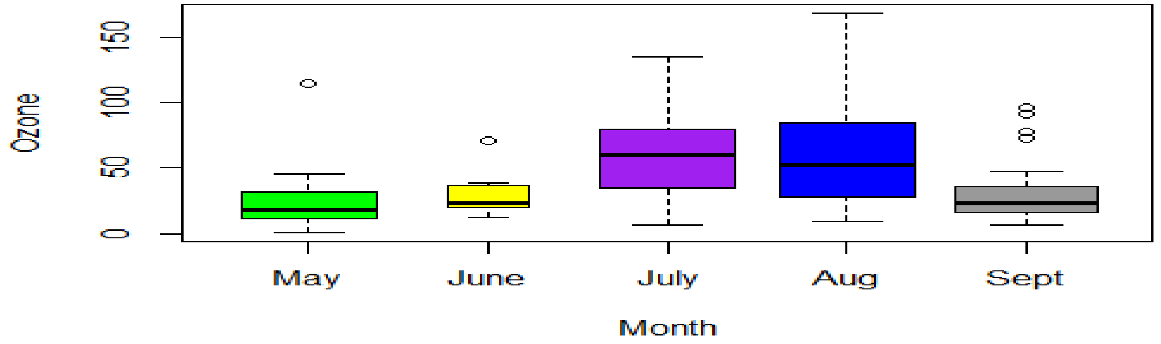
Exploratory Data Analysis: Visualizing a Single Variable Boxplot

- boxplot(Ozone~Month,data=airquality,names = c("May","June","July","Aug","Sept"),col = c("green","yellow","purple","blue","grey60"))



- boxplot(Ozone~Month,data=airquality,names = c("May","June","July","Aug","Sept"),col = c("green","yellow","purple","blue","grey60"),varwidth=TRUE)

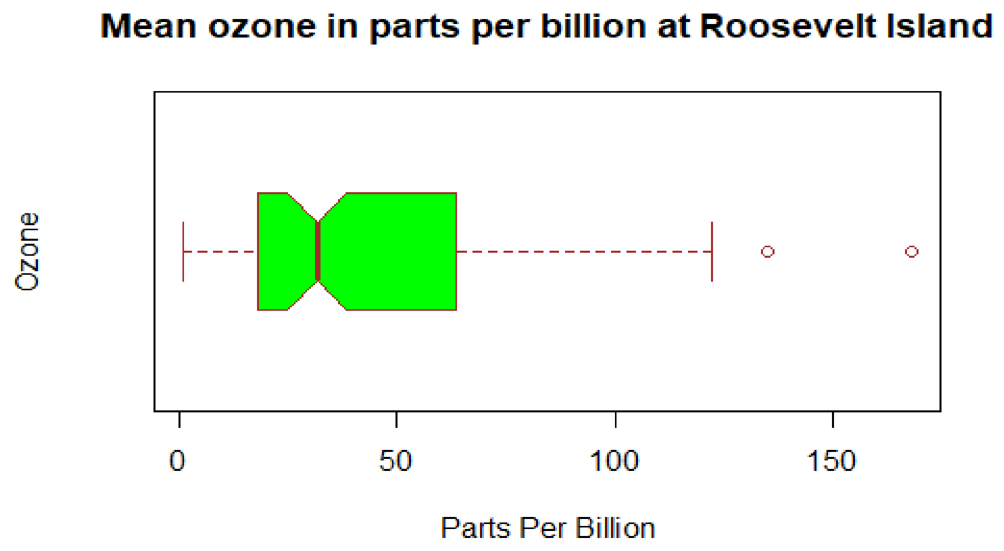
- varwidth is a logical value. Set as true to draw width of the box proportionate to the sample size.



Exploratory Data Analysis: Visualizing a Single Variable
Boxplot

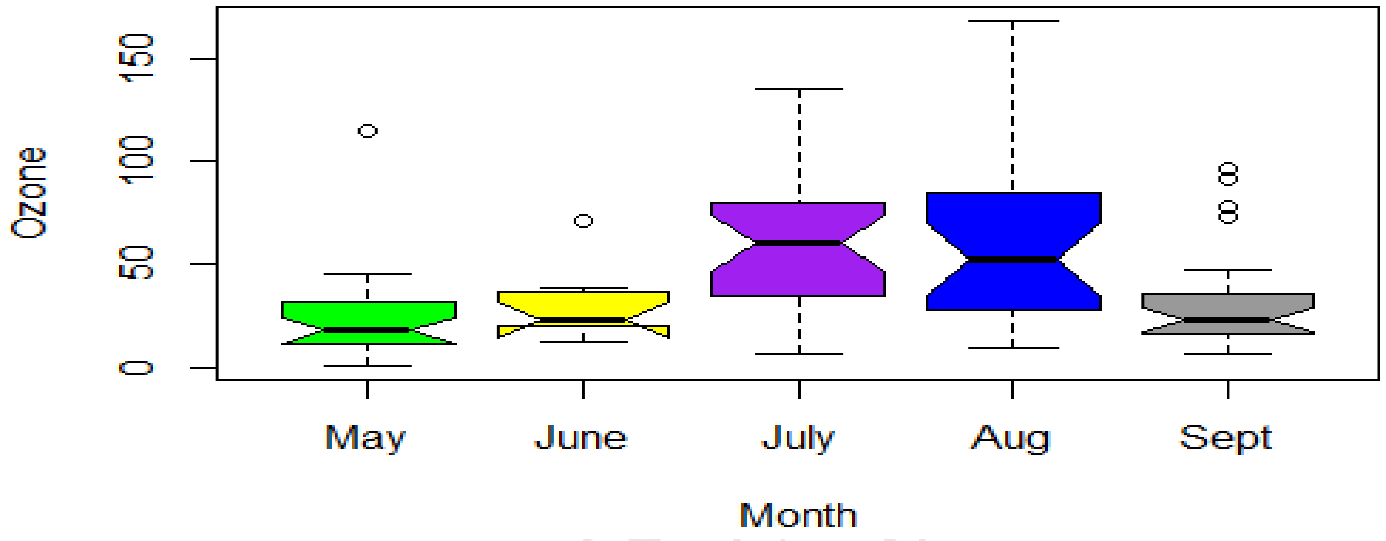
- We can **pass in additional parameters** to control the way our plot looks.
- Some of the frequently used ones are, **main**-to give the title, **xlab and ylab**-to provide labels for the axes, **col**- define color etc.
- Additionally, with the argument horizontal = TRUE, we can plot it horizontally and with notch = TRUE we can add a notch to the box. (We can draw boxplot with notch to find out how the medians of different data groups match with each other)
- Add **horizontal=TRUE** to reverse the axis orientation.

```
boxplot(airquality$Ozone,
    main = "Mean ozone in parts per billion at Roosevelt Island",
    xlab = "Parts Per Billion",
    ylab = "Ozone",
    col = "Green",
    border = "brown",
    horizontal = TRUE,
    notch = TRUE
)
```



Exploratory Data Analysis: Visualizing a Single Variable Boxplot

- boxplot(Ozone~Month,data=airquality,names = c("May","June","July","Aug","Sept"),col = c("green","yellow","purple","blue","grey60"),notch=TRUE)



Return Value of boxplot()

Exploratory Data Analysis: Visualizing a Single Variable Boxplot

- The boxplot() function returns a list with 6 components shown as follows.

```
b <- boxplot(airquality$Ozone)
b
     $stats
          [,1]
     [1,]   1.0   → 0% Quantile
     [2,]  18.0   → 25% Quantile
     [3,]  31.5   → 50% Quantile
     [4,]  63.5   →75% Quantile
     [5,] 122.0 → 100% Quantile
     attr(,"class")
          1
     "integer“
      $n
     [1] 116
```

```
$conf
 [,1]
[1,] 24.82518
[2,] 38.17482
$out
[1] 135 168
$group
[1] 1 1
$names
[1] "1"
```

n-the number of observation the boxplot is drawn with (notice that NA's are not taken into account)

conf-upper/lower extremes of the notch, out-value of the outliers

group-a vector of the same length as out whose elements indicate to which group the outlier belongs

names-a vector of names for the groups.

Multiple Boxplots

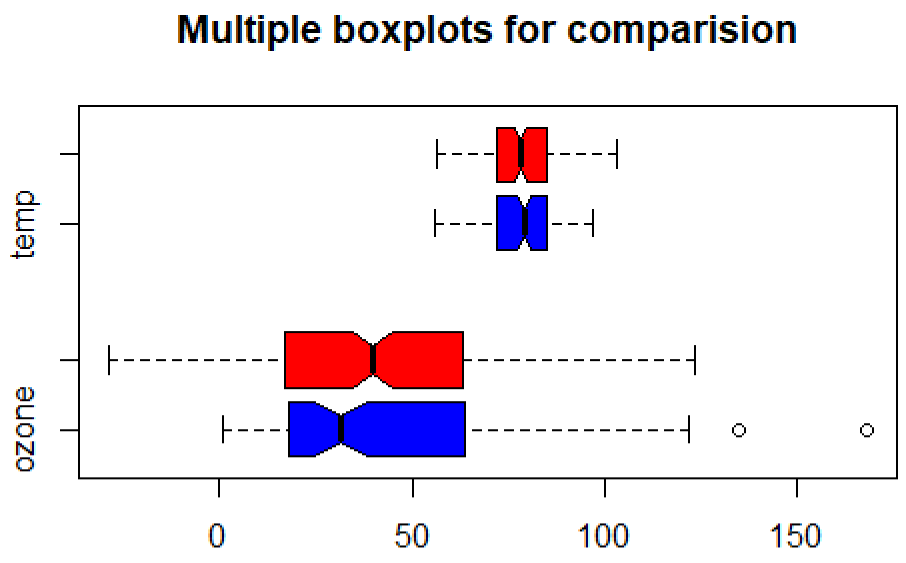
- We can draw **multiple boxplots in a single plot**, by passing in a **list, data frame or multiple vectors**.
- Let us consider the **Ozone** and **Temp field of airquality dataset**.
- Let us also generate **normal distribution with the same mean and standard deviation** and plot them side by side for comparison.

```
# prepare the data
ozone <- airquality$Ozone
temp <- airquality$Temp
# generate normal distribution with same mean and sd
ozone_norm <- rnorm(200,mean=mean(ozone, na.rm=TRUE), sd=sd(ozone, na.rm=TRUE))
temp_norm <- rnorm(200,mean=mean(temp, na.rm=TRUE), sd=sd(temp, na.rm=TRUE))
```

- Now we make 4 boxplots with this data. We use the arguments at and names to denote the place and label.

Multiple Boxplots

```
boxplot(ozone, ozone_norm, temp, temp_norm,
    main = "Multiple boxplots for comparision",
    at = c(1,2,4,5),
    names = c("ozone", "normal", "temp", "normal"),
    col = c("blue","red"),
    border = "black",
    horizontal = TRUE,
    notch = TRUE
)
```



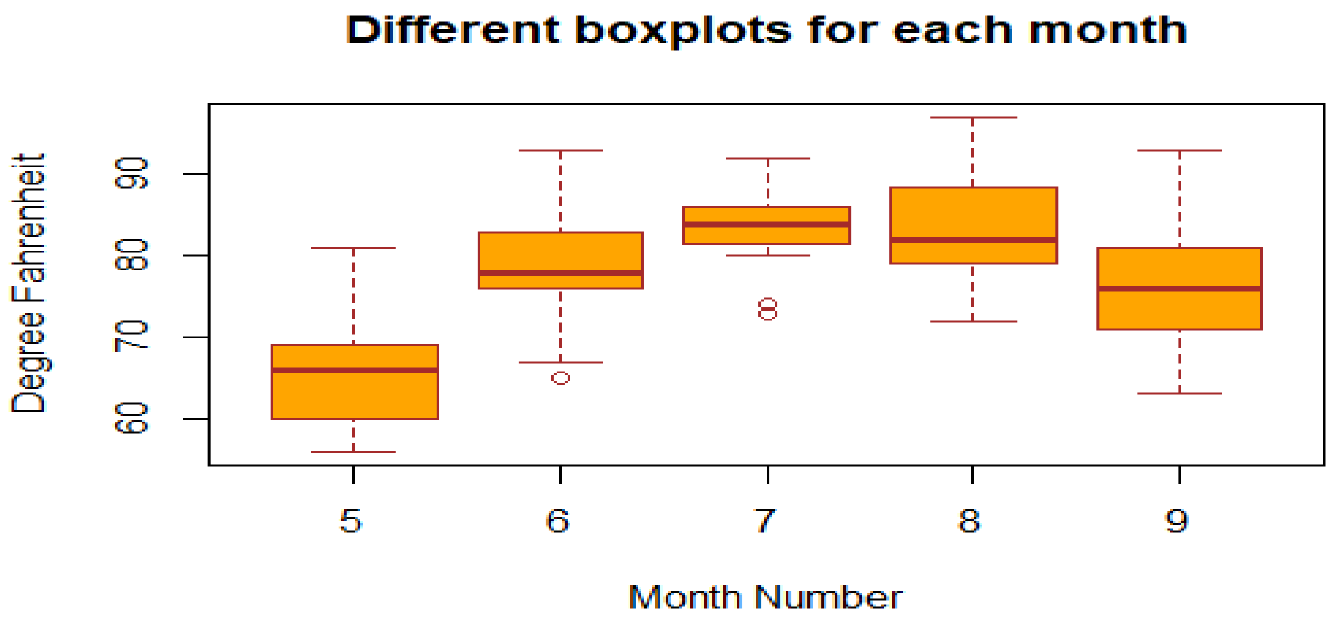
Boxplot form Formula

- The function **boxplot() can also take in formulas of the form y~x** where, **y is a numeric vector which is grouped according to the value of x**.

- For example, in the dataset airquality, the **Temp can be our numeric vector. Month can be our grouping variable**, so that we get the boxplot for each month separately.

- In the dataset airquality, month is in the form of number (1=January, 2-Febuary and so on).

```
boxplot(Temp~Month,
    data=airquality,
    main="Different boxplots for each month",
    xlab="Month Number",
    ylab="Degree Fahrenheit",
    col="orange",
    border="brown"
)
```



It is clear from the above figure that the **month number 7 (July) is relatively hotter than the rest**.

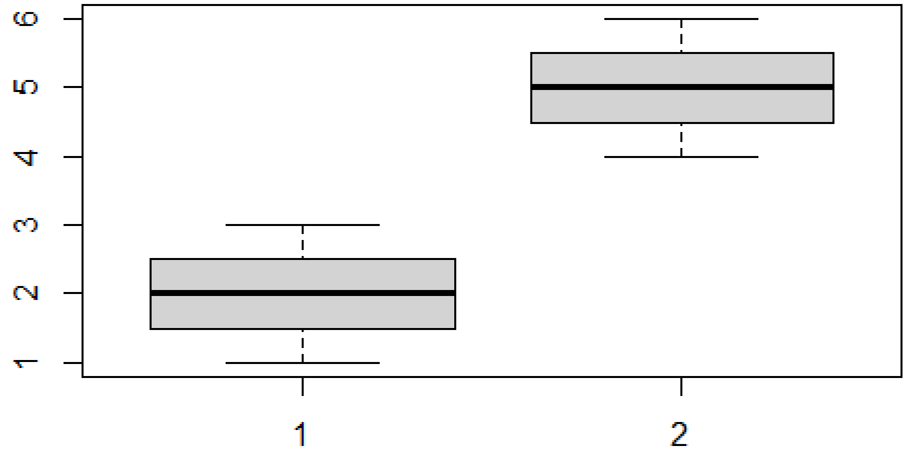
boxplot.matrix( )

- The **boxplot.matrix( )** function in the sfsmisc package draws a boxplot for each column (row) in a matrix.

M6<-cbind(c(1,2,3),c(4,5,6))

M6

boxplot.matrix(M6)



- There are many arguments supported by the Boxplot in R programming language, and the following are some of the arguments:
  - data: Please specify the DataFrame, or List that contains the data to draw boxplot. In this example, it is airquality
  - subset: You can restrict the R barplots by specifying the vector of values. In this example, you can restrict the barplot box for August month.
  - x: Please specify the data from which you want to draw the R box plot. Here, you can use a numeric vector, or a list containing the numeric vector.
  - range: This R Programming argument decides how far the whisker extends out of the box.
  - width: It is optional, but you can use this to specify a vector that contains the widths of each box.
  - varwidth: It is a Boolean argument. If it is TRUE, boxes draw with widths proportional to the square roots of the no. of observations in the group.
  - border: It is an optional argument. Please specify the vector of color you want to add to the outlines of the boxplot borders.
  - plot: It is a Boolean argument. If it is FALSE, it returns the summaries on which the R boxplots based on.
  - log: You have to specify a character string of three options. If X-Axis is to be logarithmic then “x”, If Y-Axis is to be logarithmic “y”, if both X-Axis and Y-Axis are to be logarithmic, then specify either “xy” or “yx”
  - add: It is a Boolean argument, and by default, it is FALSE. If it is TRUE, the boxplot should add to an already existing plot.
  - horizontal: It is a Boolean argument. If it is FALSE, the R boxplot drew vertically. If it is TRUE, the boxplot drew horizontally.
  - at: It is a numeric vector, which gives the locations where the boxplot drew. It is very helpful when we are adding a new

Boxplot in ggplot2 Package

- So far, we have created all the graphs and images with the boxplot function of Base R. However, there are also many packages that provide pretty designs and additional modification possibilities for boxplots.

- In the example, I'll show you how to create a boxplot with the ggplot2 package. Let's install and load the package to RStudio:

```
install.packages("ggplot2")                    # Install and load ggplot2
library("ggplot2")
```

http://r-statistics.co/Top50-Ggplot2-Visualizations-MasterList-R-Code.html#Box%20Plot

- str(airquality)

- boxplot(airquality$Ozone)
- boxplot(Ozone~Month,data=airquality,col="pink")
- boxplot(Ozone~Month,data=airquality,col="pink",names = c("May","June","July","Aug","Sept"))
- boxplot(Ozone~Month,data=airquality,names = c("May","June","July","Aug","Sept"),col = c("green","yellow","purple","blue","grey60"))
- boxplot(Ozone~Month,data=airquality,names = c("May","June","July","Aug","Sept"),col = c("green","yellow","purple","blue","grey60"),varwidth=TRUE)

- boxplot(airquality$Ozone,
-         main = "Mean ozone in parts per billion at Roosevelt Island",
-         xlab = "Parts Per Billion",
-         ylab = "Ozone",
-         col = "darkGreen",
-         border = "brown",
-         horizontal = FALSE,
-         notch = TRUE
-)

Scatter Plot

- **Scatterplots show many points plotted in the Cartesian plane. Each point represents the values of two variables. One variable is chosen in the horizontal axis** and **another in the vertical axis.** (to visualize the distribution of a variable in terms of points in a Cartesian plane)
- There are **many ways to create a scatterplot in R**. The basic function is **plot(x, y)**, where x and y are **numeric vectors** denoting the x and y points to plot.

Syntax

The basic syntax for creating scatterplot in R is −

plot(x, y, main, xlab, ylab, xlim, ylim)

- x is the **data set whose values are the horizontal coordinates**. y is the **data set whose values are the vertical coordinates**.
- **main is the tile of the graph**. **xlab is the label** in the **horizontal axis**. **ylab is the label** in the **vertical axis**.
- **xlim is the limits of the values of x used for plotting**. **ylim is the limits of the values of y used for plot**ting.

Scatter Plot

- To illustrate, first read the **Employee data included as part of lessR package**.

```
library("lessR")
d <- Read("Employee")
D
head(d)
```

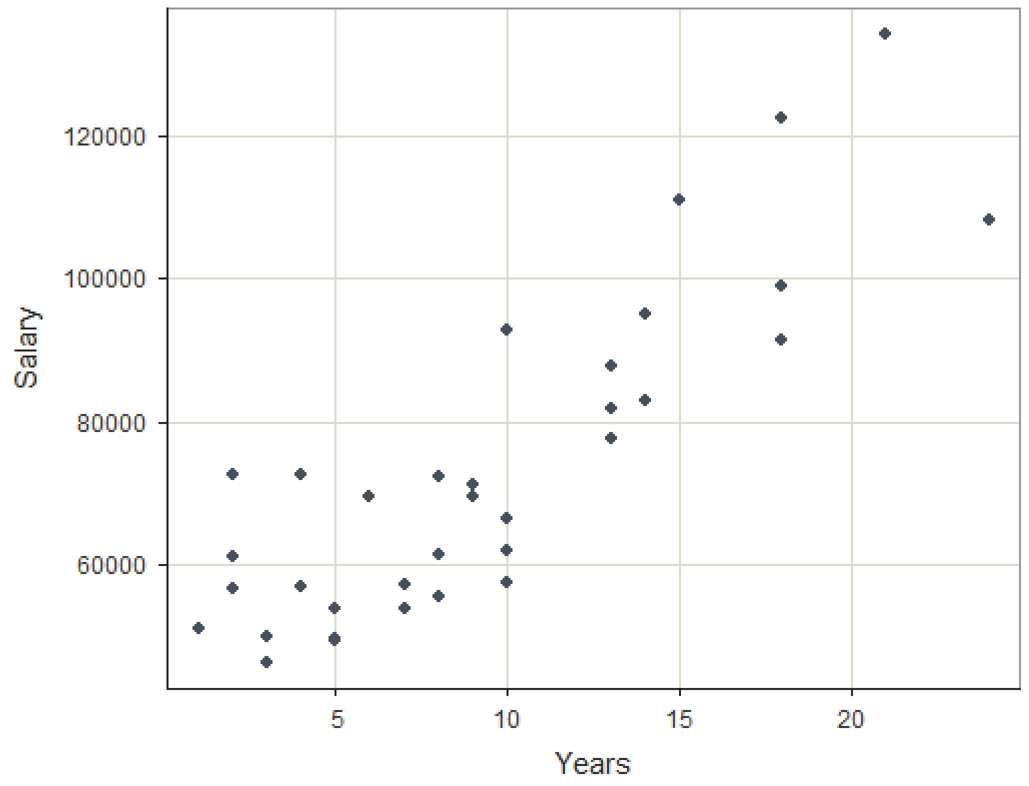
```
 Name              Years Gender      Dept      Salary    JobSat  Plan  Pre   Post
Ritchie, Darnell     7       M       ADMN  53788.26   med     1     82    92
Wu, James           NA       M        SALE  94494.58    low    1     62    74
Hoang, Binh         15       M       SALE 111074.86    low    3     96    97
Jones, Alissa        5       F        <NA>  53772.58   <NA>   1     65    62
Downs, Deborah      7       F         FINC  57139.90     high   2     90    86
Afshari, Anbar      6       F        ADMN  69441.93     high   2    100   100
```

```
details(d)
```

```
Total number of cells in data table:  296
Total number of cells with the value missing:  4
```

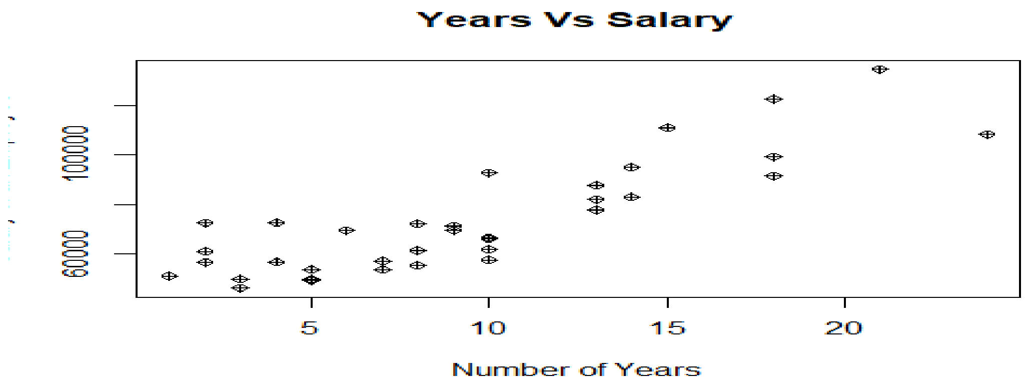
Scatter Plot

Plot(Years, Salary)



Scatter Plot

```
attach(d)
plot(Years,Salary, main="Years Vs Salary", xlab="Number of Years", ylab="Salary of an Employee", pch=10)
```



- **Attach() function** in R makes the **database attached to the R search path**.

For Eg:

```
data <- data.frame(x1 = c(9, 8, 3, 4, 8), x2 = c(5, 4, 7, 1, 1),x3 = c(1, 2, 3, 4, 5))
data
 x1                                   # Try to print x1 column without attach
```

# Error: object 'x1' not found

However, if we attach the data frame first

```
attach(data)                          # Attach data to Global Environment or R search path
```

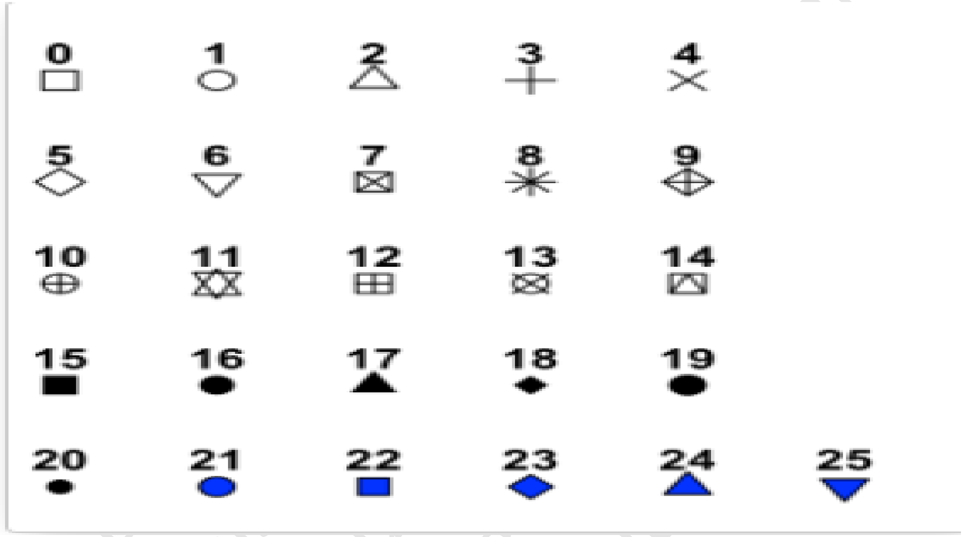
Now, we can work with the X1 column

```
x1                                    # Print x1 column to RStudio console
```

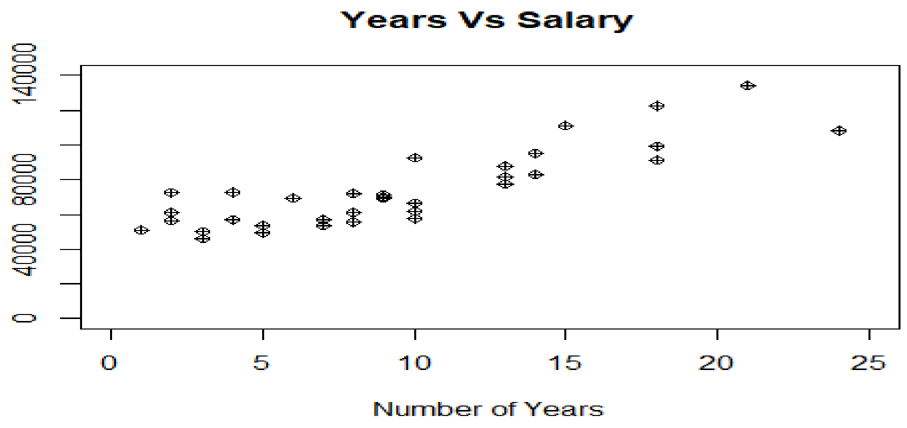
# 9 8 3 4 8

Scatter Plot

- **pch is the graphical argument** used to specify **point shapes**.
- The different **points symbols** commonly used in **R** are shown in the figure below :

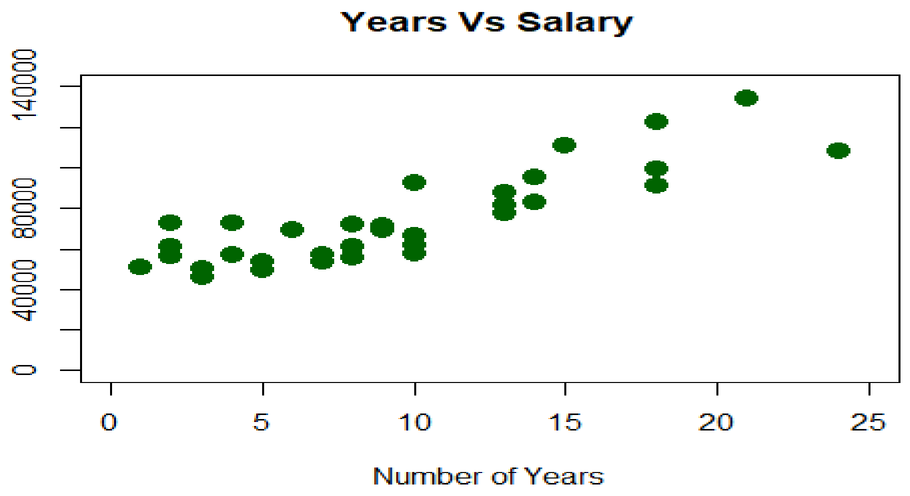


plot(Years,Salary, main="Years Vs Salary",xlab="Number of Years", ylab="Salary of an Employee",xlim=c(0,25),ylim=c(0,140000),pch=10)

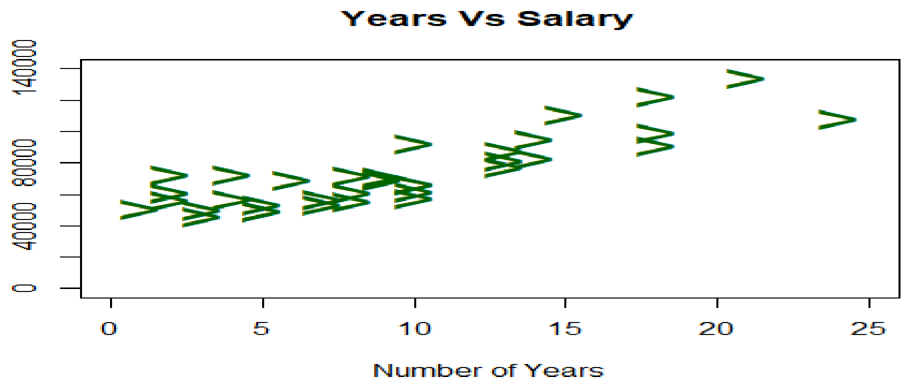


Scatter Plot

```
plot(Years,Salary, main="Years Vs Salary", xlab="Number of Years", ylab="Salary of an
Employee",xlim=c(0,25),ylim=c(0,140000),col="darkgreen", cex=2.5,pch=20)
```



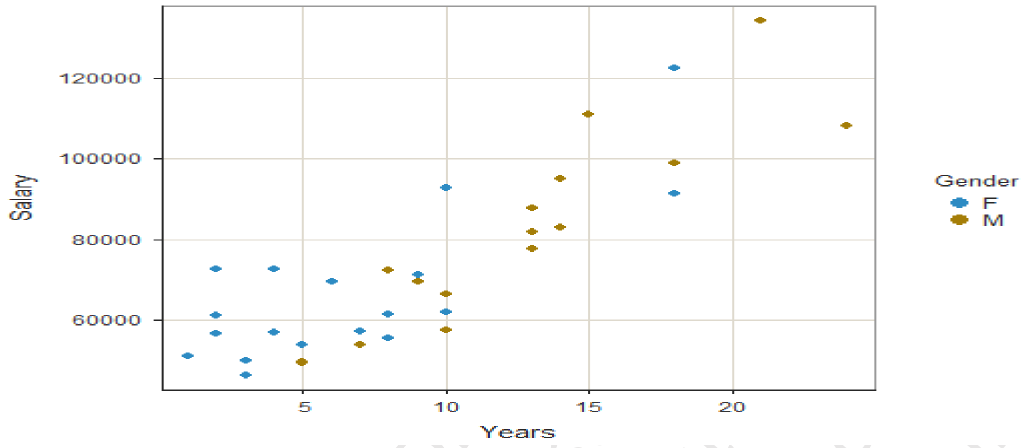
```
plot(Years,Salary, main="Years Vs Salary", xlab="Number of Years", ylab="Salary of an
Employee",xlim=c(0,25),ylim=c(0,140000),col="darkgreen", cex=2.5,pch=">")
```



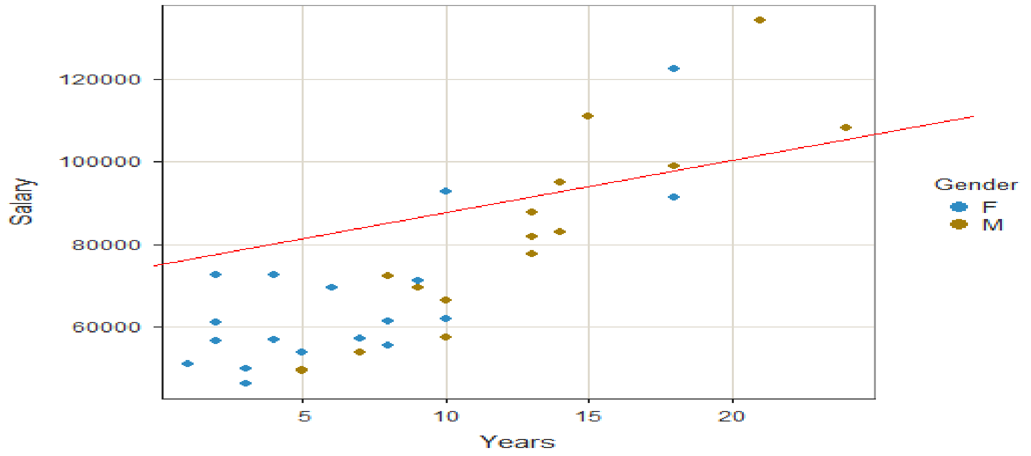
Scatter Plot

- **Plot against levels of categorical variable** Gender with the **by** parameter.

Plot(Years, Salary, by=Gender)



abline(lm(Salary~Years),col="red")   # regression line (y~x)



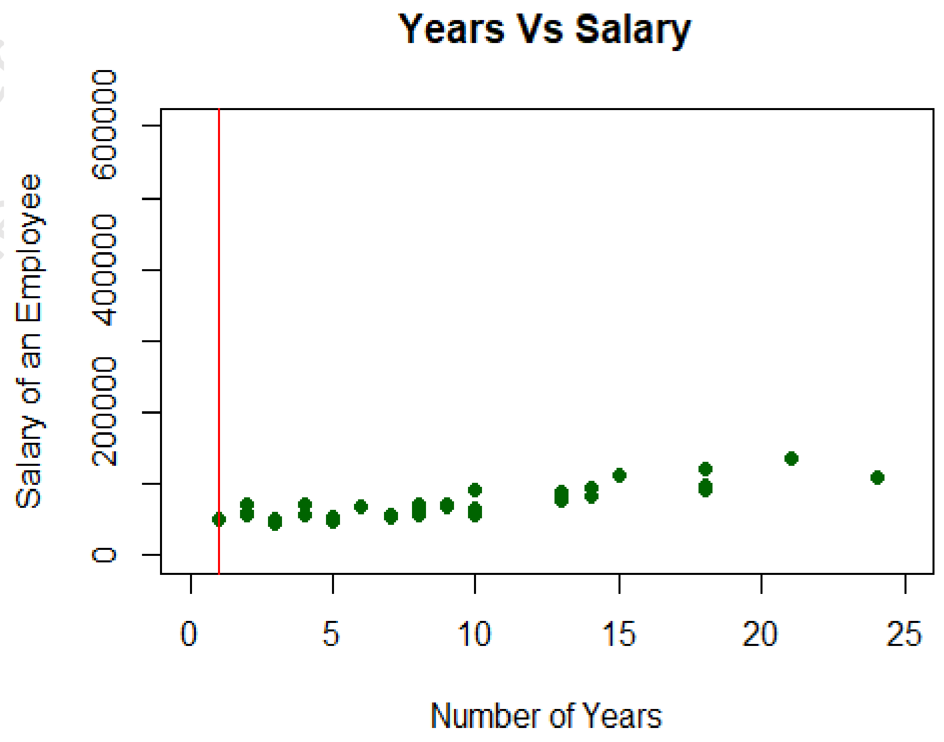
Scatter Plot

- The R function **abline()** can be used to add **vertical**, **horizontal** or **regression lines** to a graph.

```
plot(Years,Salary, main="Years Vs Salary", xlab="Number of Years", ylab="Salary of an
Employee",xlim=c(0,25),ylim=c(0,600000),col="darkgreen", cex=1.5,pch=20)


min(Years,na.rm=TRUE)


abline(v=min(Years,na.rm=TRUE),col="Red")
```



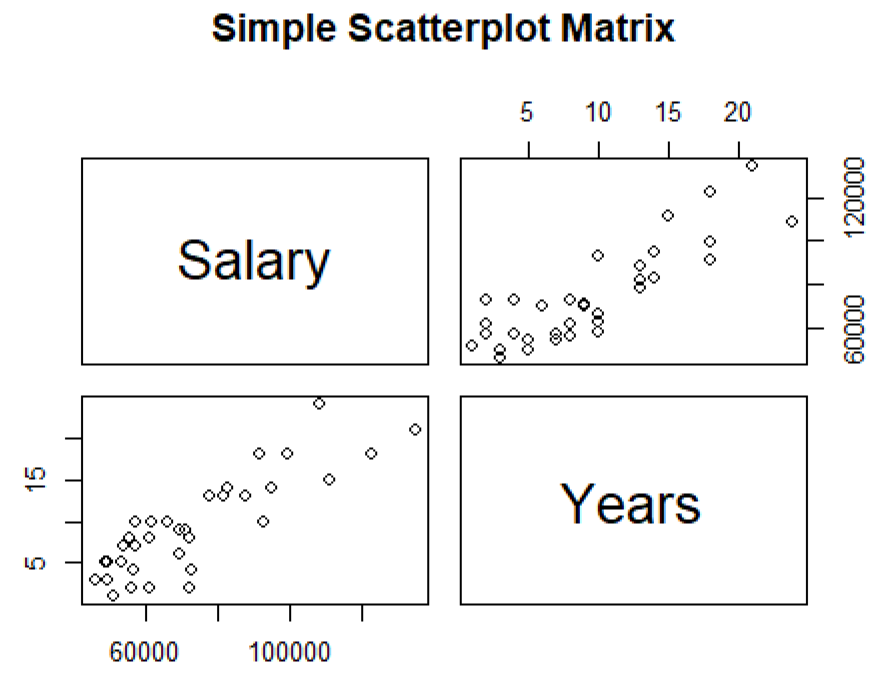
Scatter Plot

- The **scatterplot( ) function in the car package offers many enhanced features**, including **fit lines, marginal box plots, conditioning on a factor**, and **interactive point identification**. Each of these features is optional.

Scatter Plot

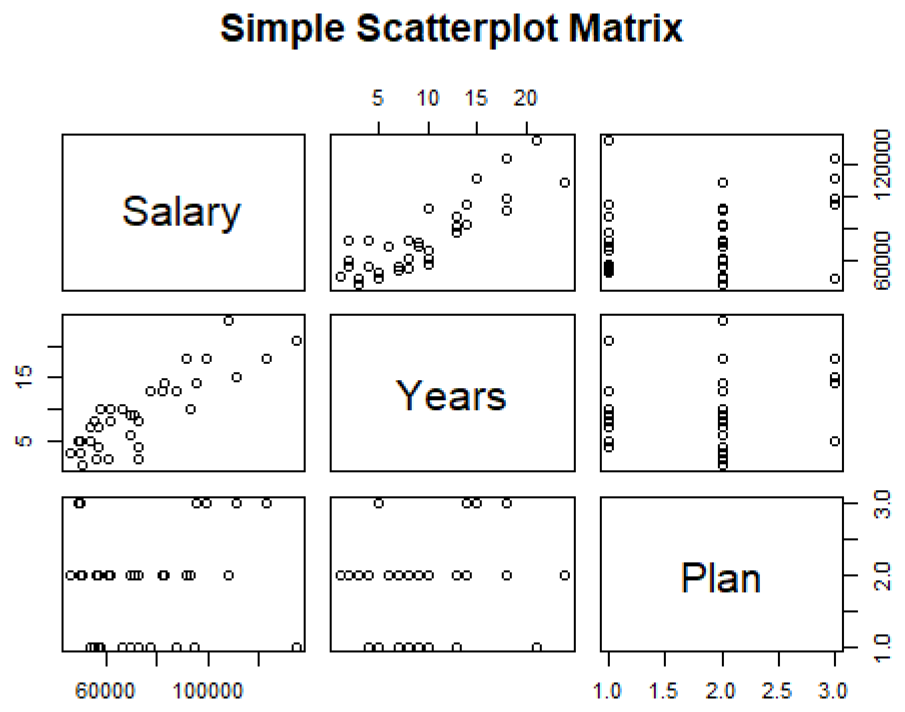
- **Scatterplot Matrix**
- If **our data set contains large number of variables, finding relation between** them is difficult. In R, we can create **scatter plots of all pairs of variables at once**.
- Following example plots all columns of iris data set, producing a matrix of scatter plots (pairs plot).

pairs(~Salary+Years,data=d,main="Simple Scatterplot Matrix")



Scatter Plot

```
pairs(~Salary+Years+Plan,data=d, main="Simple Scatterplot Matrix")
```



Scatter Plot

Scatterplot Matrices from the glus Package

```
library(gclus)

mtcars

dta <- mtcars[c(1,3,5,6)] # get data

dta

dta.r <- abs(cor(dta)) # get correlations

dta.r

dmat.color(dta.r)

dta.col <- dmat.color(dta.r) # get colors

dta.col

# reorder variables so those with highest correlation

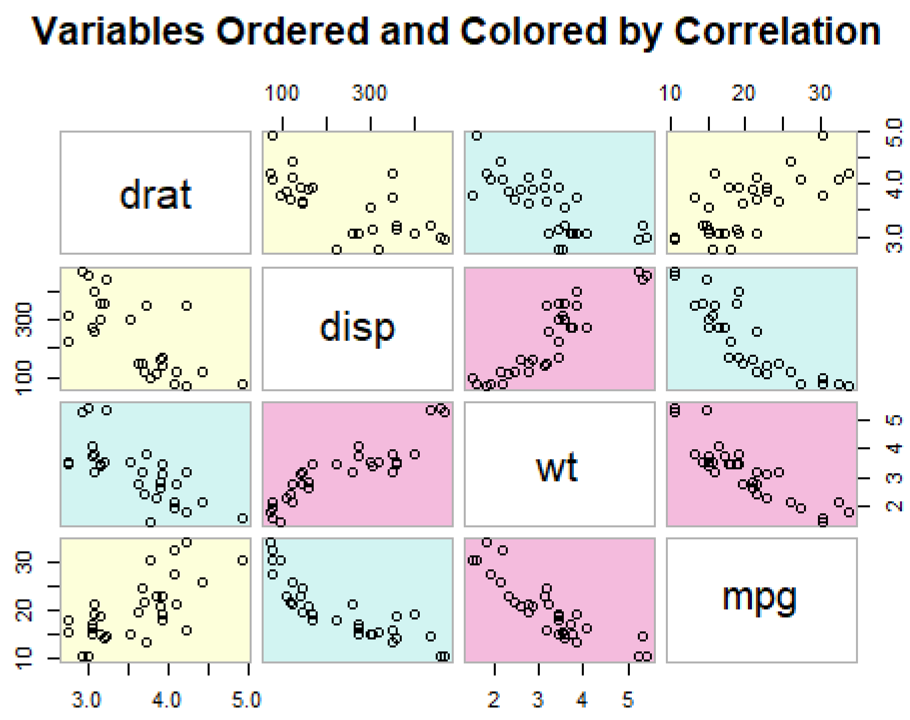
# are closest to the diagonal

dta.o <- order.single(dta.r)

dta.o

cpairs(dta, dta.o, panel.colors=dta.col, gap=.5,

    main="Variables Ordered and Colored by Correlation" )
```



Scatter Plot

High Density Scatterplots

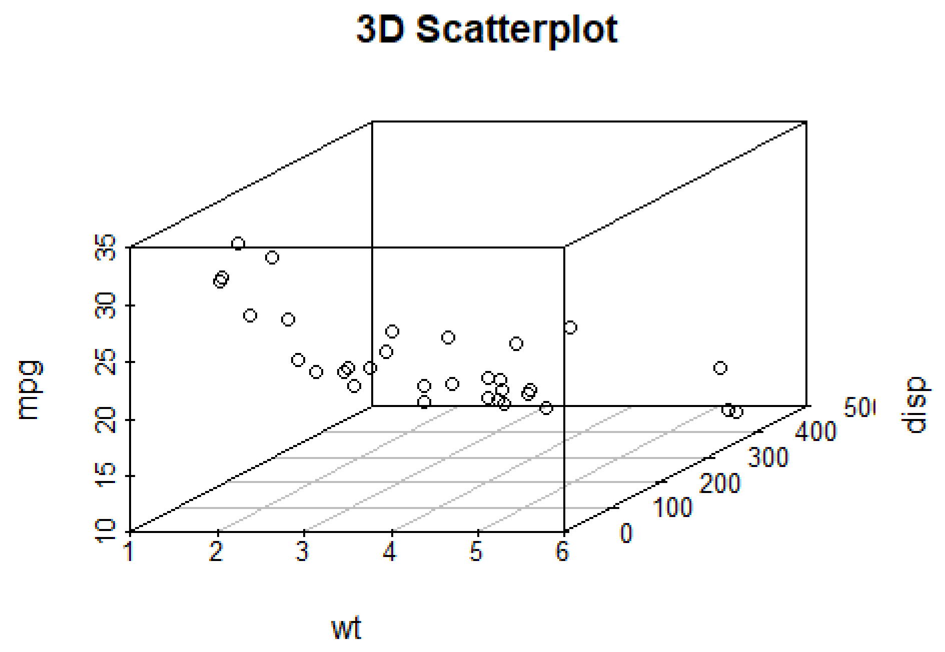
When there are many data points and significant overlap, scatterplots become less useful. There are several approaches that be used when this occurs. The **hexbin(x, y)** function in the hexbin package provides bivariate binning into hexagonal cells (it looks better than it sounds).

https://www.statmethods.net/graphs/scatterplot.html

3D Scatterplots

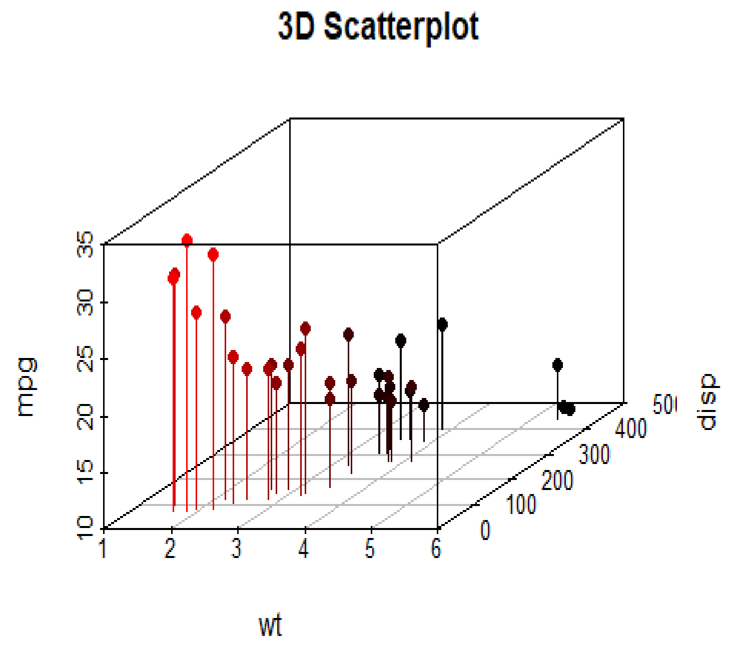
You can create a 3D scatterplot with the scatterplot3d package. Use the function **scatterplot3d(*x, y, z*)**.

```
library(scatterplot3d)
attach(mtcars)
scatterplot3d(wt,disp,mpg, main="3D Scatterplot")
```



- # 3D Scatterplot with Coloring and Vertical Drop Lines
```
library(scatterplot3d)
attach(mtcars)
scatterplot3d(wt,disp,mpg, pch=16, highlight.3d=TRUE,
  type="h", main="3D Scatterplot")
```
- highlight.3dpoints will be drawn in different colors related to y coordin ,
  else color will be used)

- # 3D Scatterplot with Coloring and Vertical Lines
```
# and Regression Plane
library(scatterplot3d)
attach(mtcars)
s3d <-scatterplot3d(wt,disp,mpg, pch=16, highlight.3d=TRUE,
  type="h", main="3D Scatterplot")
fit <- lm(mpg ~ wt+disp)
s3d$plane3d(fit)
```



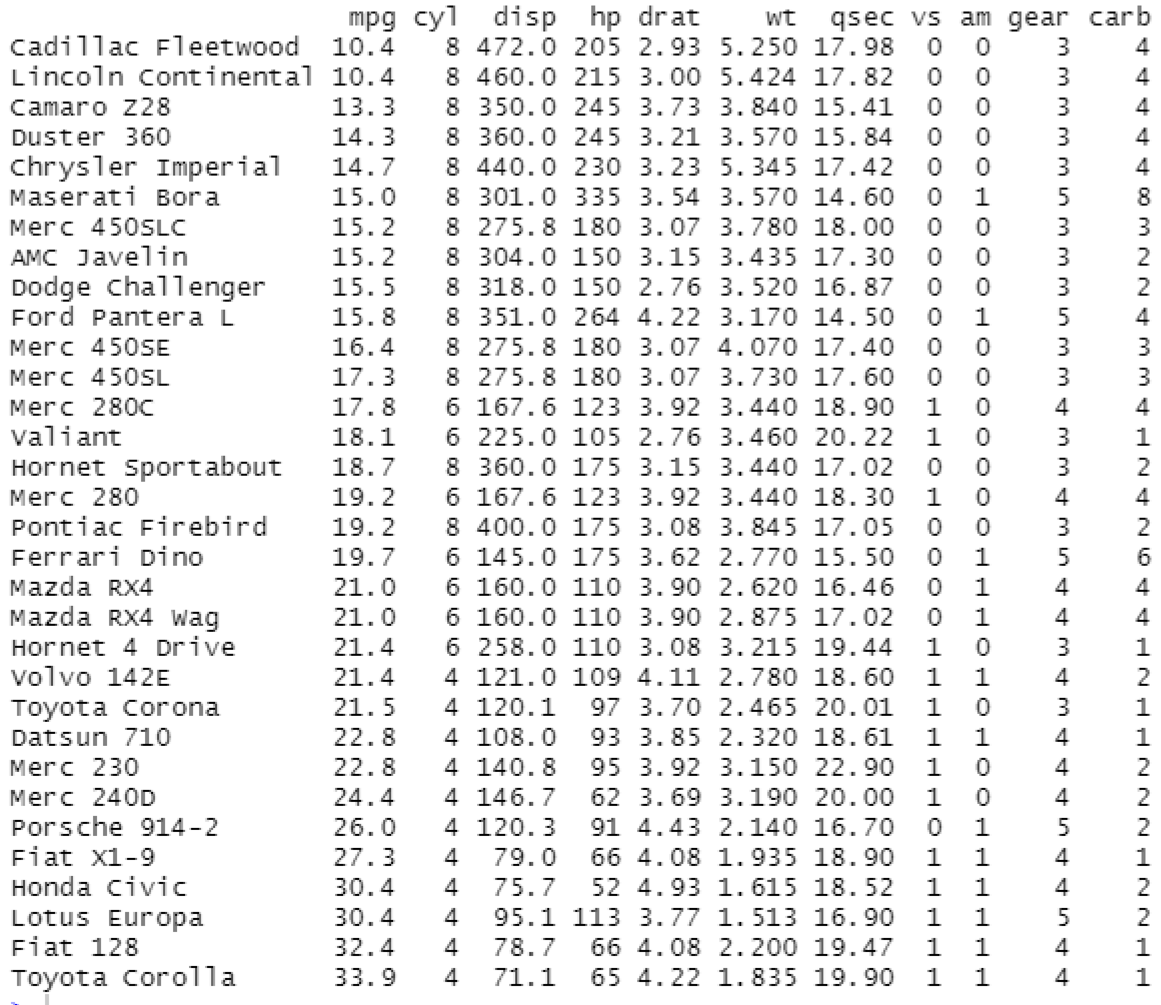
- Ggplot()
- The R code for generating Figure 3-7 is shown next. It requires the R package ggplot2 [11]. which can be installed simply by running the command install . p ackages ("ggp lot2"). The anscombe REVIEW OF BASIC DATA ANALYTIC METHODS USING R dataset for the plot is included in the standard R distribution. Enter data ( ) for a list of datasets included in the R base distribution. Enter data (Da tase tName) to make a dataset available in the current workspace. In the code that follows, variable levels is created using the gl (} function, which generates factors offour levels (1, 2, 3, and 4), each repeating 11 times. Variable myda ta is created using the with (data, expression) function, which evaluates an expression in an environment

Dot Chart

- Dot plot in R also known as **dot chart** is an **alternative to bar charts**, where the **bars are replaced by dots**.

- We'll use **mtcars** data sets.

mtcars



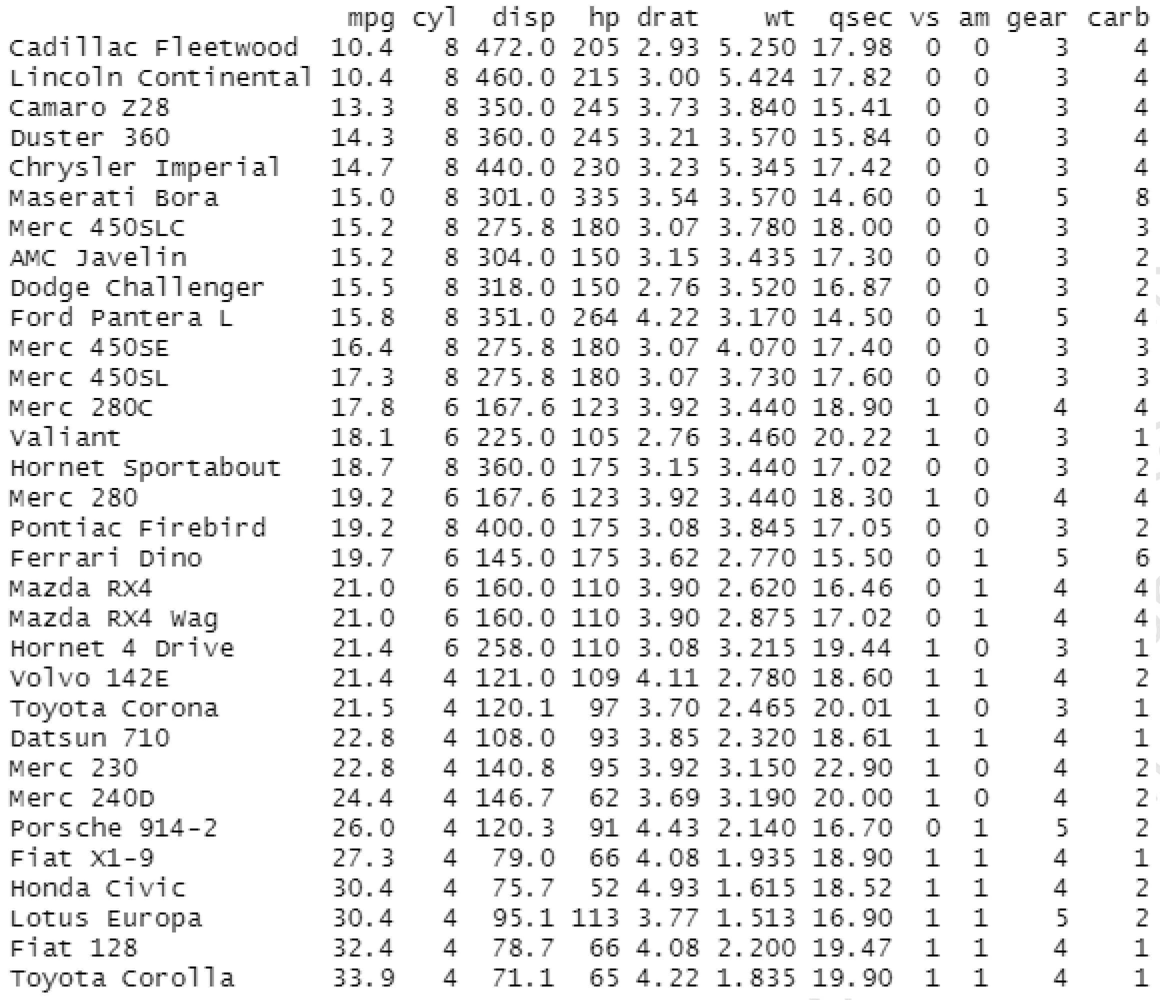
```
                     mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
Camaro Z28          13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4
Duster 360          14.3   8 360.0 245 3.21 3.570 15.84  0  0    3    4
Chrysler Imperial   14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4
Maserati Bora       15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
Merc 450SLC         15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3
AMC Javelin         15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2
Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4
Merc 450SE          16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3
Merc 450SL          17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3
Merc 280C           17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4
Valiant             18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
Hornet Sportabout   18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2
Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
Pontiac Firebird    19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2
Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
Mazda RX4           21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag       21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
Hornet 4 Drive      21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
Volvo 142E          21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
Toyota Corona       21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
Datsun 710          22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
Merc 230            22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
Merc 240D           24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
Porsche 914-2       26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2
Fiat X1-9           27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
Honda Civic         30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
```

mpg stands for miles per gallon, and is used to show how far your car is able to travel for every gallon (or 4.55 litres) of fuel it uses. As an example, if you own a car that can return 50mpg and its fuel tank only has one gallon of petrol or diesel in it, you should be able to drive 50 miles before the car runs out of fuel.

Dot Chart

- We start by ordering the data set according to mpg variable.

mtcars <- mtcars[order(mtcars$mpg),]

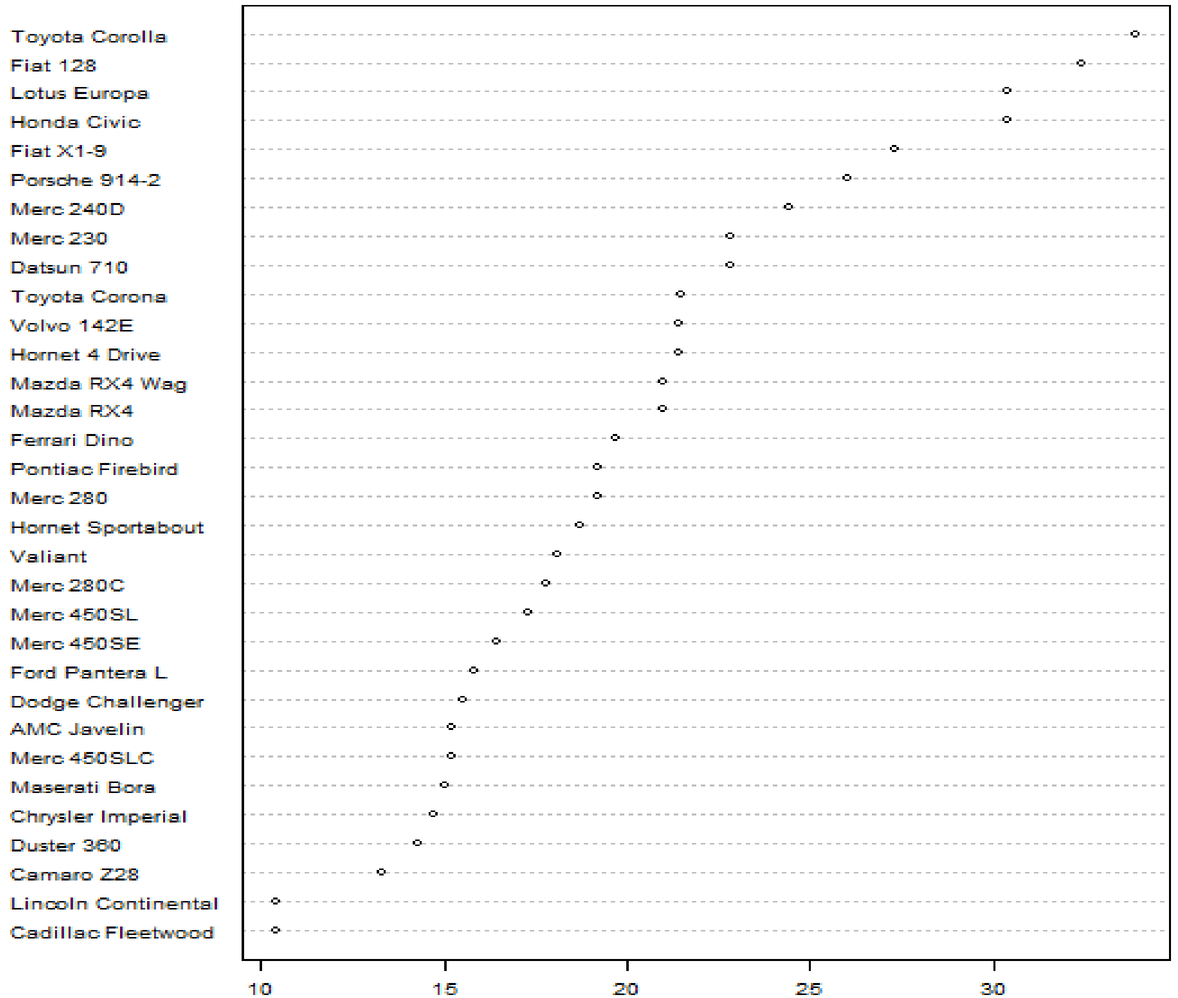


```
                     mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
Camaro Z28          13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4
Duster 360          14.3   8 360.0 245 3.21 3.570 15.84  0  0    3    4
Chrysler Imperial   14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4
Maserati Bora       15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
Merc 450SLC         15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3
AMC Javelin         15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2
Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4
Merc 450SE          16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3
Merc 450SL          17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3
Merc 280C           17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4
Valiant             18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
Hornet Sportabout   18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2
Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
Pontiac Firebird    19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2
Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
Mazda RX4           21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag       21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
Hornet 4 Drive      21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
Volvo 142E          21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
Toyota Corona       21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
Datsun 710          22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
Merc 230            22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
Merc 240D           24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
Porsche 914-2       26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2
Fiat X1-9           27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
Honda Civic         30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
```

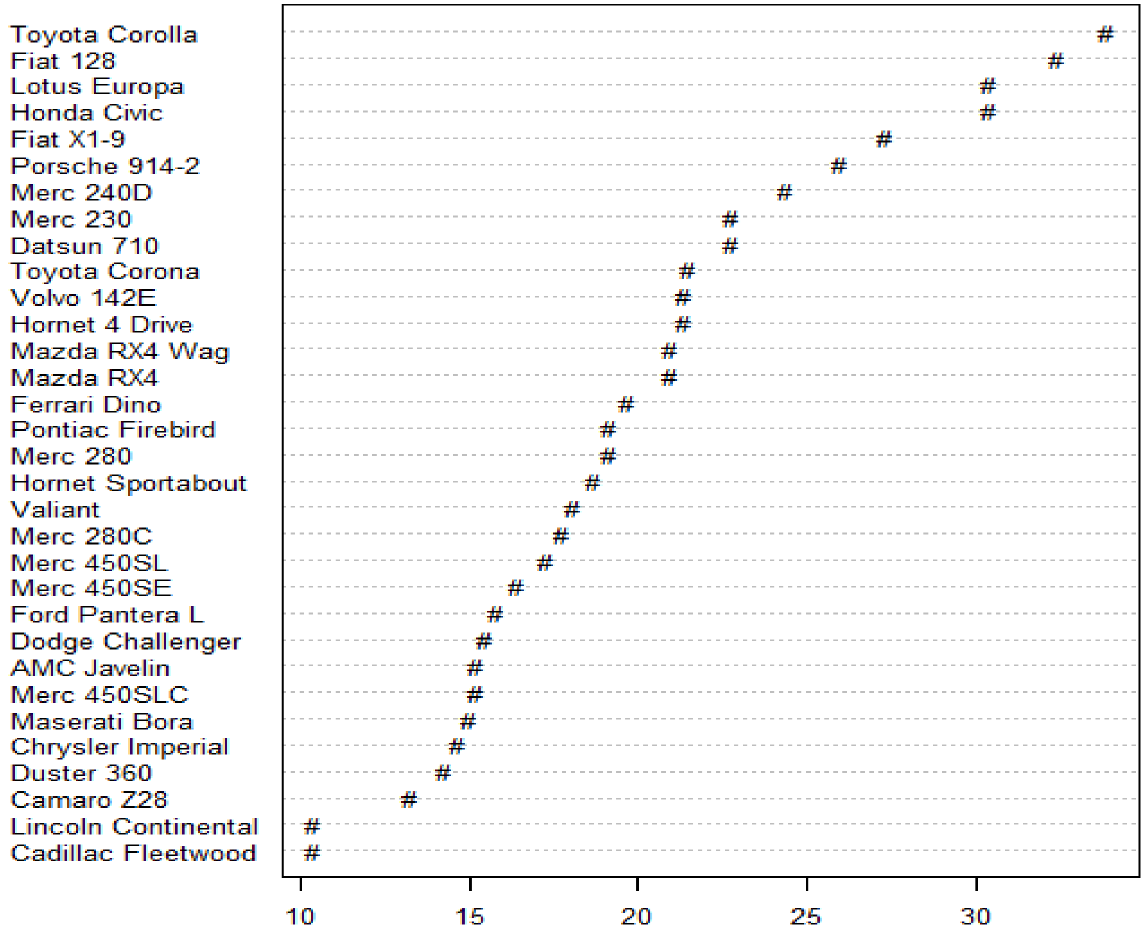
Dot Chart

- **dot plot can be draw using the R function dotchart().**

dotchart(mtcars$mpg, labels = row.names(mtcars),cex = 0.6, xlab = "mpg")



dotchart(mtcars$mpg, labels = row.names(mtcars),cex = 0.8, pch="#",xlab = "mpg")



gcolor the color(s) to be used for points and labels.

gcolor the color(s) to be used for points and labels.
the single color to be used for group labels and values.
gcolor the single color to be used for group labels and values.
the single color to be used for group labels and values.

Dot Chart

- **Plot and color by groups cyl**

grps <- as.factor(mtcars$cyl) // Create factor on Cylinder variable CY

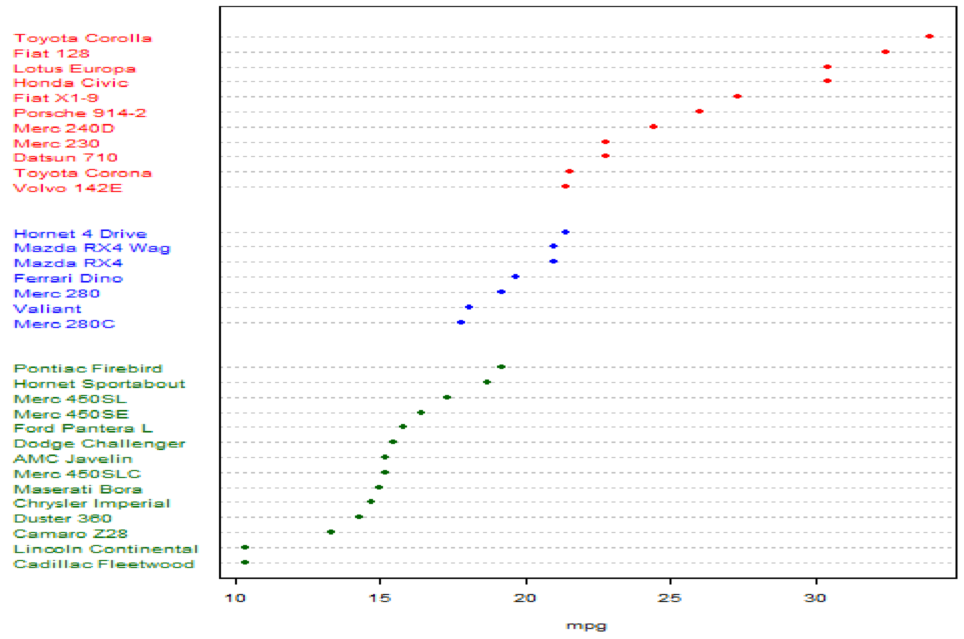
grps

OUTPUT

```
 8 8 8 8 8 8 8 8 8 8 8 8 6 6 8 6 8 6 6 6 6 4 4 4 4 4 4 4 4 4 4
Levels: 4 6 8
```

my_cols <- c("RED", "BLUE", "DARK GREEN")

dotchart(mtcars$mpg, labels = row.names(mtcars),groups = grps, gcolor =my_cols, color = my_cols[grps],cex = 0.6, pch = 19, xlab = "mpg")



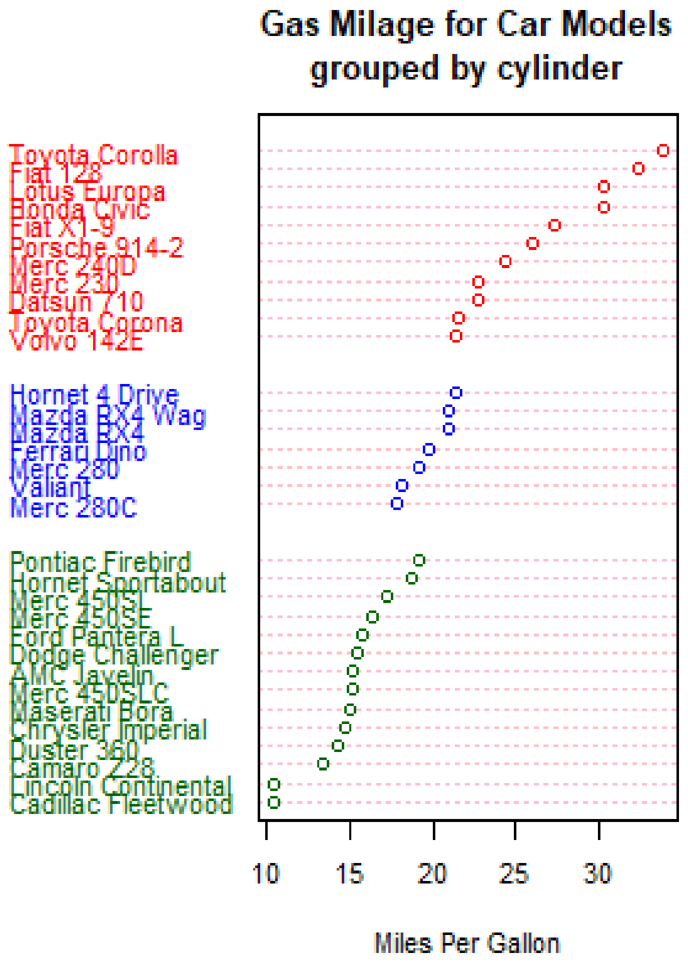
labels: a vector representing labels for each point.

groups: a grouping variable grps→ catogorical factor created based on cylinder.

gcolor: single color to be used for group labels and values.

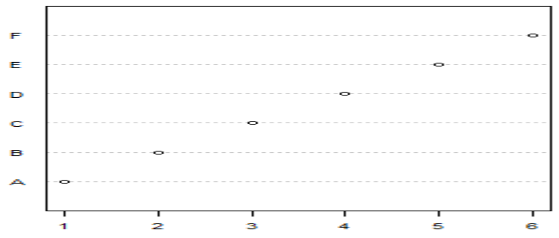
color: color(s) to be used for points and labels.

```
dotchart(mtcars$mpg,labels=row.names(mtcars),cex=.7,groups= mtcars$cyl, main="Gas Milage for Car
Models\ngrouped by cylinder", xlab="Miles Per Gallon", color=mtcars$color, lcolor = "PINK")
```

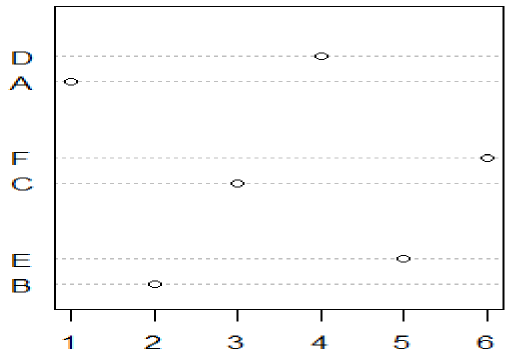


lcolor: color(s) to be used for the horizontal lines.

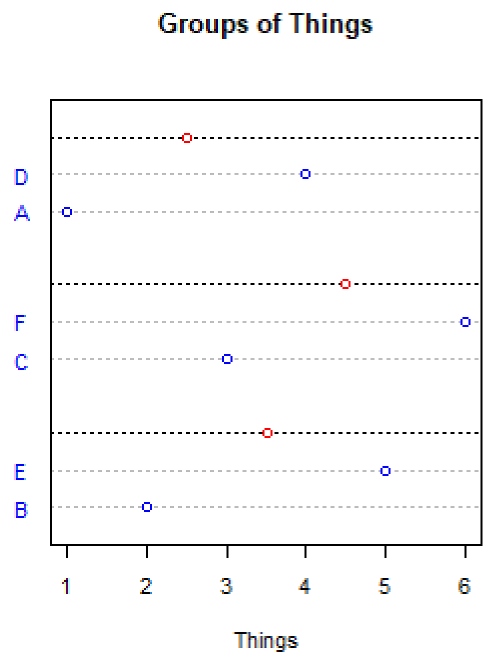
```
vectorToPlot <- c(1:6)
names(vectorToPlot) <- c(LETTERS[1:6])
dotchart(vectorToPlot, cex = .7)
```



```
myGroup <- factor(c("group1","group3","group2","group1","group3","group2"))
myGroup
group1 group3 group2 group1 group3 group2
Levels: group1 group2 group3
dotchart(vectorToPlot, groups = myGroup)
```



```
dotchart(vectorToPlot, gcolor = "red", groups = myGroup,
color="BLUE", gdata = c(median(vectorToPlot[myGroup ==
"group1"]), median(vectorToPlot[myGroup == "group2"]),
median(vectorToPlot[myGroup == "group3"])),cex = .7,
main = "Groups of Things", xlab = "Things")
```



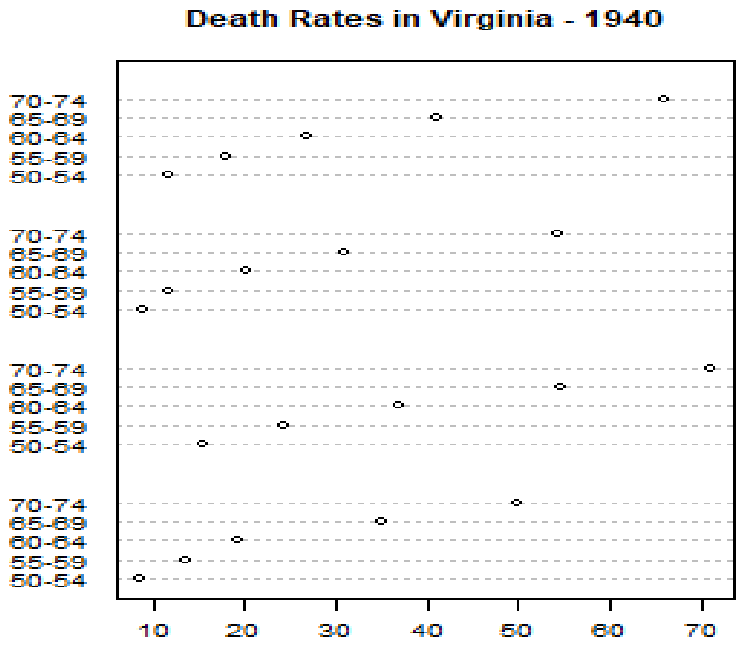
Dot Chart

Dot chart of a matrix

VADeaths

```
      Rural Male Rural Female Urban Male Urban Female
50-54       11.7          8.7       15.4          8.4
55-59       18.1         11.7       24.3         13.6
60-64       26.9         20.3       37.0         19.3
65-69       41.0         30.9       54.6         35.1
70-74       66.0         54.3       71.1         50.0
```

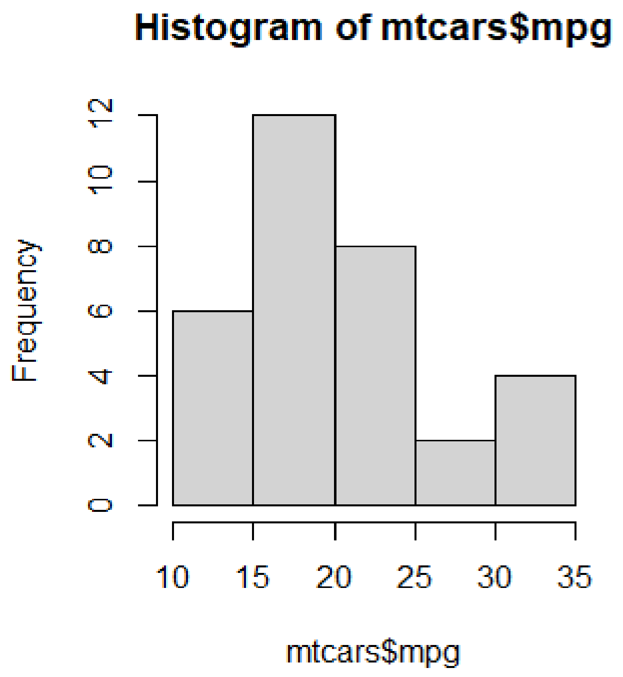
dotchart(VADeaths, cex = 0.6, main = "Death Rates in Virginia - 1940")

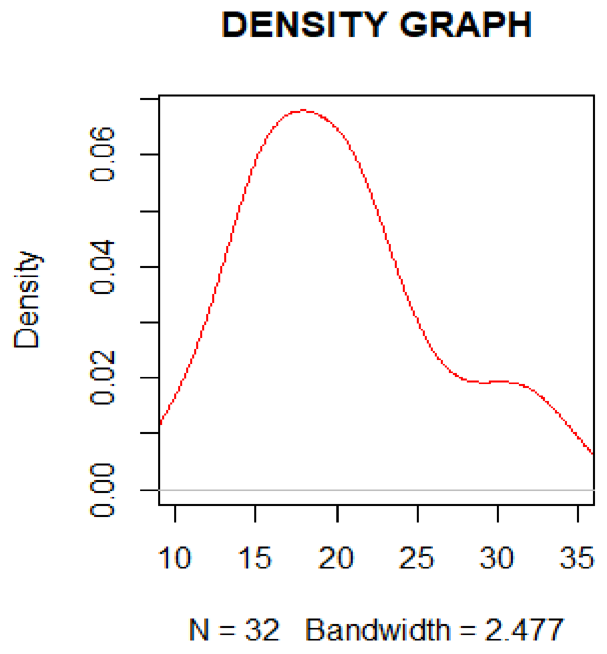


Density Plot

- A **density plot shows the distribution of a numeric variable**. It is similar to histogram. Histogram represents count where as density represents probability value equal to each count.
- Density is proportional to the chance that any value in our data is approximately equal to that value.
- In fact, for a histogram, the density is calculated from the counts, so the only difference between a histogram with frequencies and one with densities, is the scale of the y-axis. For the rest, they look exactly the same.
- we can estimate the density function of a variable using the density() function.

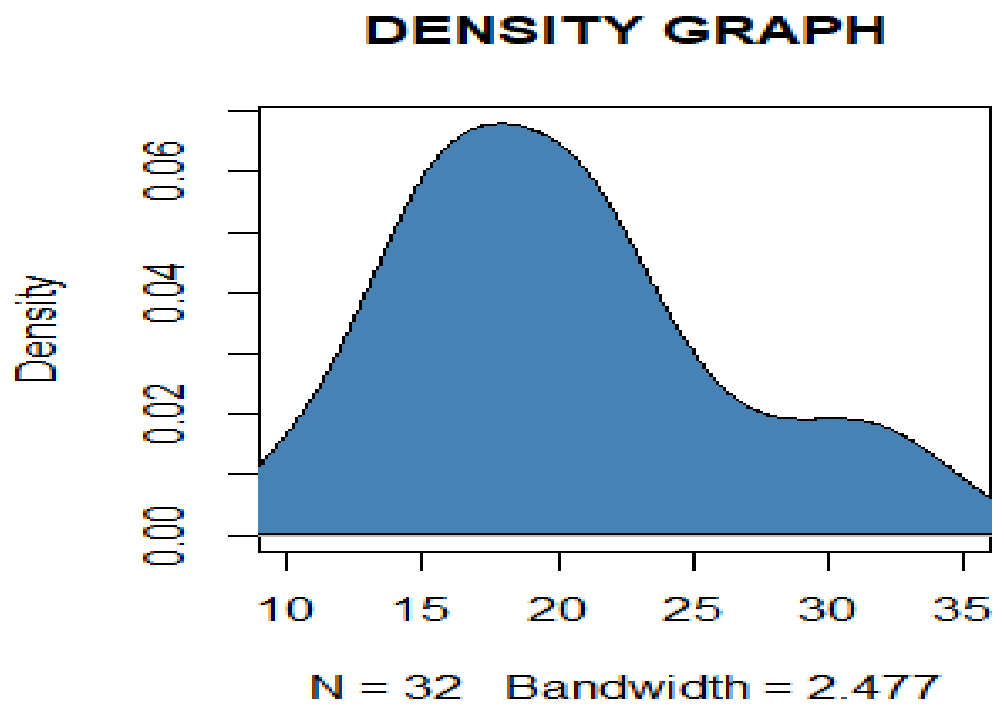
```
hist(mtcars$mpg)
d <- density(mtcars$mpg)
plot(d,col="RED",xlim=c(10,35),main="DENSITY GRAPH")
```





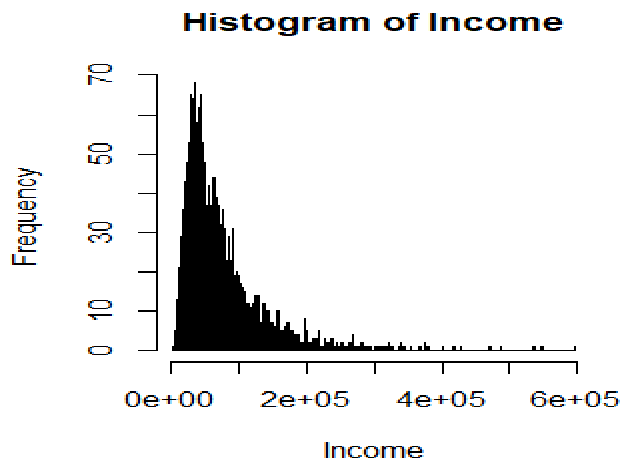
Observation: in both figures shows peak for the count range between 15 to 20 mpg value almost 12 in histogram, but in density graph y axis range is in the form of probability

```
polygon(d, col = "steelblue")
```



Density Plot

```
# randomly generate 4000 observations from the log normal distribution
income<- rlnorm(4000, meanlog = 4, sdlog = 0.7)   // generats logarithmic normal distribution whose logarithm has mean equal to meanlog and standard deviation equal to sdlog.
summary (income)
Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  3.891  33.637  54.353  70.164  89.187 596.477
income <- 1000*income
summary (income)
Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   3891   33637   54353   70164   89187  596477
# plot the histogram
hist(income, breaks=500, xlab="Income", main="Histogram of Income")
```



Density Plot

# density plot

plot(density(log10(income), adjust=0.5),main="Distribution of Income (log10 scale)")

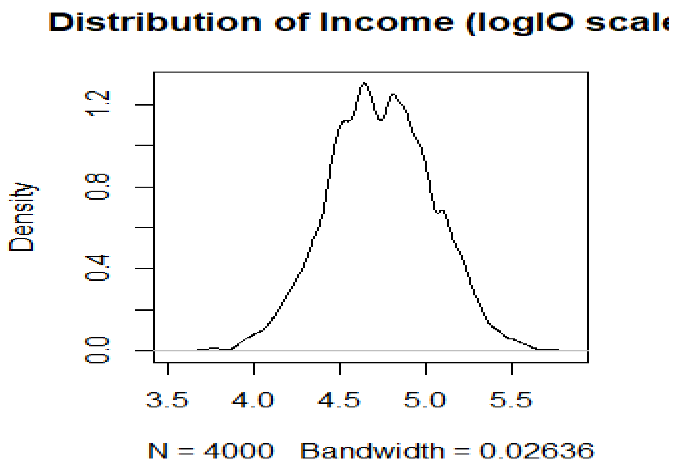
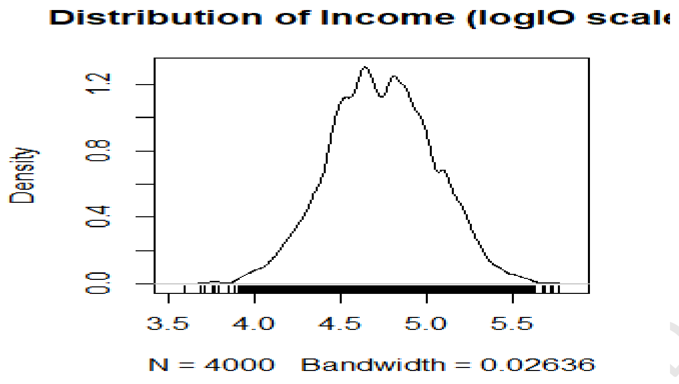


Figure shows a density plot of the logarithm of household income values, which emphasizes the distribution. The income distribution is concentrated in the center portion of the graph.
The rug (} function creates a one-dimensional density plot on the bottom of the graph to emphasize the distribution of the observation.

# add rug to the density plot

rug(log10(income))

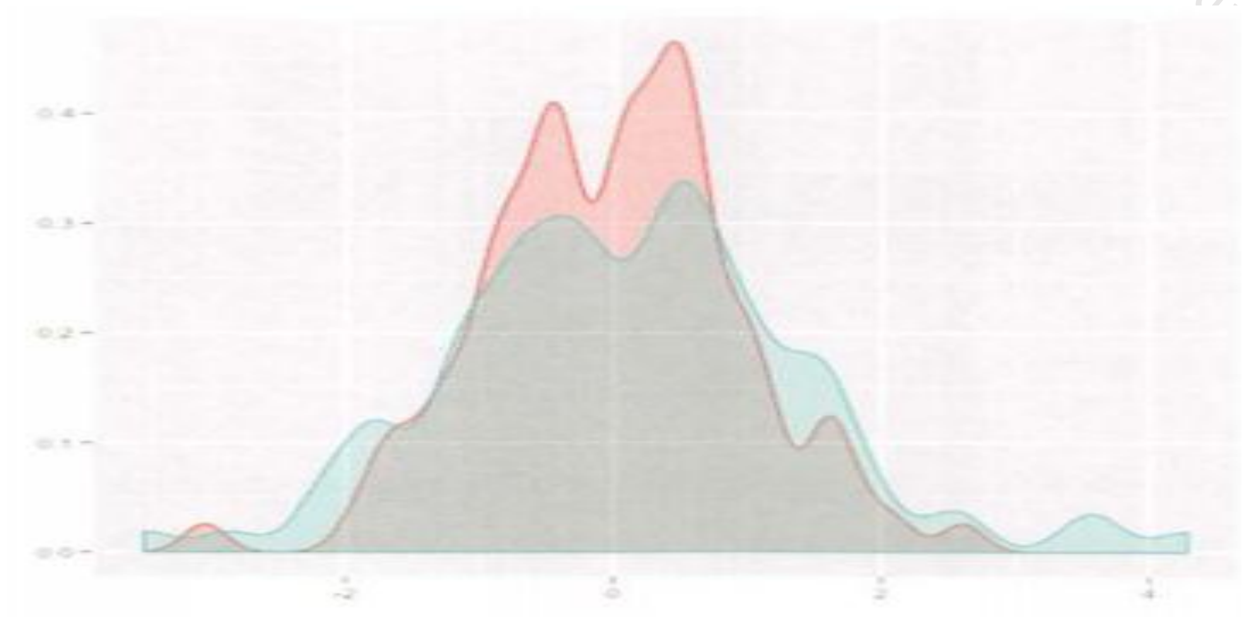


dotchart(x, labels = NULL, groups = NULL, gcolor = par("fg"), color = par("fg"))

- **x**: numeric vector or matrix
- **labels**: a vector of labels for each point.
- **groups**: a grouping variable indicating how the elements of x are grouped.
- **gcolor**: color to be used for group labels and values.
- **color**: the color(s) to be used for points and labels.

Statistical Methods for Evaluation

- **Hypothesis Testing** is a technique to assess the relationship between two samples of data.(Theoretical testing)


Distributions of two samples of data

- The basic concept of **hypothesis testing is to form an assertion** (statement) and **test it with data**. (Sample data)

For Eg: Drinking sugary drinks daily leads to obesity.

- **Statistical analysts test a hypothesis by measuring** and **examining a random sample of the population** being analyzed.

- When performing hypothesis tests, the **common assumption is that there is no difference between two samples**.

  Statisticians refer to this type of hypothesis as the **null hypothesis.** This is referred as $\mathbf{H_0}$.

Hypothesis Testing

Null Hypothesis

- A Null hypothesis H_0 exists when a **researcher believes there is no relationship between the two variables**, or **there is a lack of information** to state a scientific hypothesis. This is something to attempt to disprove or discredit.

Alternative Hypothesis

- The Alternative hypothesis H_A is that there is a difference between two samples.
- **Example-1**

  If the task is to identify the effect of drug A compared to drug B on patients, the Null hypothesis and Alternative hypothesis would be this:

  H_0 : Drug A and Drug B have the same effect on patients.

  H_A : Drug A has a greater effect than Drug B on patients.

Hypothesis Testing

- **Example-2,**

  If the task is to identify whether advertising Campaign C is effective on reducing customer churn, the Null hypothesis and Alternative hypothesis would be as follows:

  H_0 : Campaign C does not reduce customer churn better than the current campaign method.

  H_A : Campaign C does reduce customer churn better than the current campaign.

- It is **important to state the Null hypothesis and Alternative hypothesis**, because misstating them is likely to **undermine the subsequent steps** of the hypothesis testing process. (it is important to make null hypothesis and alternative hypothesis, otherwise it will be difficult to prove during model building and testing phase to prove that your built model is better than existing model).

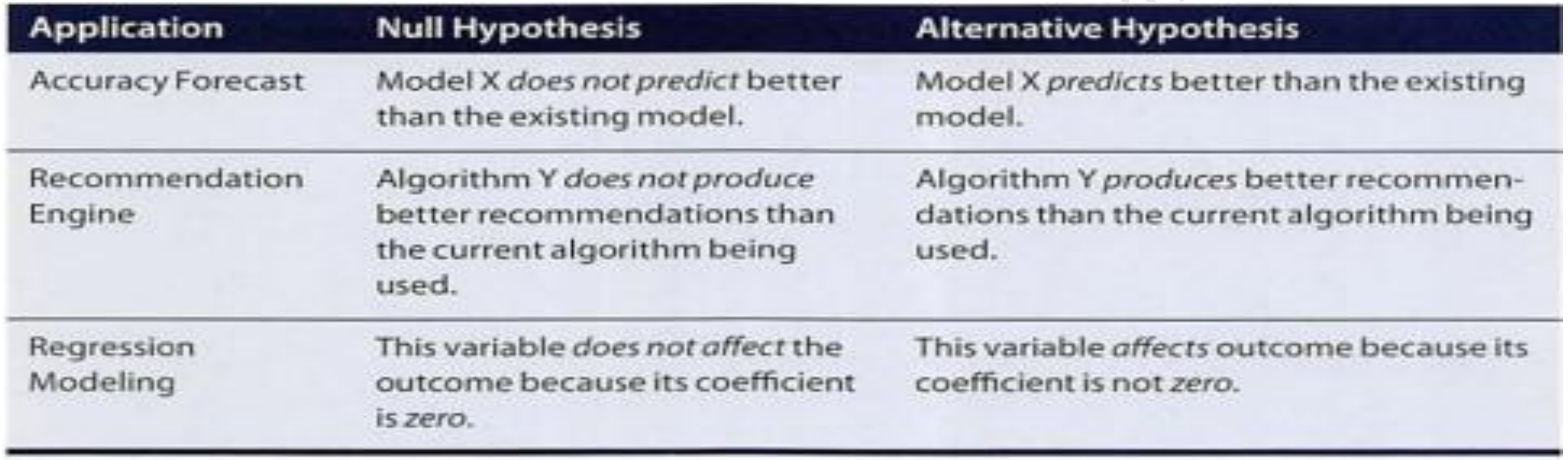
- A **hypothesis test leads to either rejecting the Null hypothesis in favor of the Alternative** or **not rejecting the Null hypothesis.**

- The **purpose** of a **hypothesis** testing is to find the answer to a question.

- Basically, we're looking at reject the **Null hypothesis** with the **Alternate hypothesis**.

Hypothesis Testing

- Below Table includes some examples of **Null** and **Alternative hypotheses** that should be answered during the analytic lifecycle.



Application	Null Hypothesis	Alternative Hypothesis
Accuracy Forecast	Model X *does not predict* better than the existing model.	Model X *predicts* better than the existing model.
Recommendation Engine	Algorithm Y *does not produce* better recommendations than the current algorithm being used.	Algorithm Y *produces* better recommendations than the current algorithm being used.
Regression Modeling	This variable *does not affect* the outcome because its coefficient is *zero*.	This variable *affects* outcome because its coefficient is not *zero*.

- Once a **model is built over the training data**, it **needs to be evaluated over the testing data to see if the proposed model predicts better than the existing model** currently being used.
- The **Null hypothesis is that the proposed model does not predict better than the existing model.** The **Alternative hypothesis is that the proposed model indeed predicts better than the existing model**.
- In **accuracy forecast**, the **Null model could be that the sales of the next month are the same as the prior month**. The hypothesis test needs to evaluate if the proposed model provides a better prediction.

Hypothesis Testing

- Take a **recommendation engine** as an example. The Null hypothesis could be that the **new algorithm does not produce better recommendations than the current algorithm** being deployed. The **alternative hypothesis is that the new algorithm produces better recommendations than the old algorithm**.

- When evaluating a model, sometimes it needs to be determined if a given **input variable improves the model**.

- In regression analysis, for example, if the regression coefficient for a variable is zero. The **Null hypothesis is that the coefficient is zero**, which **means the variable does not have an impact on the outcome**. The **alternative hypothesis is that the coefficient is nonzero**, which means the **variable does have an impact on the outcome**.

Hypothesis Testing

Difference of Means

- A common **hypothesis test is to compare the means of two populations.**

- **Hypothesis testing is a common approach to draw inferences on whether or not the two populations**, denoted **pop1** and **pop2**, **are different from each other**.

- There are **two hypothesis tests to compare the means of the respective populations** based on samples randomly drawn from each population.

- Specifically, the **two hypothesis tests consider the following Null and Alternative hypotheses**.

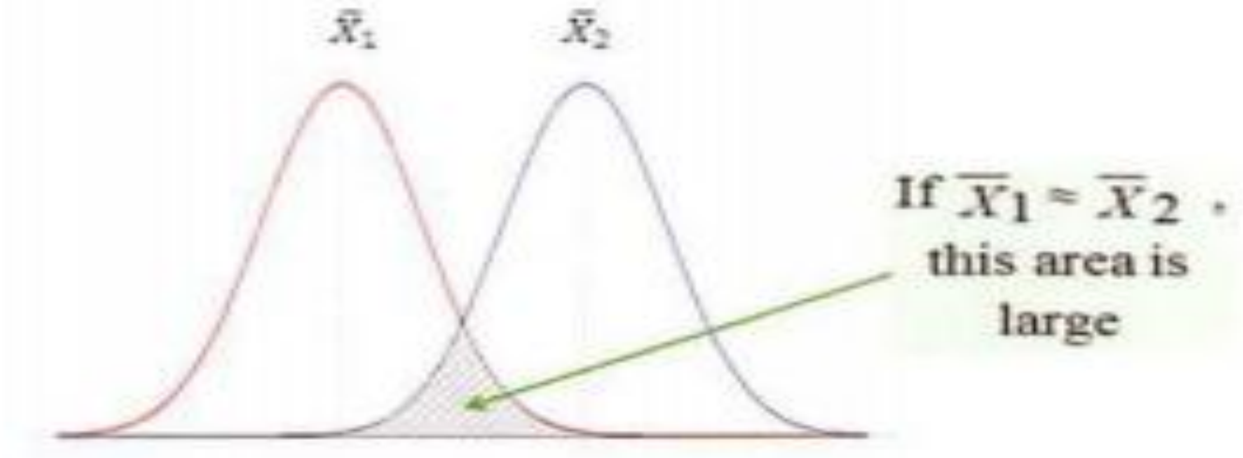
  $\mu_1 = \mu_2$

  $\mu_1 != \mu_2$

- The μ_1 and μ_2 denote the **population means of pop1 and pop2, respectively**.

Hypothesis Testing

- The basic **testing approach is to compare the observed sample means, X_1 and X_2 corresponding to each population**.
- **If the values of X_1 and X_2 are approximately equal to each other**, the **distributions of X_1 and X_2 overlap substantially** as shown in below figure **and the Null hypothesis is supported**.
- A **large observed difference between the sample means indicates that the Null hypothesis should be rejected**.
- Formally, the **difference in means can be tested using Student's t-test** or the **Welch's t-test**.



Overlap of the two distributions is large if $\bar{X}_1 \approx \bar{X}_2$

Student's t-test

- Student's t-test assumes that **distributions of the two populations have equal but unknown variances**.
- Suppose **n1** and **n2 samples are randomly and independently selected from two populations** pop1 and pop2, respectively.
- If each population is normally distributed with the same mean (**$\mu_1 = \mu_2$**) and with the same variance, then T (the t-statistic), given in below equation, follows a t-distribution with (n1 + n2 – 2) degrees of freedom (df).

$$T = \frac{\bar{X}_1 - \bar{X}_2}{S_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

where

$$S_p^2 = \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{n_1 + n_2 - 2}$$

Student's t-test

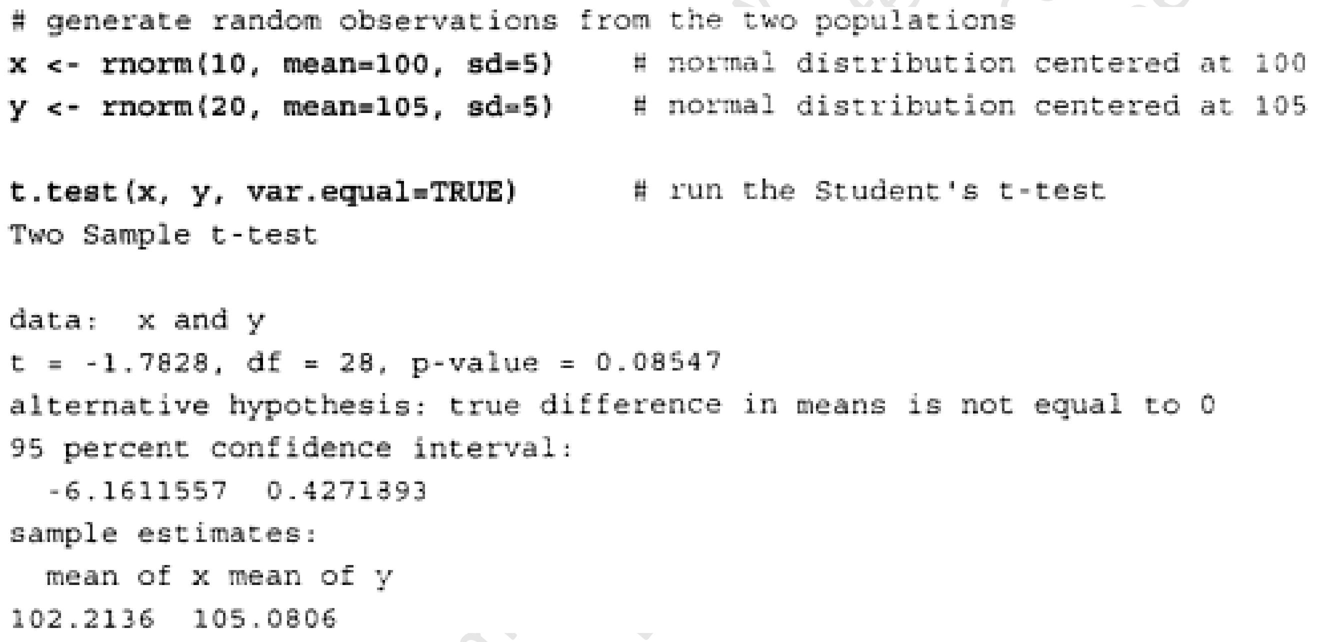
- Where **N** is the number of values in the data set (sample size). Take a look at the sample computation.
- If there is a data set of 4, (N=4).
- Call the data set X and create a list with the values for each data.
- For this example data set X includes: 15, 30, 25, 10
- This data set has a **mean**, or average of 20. Calculate the mean by adding the values and dividing by N:
- (15+30+25+10)/4= 20
- Using the formula, the degrees of freedom would be calculated as df = N-1:
- In this example, it looks like, df = 4-1 = 3
- This indicates that, in this data set, three numbers have the freedom to vary as long as the mean remains 20.
- https://www.statisticshowto.com/probability-and-statistics/hypothesis-testing/degrees-of-freedom/

Student's t-test

- The shape of the t-distribution is similar to the normal distribution.
- if the observed value of T is far enough from zero such that the probability of observing such a value of T is unlikely, one would reject the null hypothesis that the population means are equal.
- Thus, for a small probability, say $\alpha = 0.05$, T* is determined.
- After the samples are collected and the observed value of T is calculated according to equation, the null hypothesis (**$\mu_1 = \mu_2$**) is rejected if T> T*.
- In hypothesis testing, in general, the small probability ‘n’ is known as the **significance level** of the test.
- for n = 0.05, if the means from the two populations are truly equal, then in repeated random sampling, the observed magnitude of T would only exceed T* 5% of the time.

Student's t-test

- In the following R code example, 10 and 20 observations are randomly selected from two normally distributed populations and assigned to the variables x and y. The two populations have a mean of 100 and 105, respectively, and a standard deviation equal to 5. Student's t-test is then conducted to determine if the obtained random samples support the rejection of the null hypothesis.



```
# generate random observations from the two populations
x <- rnorm(10, mean=100, sd=5)    # normal distribution centered at 100
y <- rnorm(20, mean=105, sd=5)    # normal distribution centered at 105

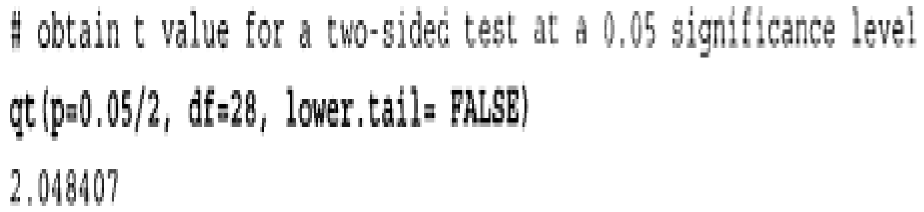
t.test(x, y, var.equal=TRUE)      # run the Student's t-test
Two Sample t-test

data:  x and y
t = -1.7828, df = 28, p-value = 0.08547
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
  -6.1611557  0.4271393
sample estimates:
  mean of x mean of y
102.2136  105.0806
```

- From the R output, the observed value of T is t = -1.7828. The negative sign is due to the fact that the sample mean of x is less than the sample mean of y.

Student's t-test

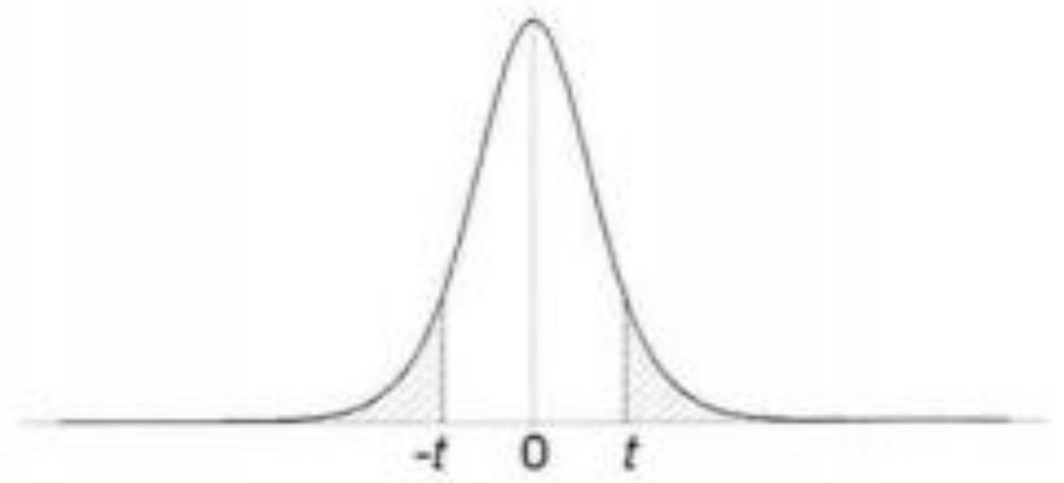
- Using the qt () function in R corresponds to a 0.05 significance level, a T value of 2.0484 (qt gives the quantile function, is used, for example, when constructing confidence intervals, to find the endpoints of an interval)



```
# obtain t value for a two-sided test at a 0.05 significance level
qt(p=0.05/2, df=28, lower.tail= FALSE)
2.048407
```

- Because the magnitude of the observed T statistic is less than the T value corresponding to the 0.05 significance level T|1.78281|< 2.0484), the null hypothesis is not rejected.
- However, based on the p -value, if the significance level was chosen to be 0.10, instead of 0.05, the null hypothesis would be rejected. T value of magnitude 1.7828 or greater would occur at higher probability than 0.05.
- Because the alternative hypothesis is that the means are not equal (**μ_1 != μ_2**) , the possibilities of both **μ_1** > **μ_2** and **μ_1** < **μ_2** need to be considered.
- This form of Student's t-test is known as a two-sided hypothesis test.

- Figure illustrates the t-statistic for the area under the tail of a t-distribution. The –t and t are the observed values of the t-statistic.
- In the R output, t = 1.7828. The left shaded area corresponds to the P(T ~ - 1.7828), and the right shaded area corresponds to the P(T ~ 1.7828).



Area under the tails (shaded) of a student's t-distribution

- **Formula for Degrees of Freedom**
- The statistical formula to determine degrees of freedom is quite simple. It states that degrees of freedom equal the number of values in a data set minus 1, and looks like this:
- df = N-1
- Where **N** is the number of values in the data set (sample size). Take a look at the sample computation.
- If there is a data set of 4, (N=4).
- Call the data set X and create a list with the values for each data.
- For this example data, set X includes: 15, 30, 25, 10
- This data set has a **mean**, or average of 20. Calculate the mean by adding the values and dividing by N:
- (15+30+25+10)/4= 20
- Using the formula, the degrees of freedom would be calculated as df = N-1:
- In this example, it looks like, df = 4-1 = 3
- This indicates that, in this data set, three numbers have the freedom to vary as long as the mean remains 20.

- t-Distribution
- Definition: The t-Distribution, also known as Student's t-Distribution is the probability distribution that estimates the population parameters when the sample size is small and the population standard deviation is unknown.
-
- It resembles the normal distribution and as the sample size increases the t-distribution looks more normally distributed with the values of means and standard deviation of 0 and 1 respectively.
- The *t*-distribution describes the standardized distances of sample means to the population mean when the population standard deviation is not known, and the observations come from a normally distributed population.

- The idea is that the **null hypothesis** generally assumes that there is nothing new or surprising in the population
- https://www.sagepub.com/sites/default/files/upm-binaries/40007_Chapter8.pdf

P Values

- It’s good science to let people know if your study results are solid, or if they could have happened by chance. The usual way of doing this is to test your results with a p-value. A p value is a number that you get by running a hypothesis test on your data. A P value of 0.05 (5%) or less is usually enough to claim that your results are repeatable.

UNIT-3

Advanced Analytical Theory and Methods: Clustering

- Clustering is the use of **unsupervised techniques** for **grouping similar objects**. (Unsupervised→ Like not based on some specific constraint, not straight forward technique→ like group based on age or group based on salary→ based on few parameters analysing similarities among the objects and grouping the objects into clusters)
- In machine learning, **unsupervised refers** to the problem of **finding hidden structure within unlabelled data** (unlabelled data→ data that cannot be categorized).
- Clustering techniques are unsupervised in the sense that the data scientist does not determine, in advance, the labels to apply to the clusters.
- The **structure of the data describes the objects of interest** and **determines how best to group the objects**.
- For example, based on **customers' personal income**, it is **straightforward to divide the customers into three groups**:
  - **Earn less than $10,000**
  - **Earn between $ 10,000 and $99,999**
  - **Earn $100,000 or more**

Clustering

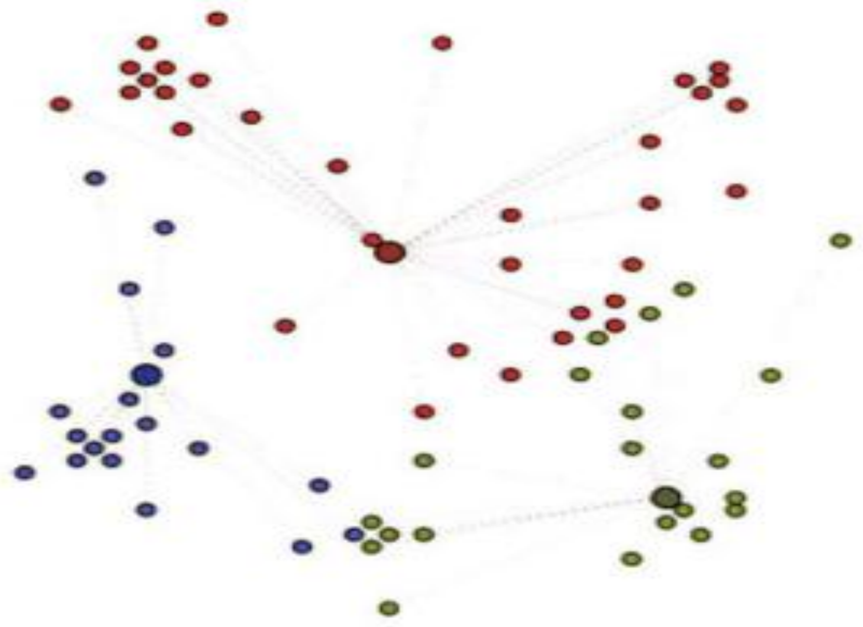
- In this case, the **income levels were chosen somewhat subjectively** based on easy-to-communicate points of **delineation**.
- There is **no inherent reason to believe that the customer making $90,000 will behave any differently than the customer making $ 110,000**. (In this clustering, there is no inherent reason for clustering that tells behaviour of the customers based on income)
- As **additional dimensions are introduced by adding more variables about the customers**, the task of **finding meaningful groupings becomes more complex**.
- For instance, suppose **variables such as age, years of education, household size**, and **annual purchase expenditures** were considered along with the personal income variable.(What cluster using based on income is not a meaningful cluster)
- Rather, **Clustering methods find the similarities between objects according to the object attributes** and **group the similar objects into clusters**.
- A popular **clustering method is k-means**.

K-means

- Given a **collection of objects each with ‘n’ measurable attributes, k-means is an analytical technique** that, for a chosen value of k, **identifies k clusters of objects based on the objects' proximity to the center of the k groups**.

- The **center is determined as the mean of each cluster's n-dimensional vector of attributes**.

- Figure illustrates **three clusters of objects with two attributes**. Each object in the dataset is represented by a **small dot color-coded to the closest large dot**, the mean of the cluster.



Possible k-means clusters for k=3

K-means-Overview of the Method

- To illustrate the method to find **‘k’ clusters from a collection of ‘M’ objects with ‘n’ attributes**, the two dimensional case (n = 2) is examined. It is much easier to visualize the k-means method in two dimensions.

- Because **each object in this example has two attributes**, it is useful to consider each object corresponding to the **point (x,y), where x and y denote the two attributes** and i = 1, 2 ... M.

- For a given cluster of **m points** (m<=M), the **point that corresponds to the cluster's mean is called a Centroid**.

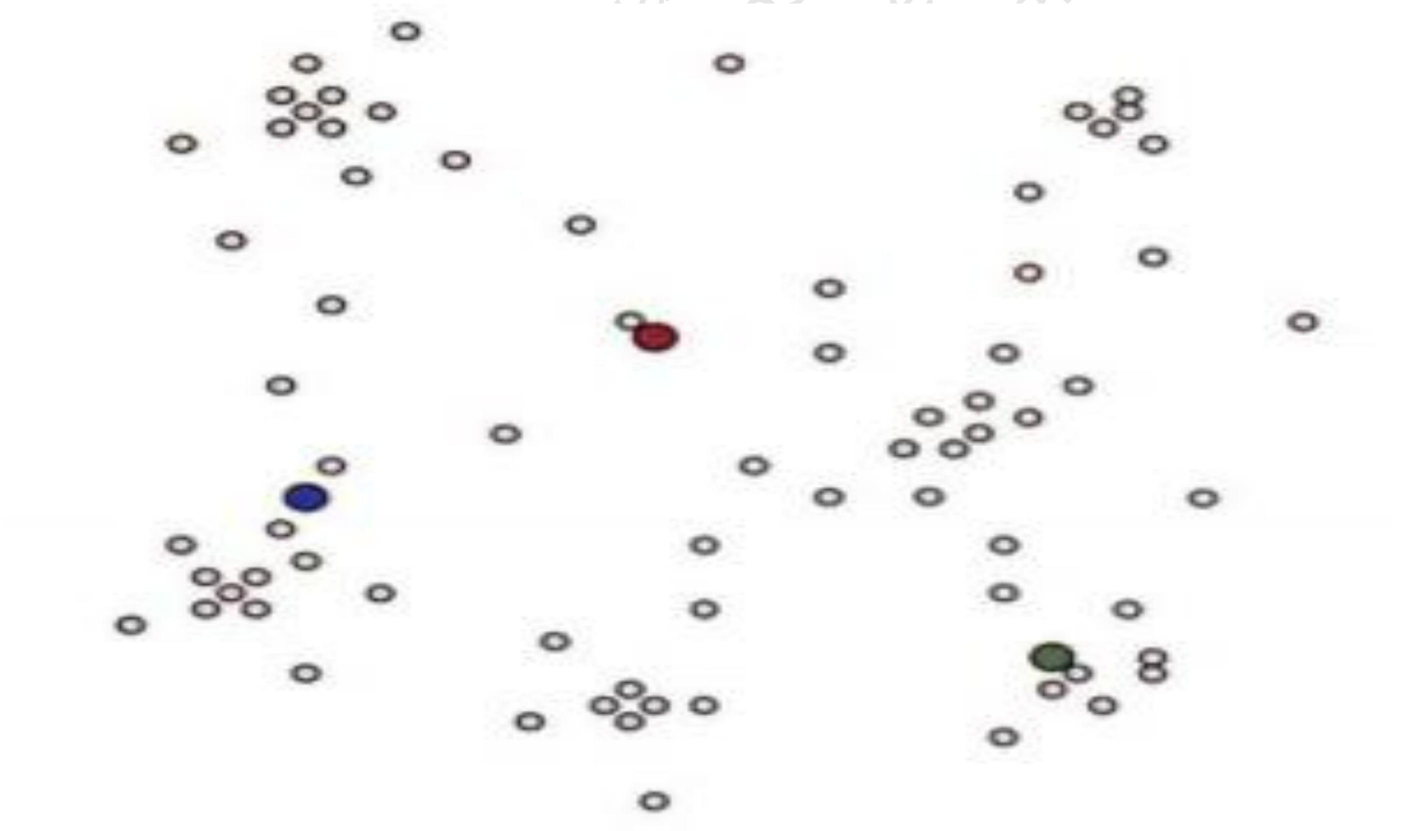
- In mathematics, a centroid refers to a point that corresponds to the **center of mass for an object**.

- The **k-means algorithm** to find k clusters can be described in the following **four steps**.

K-means-Overview of the Method (Cont…)

1) **Choose the value of k and the k initial guesses for the centroids**.

- In this example, **k = 3**, and the **initial centroids are indicated by the points shaded in red, green, and blue** as shown in Figure.



Initial starting points for the centroids

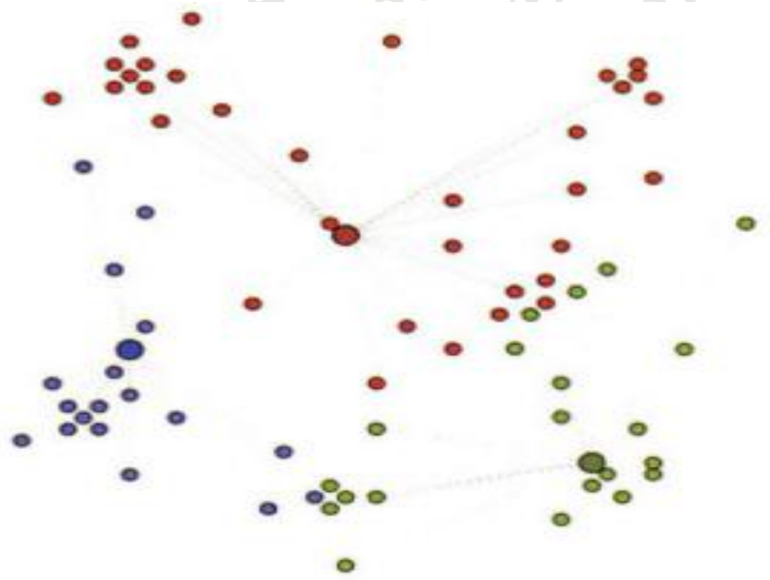
K-means-Overview of the Method (Cont.…)

2) **Compute the distance from each data point (x, y) to each centroid**. Assign **each point to the closest centroid**. **This association defines the first k clusters**.

- In two dimensions, **the distance ‘d’ between any two points (x1 , y1) and (x2 , y2) in the Cartesian plane is typically expressed by using the Euclidean distance measure** using the Equation

$$d = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2}$$

- In the below figure, **the points closest to a centroid are shaded with the corresponding color**.


Points are assigned to the closest centroid

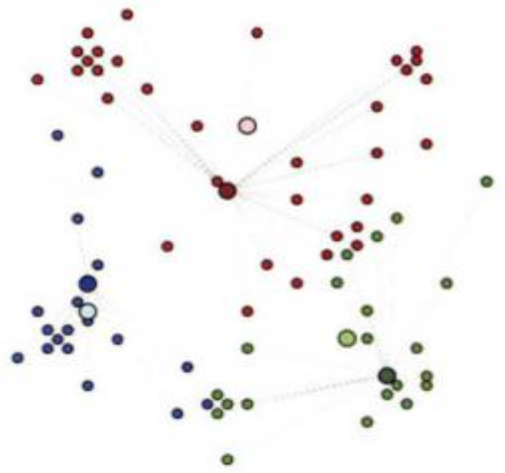
K-means-Overview of the Method (Cont…)

3) Compute the centroid (the center of mass) **of each newly defined cluster from Step 2**.

- In two dimensions, the **centroid ($X_{C,}$ Y_C) of them m points in a k-means cluster is calculated using the Equation**

$$(x_c, y_c) = \left(\frac{\sum_{i=1}^{m} x_i}{m}, \frac{\sum_{i=1}^{m} y_i}{m} \right)$$

- In the below figure, the **computed centroids in Step 3 are the lightly shaded points of the corresponding color**.



Compute the mean of each cluster

- Thus, **($X_{C,}$ Y_C) is the ordered pair of the arithmetic means of the coordinates of m points** in the cluster.

- **In this step, a centroid is computed for each of the k clusters**.

K-means-Overview of the Method (Cont…)

4) **Repeat Steps 2 and 3** until the algorithm converges to an answer (Assumed: 10,15,20→Assign→11,16,20→Assign→10.8,15.8,20.8→Assign)

   a) **Assign each point to the closest centroid** computed in Step 3.

   b) **Compute the centroid of newly defined clusters**.

   c) **Repeat until the algorithm** reaches the final answer.

- **Convergence is reached when the computed centroids do not change** or **the centroids and the assigned points oscillate back and forth from one iteration to the next**.

- **K-means Overview**
  Before diving into the dataset, let us briefly discuss how k-means works:
- The process begins with k centroids initialised at random.
- These centroids are used to assign points to its nearest cluster.
- The mean of all points within the cluster is then used to update the position of the centroids.
- The above steps are repeated until the values of the centroids stabilise.

Determining the Number of Clusters

- The optimal number of clusters can be defined as follow:

1) **Compute clustering algorithm** (e.g., k-means clustering) **for different values of k**.

2) **For each k**, calculate the **total within-cluster sum of square** (**WSS**).

3) **Plot the curve** of **WSS according to the number of clusters k**.

Determining the Number of Clusters

- **Total Within-Cluster-Sum of Squares** sounds a bit complex. Let's break it down:

1) **Square the Euclidean distances between each point** and the **corresponding centroid to which it is assigned**.

2) The **WSS score is the sum of these squares for all the points within the cluster**.

3) **Total within-cluster is the sum of WSS score of all the clusters**

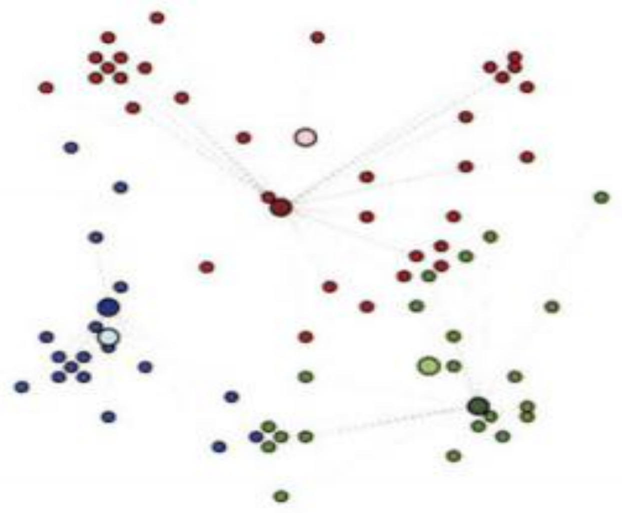
4) **Any distance metric like the Euclidean Distance** or the **Manhattan Distance** can be used.

$$W(C_k) = \sum_{x_i \in C_k} (x_i - \mu_k)^2$$

where:

- x_i is a data point belonging to the cluster C_k
- μ_k is the mean value of the points assigned to the cluster C_k

$$tot.\,withiness = \sum_{k=1}^{k} W(C_k) = \sum_{k=1}^{k} \sum_{x_i \in C_k} (x_i - \mu_k)^2$$


Compute the mean of each cluster

Determining the Number of Clusters

Elbow Method

- **Elbow Method** is probably the **most well-known method for determining the optimal number of clusters**.

- The elbow method **looks at the percentage of variance** explained as a function of the **number of clusters**:

- One should **choose a number of clusters so that adding another cluster doesn't give much better modeling of the data**. (Customer income and expenditure→ 30 customers→ 3 clusters→ 10,10,10. if 4 clusters→ not better result→ 10,10,9,1)

- More precisely, if **one plots the percentage of variance explained by the clusters against the number of clusters**, the **first clusters will add much information** (explain a lot of variance), but **at some point the marginal gain will drop**, giving an angle in the graph. The **number of clusters is chosen at this point**, hence the "**elbow criterion**".

Determining the Number of Clusters
Elbow Method

- we can use the following **algorithm to define the optimal clusters**:

1. **Compute clustering algorithm** (e.g., k-means clustering) **for different values of *k***. For instance, **by varying *k* from 1 to 10 clusters.**

2. **For each *k***, calculate the **Total Within-cluster Sum of Square (WSS).**

3. **Plot the curve of WSS** against the **number of clusters *k***.

4. **The location of a bend** (knee) **in the plot is generally considered as an indicator of the appropriate number of clusters**.

Determining the Number of Clusters

Example-1

1) **Selecting only the 1st four columns of the "iris" dataset:**

```
data <- iris[,1:4]
dim(data)
     150   4
```

2) **Creating an empty vector "tot_wss" to store the total_within_sum_of_squares for various no of clusters:**

```
tot_wss <- c()
tot_wss
     NULL
```

Determining the Number of Clusters

3) Next, we are going to do k-means 15 times for various clusters (1 to 15):

```
for(i   in   1:15)
  {
      cl <- kmeans(data,centers = i)
      tot_wss[i] <- cl $ tot.withinss
  }
tot_wss
```

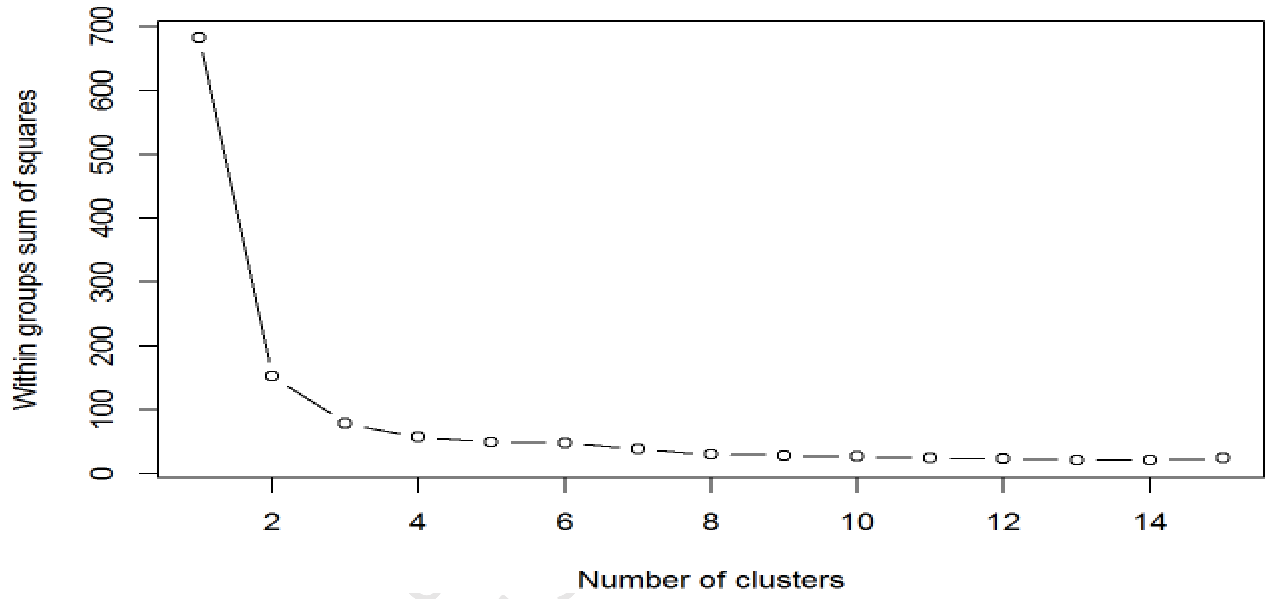
```
[1] 681.37060 152.34795  78.85144  57.22847  49.82228  47.61943  38.18643
[8]  29.98894  28.50441  26.80009  24.44235  23.37951  21.46090  20.82540
[15]  24.75149
```

Determining the Number of Clusters

4) Plotting a graph for the values of tot_wss against no-of-clusters

```
plot(x=1:15, y=tot_wss, type = "b", xlab = "Number of clusters", ylab = "Within groups sum
    of squares")
```

type = "b“ means plot both line as well as points



- From the above graph, we can observe that **as the number of clusters increases**, the **within cluster sum of squares decreases.**
- The **location of a knee in the plot is usually considered as an indicator of the appropriate number of clusters** because it means that adding another cluster does not improve much better the partition. **This method seems to suggest 4 clusters**.

https://www.r-bloggers.com/2017/02/finding-optimal-number-of-clusters/

https://rpubs.com/s_ritesh/Deciding_Clusters

https://www.rdocumentation.org/packages/stats/versions/3.6.2/topics/kmeans

https://www.datanovia.com/en/lessons/k-means-clustering-in-r-algorith-and-practical-examples/#estimating-the-optimal-number-of-clusters

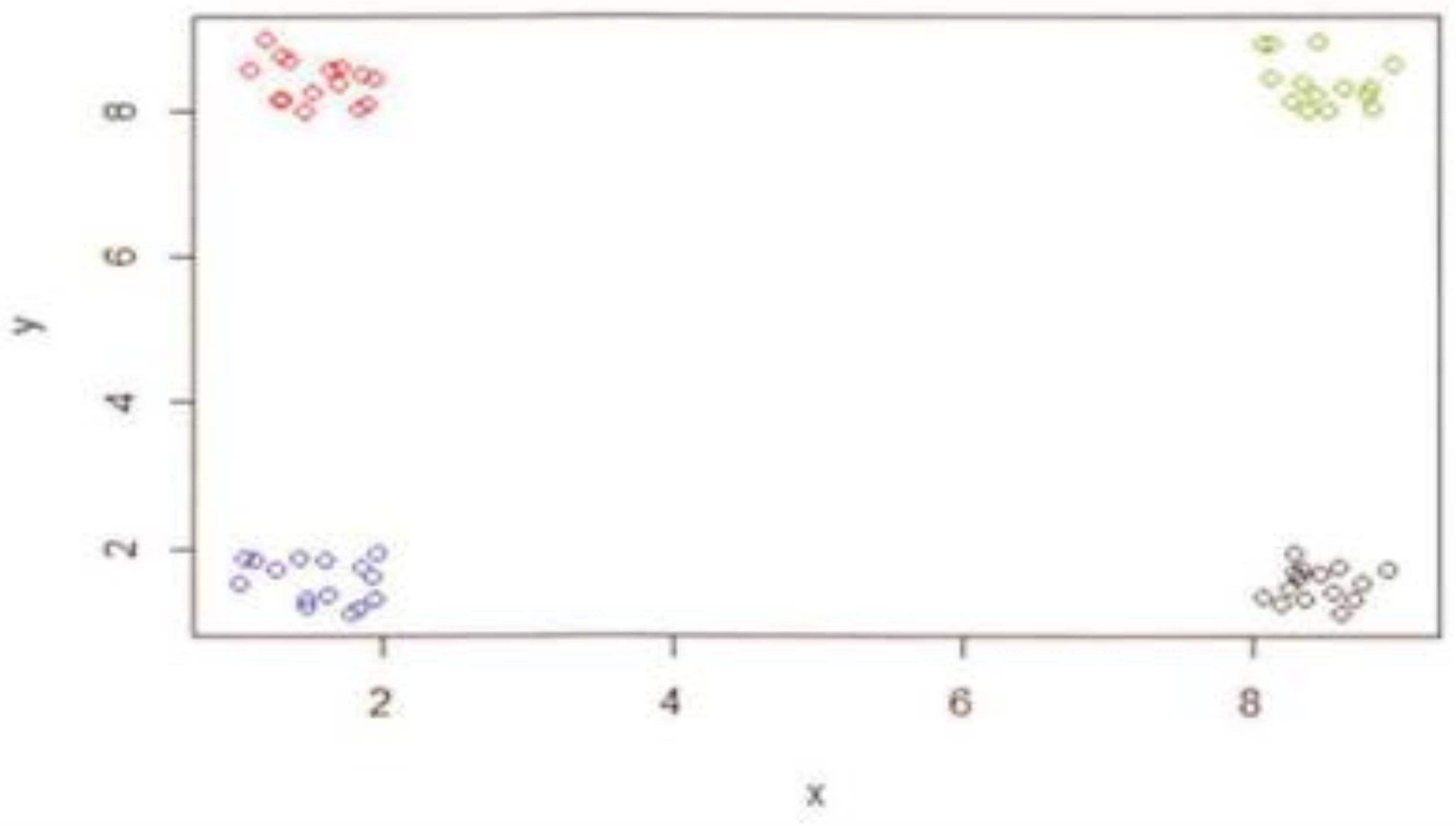
https://medium.com/analytics-vidhya/how-to-determine-the-optimal-k-for-k-means-708505d204eb

Diagnostics (Investigating in defining clusters)

- The **heuristic using WSS can provide at least several possible k values** to consider.
- **When the number of attributes is relatively small**, a common approach to further **refine the choice of k is to plot the data to determine how distinct the identified clusters are from each other**.
- In general, the following questions should be considered.
  - ➢ **Are the clusters well separated from each other?**
  - ➢ **Do any of the clusters have only a few points?**
  - ➢ **Do any of the centroids appear to be too close to each other?**

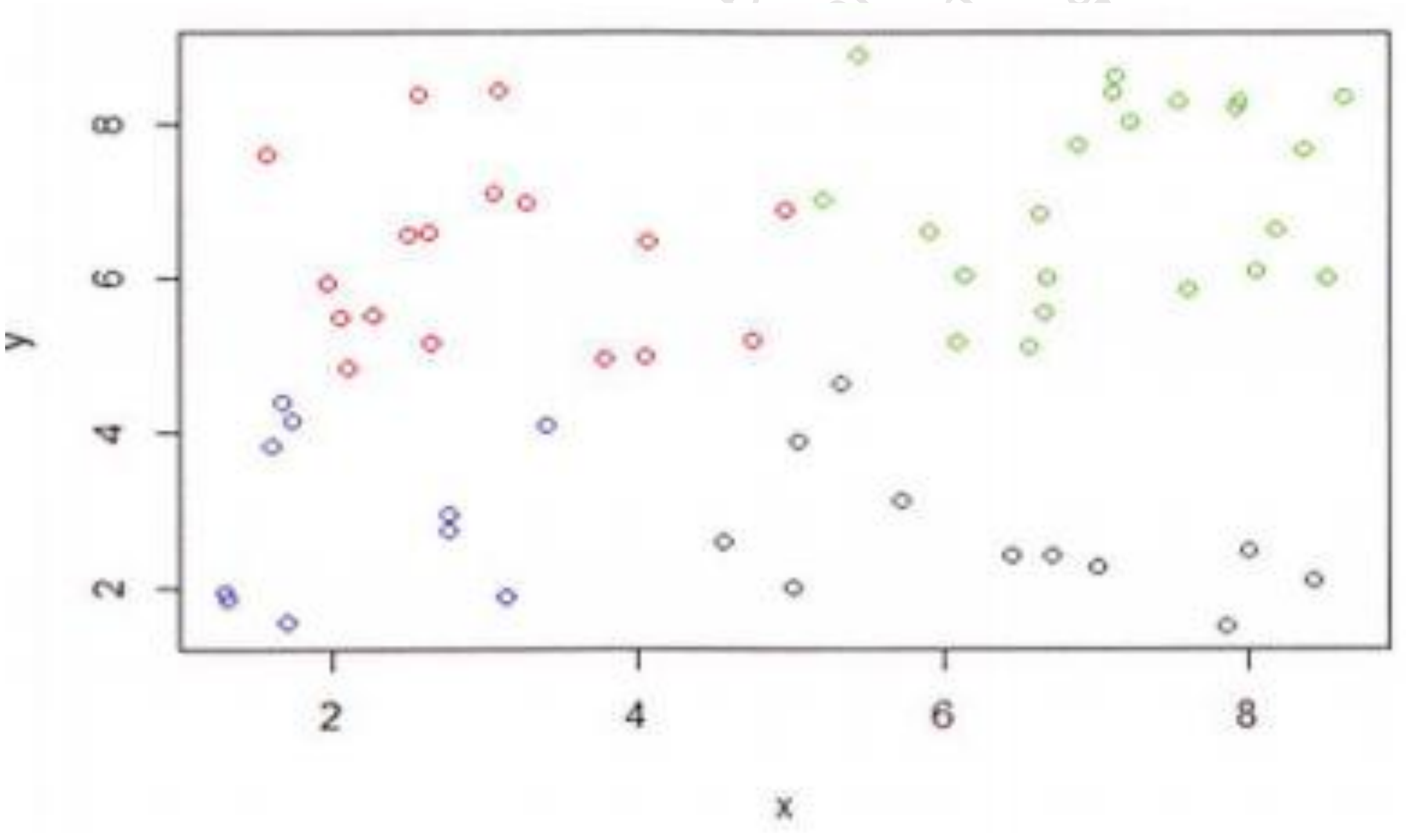
Diagnostics

- In the **first case, ideally the plot would look like the one shown in figure, when n = 2**. The **clusters are well defined, with considerable space between the four identified clusters**.



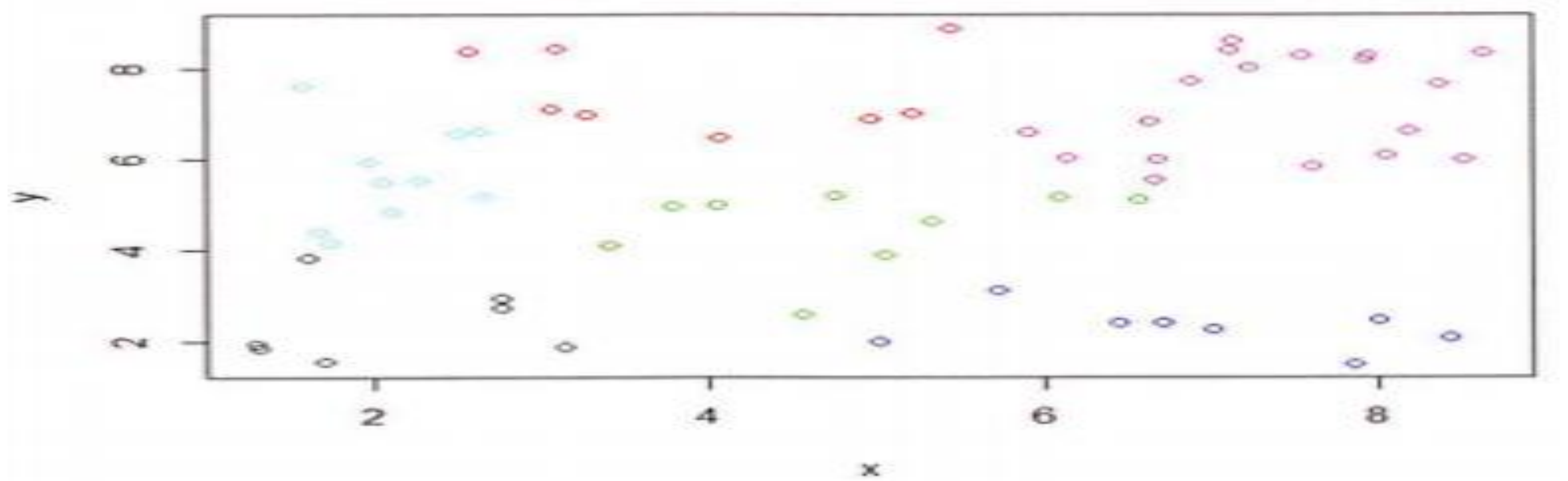
Diagnostics

- However, in **other cases**, such as figure, the **clusters may be close to each other**, and the **distinction may not be so obvious**(not clear).



Diagnostics

- In such cases, it is important to **apply some judgment on whether anything different will result by using more clusters.**
- For example, Below figure **uses six clusters to describe the same dataset as used in previous figure.** If **using more clusters does not better distinguish the groups**, it is almost certainly **better to go with fewer clusters.**



Reasons to Choose and Cautions-K-means

- **K-means is a simple and straightforward method for defining clusters.**
- **Once clusters and their associated centroids are identified,** it is easy to **assign new objects** (for example, new customers) **to a cluster** based on the object's distance from the closest centroid.
- Although **k-means is considered an unsupervised method** (Unsupervised→ Like not based on some specific constraint, not straight forward technique→ like group based on age or group based on salary), there are **still several decisions that the practitioner must make:**
  - ➢ **What object attributes should be included in the analysis?**
  - ➢ **What unit of measure** (for example, miles or kilometers) **should be used for each attribute?**
  - ➢ **Do the attributes need to be rescaled** so that **one attribute does not have a disproportionate effect on the results?**
  - ➢ **What other considerations might apply?**

Reasons to Choose and Cautions K-means-Object Attributes

Object Attributes →What object attributes should be included in the analysis?

- Regarding **which object attributes (for example, age and income) to use in the analysis**, it is important to understand **what attributes will be known at the time a new object will be assigned to a cluster.**

- For example, **information on existing customers' satisfaction** or **purchase frequency** may be available, **but such information may not be available for potential customers.**

- The **Data Scientist may have a choice of a dozen or more attributes** to use in the clustering analysis.

- Whenever possible and based on the data, it is **best to reduce the number of attributes** to the extent possible.

- **Too many attributes can minimize the impact of the most important variables.**

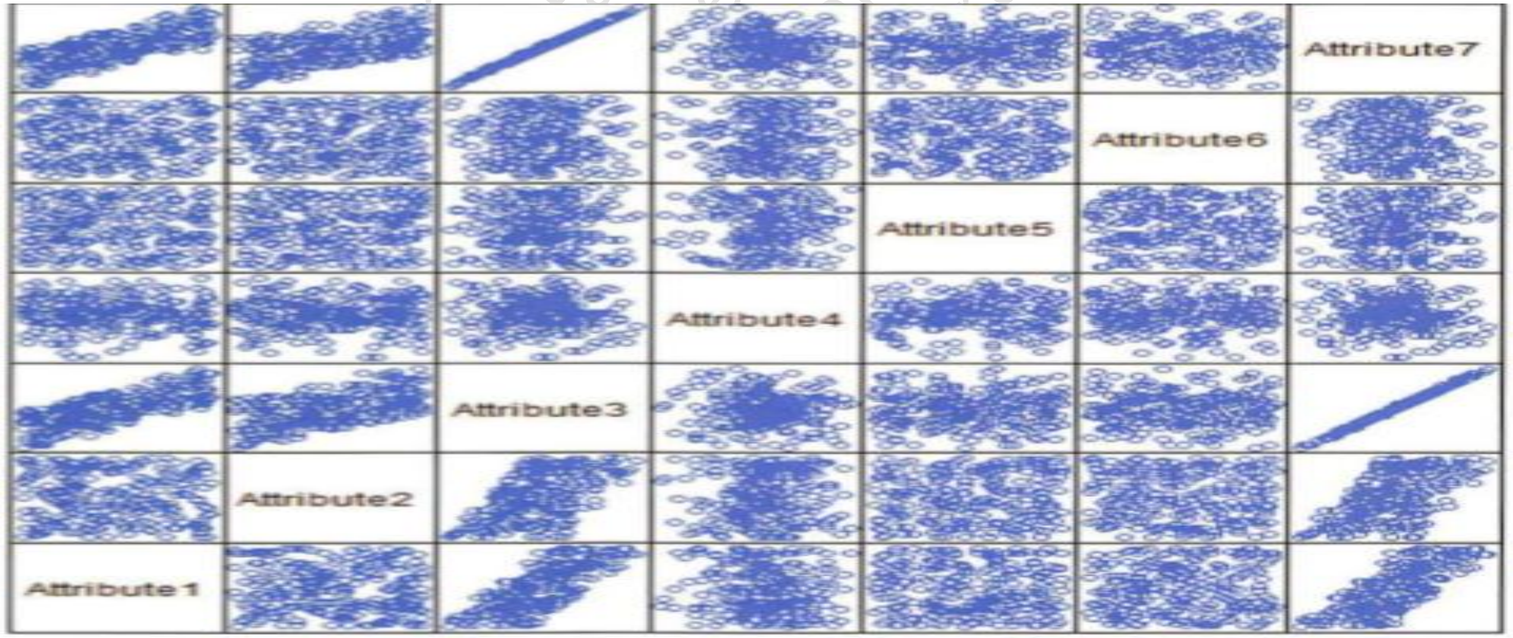
Reasons to Choose and Cautions K-means-Object Attributes

- Also, the **use of several similar attributes can place too much importance on one type of attribute.** For example, if **five attributes related to personal wealth** are included in a clustering analysis, the **wealth attributes dominate the analysis** and **possibly mask the importance of other attributes, such as age.**

- When **dealing with the problem of too many attributes**, one **useful approach is to identify any highly correlated attributes** and **use only one or two of the correlated attributes** in the clustering analysis.

Reasons to Choose and Cautions K-means-Object Attributes

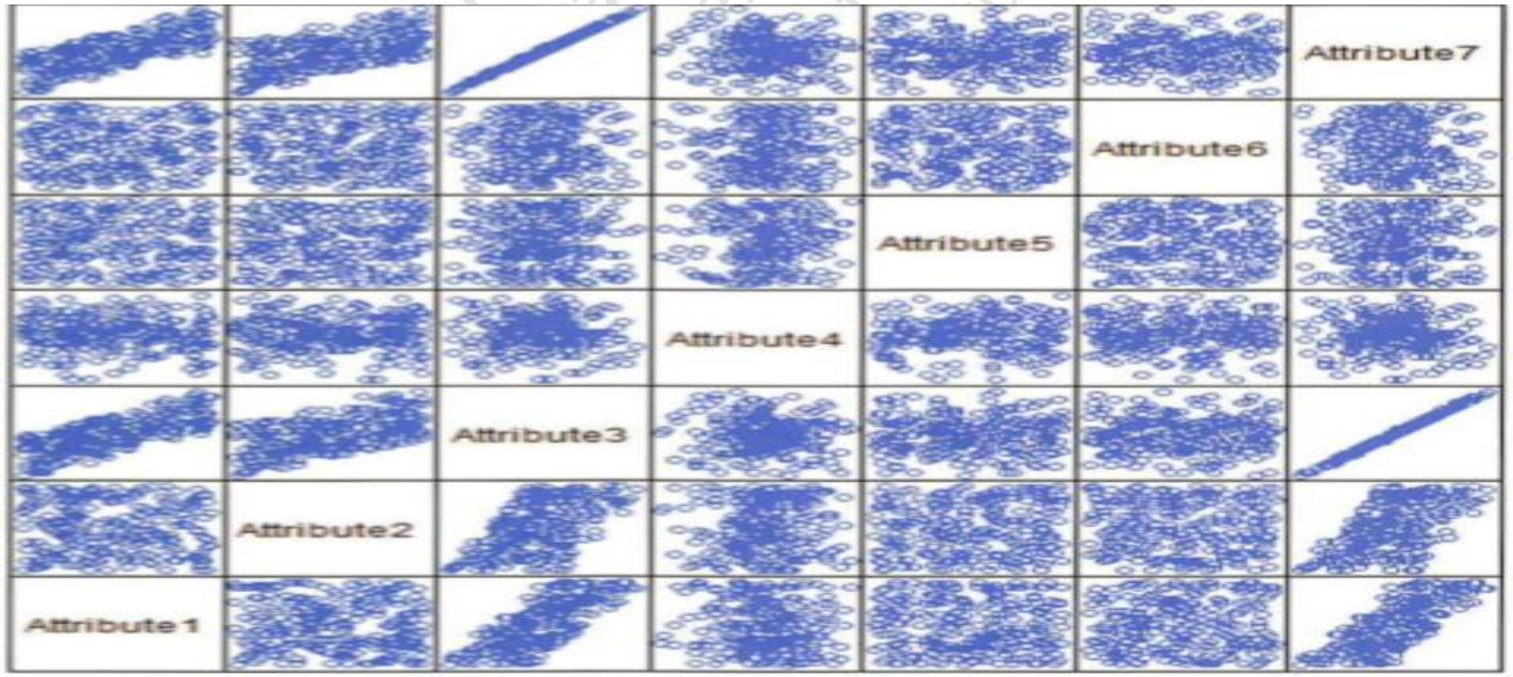
- As illustrated in figure, a **scatterplot matrix is a useful tool to visualize the pair-wise relationships between the attributes.**
- The **strongest relationship is observed to be between Attribute3 and Attribute7.**
- **If the value of one of these two attributes is known**, it appears that the **value of the other attribute is known with near certainty.**



Scatterplot matrix for seven attributes

Reasons to Choose and Cautions K-means-Object Attributes

- Other **linear relationships are also identified in the plot**. For example, consider the plot of **Attribute2 against Attribute3.**
- if the value of **Attribute2 is known**, there is **still a wide range of possible values for Attribute3**.
- Thus, **greater consideration must be given prior to dropping one of these attributes from the clustering analysis.**



Scatterplot matrix for seven attributes

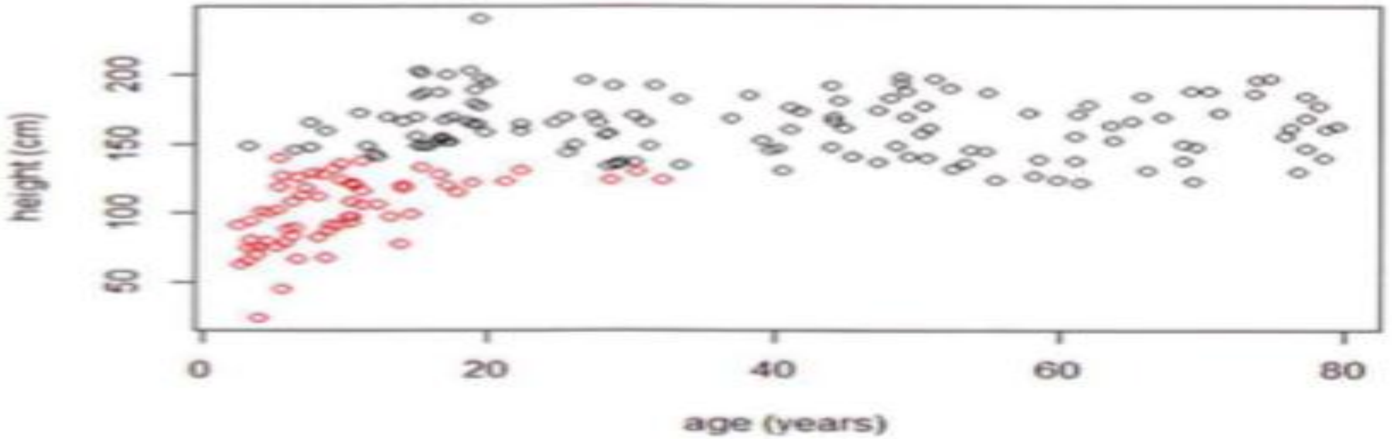
Reasons to Choose and Cautions K-means-Object Attributes

- **Another option to reduce the number of attributes is to combine several attributes into one measure**.
- For example, instead of using two attribute variables, **one for Debt and one for Assets, a Debt to Asset ratio could be used.**
- This option also addresses the problem when the **magnitude of an attribute is not of real interest**, but the **relative magnitude is a more important measure**.

Reasons to Choose and Cautions K-means-Units of Measure

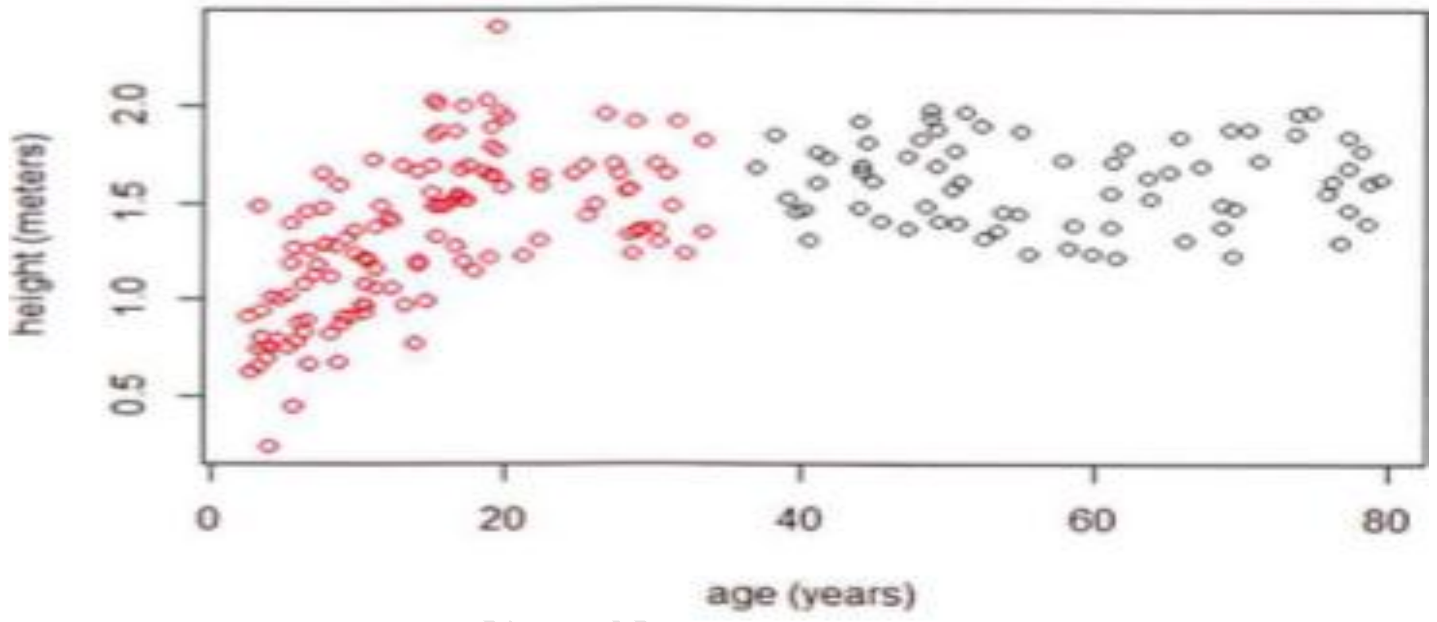
Units of Measure → What unit of measure (for example, miles or kilometers) should be used for each attribute?

- From a computational perspective, the **k-means algorithm is somewhat indifferent to the units of measure for a given attribute** (for example, meters or centimetres for a patient's height).
- However, the **algorithm will identify different clusters depending on the choice of the units of measure**.
- **For example, suppose that k-means is used to cluster patients based on age in years and height in centimetres.** For n=2, figure illustrates the two clusters that would be determined for a given dataset.



Reasons to Choose and Cautions K-means-Units of Measure

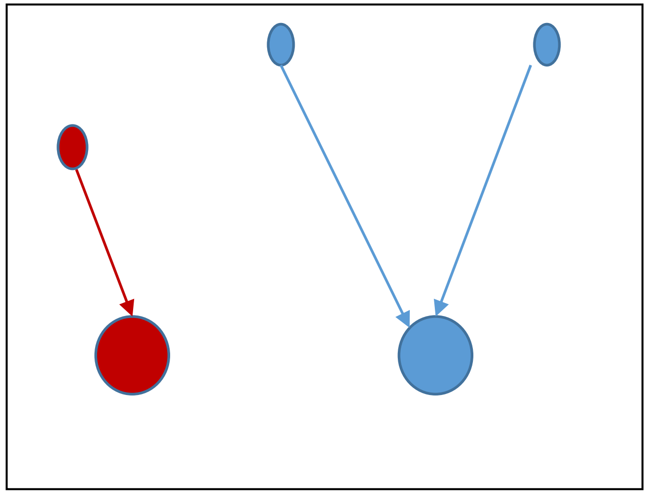
- But if the height was rescaled from centimeters to meters by dividing by 100, the resulting clusters would be slightly different, as illustrated in figure.

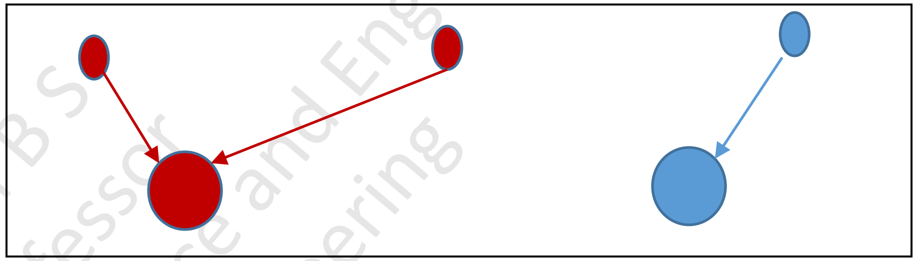


- When the height is expressed in meters, the magnitude of the ages dominates the distance calculation between two points.

Example-Units of Measure

Example-Units of Measure





Reasons to Choose and Cautions K-means- Rescaling

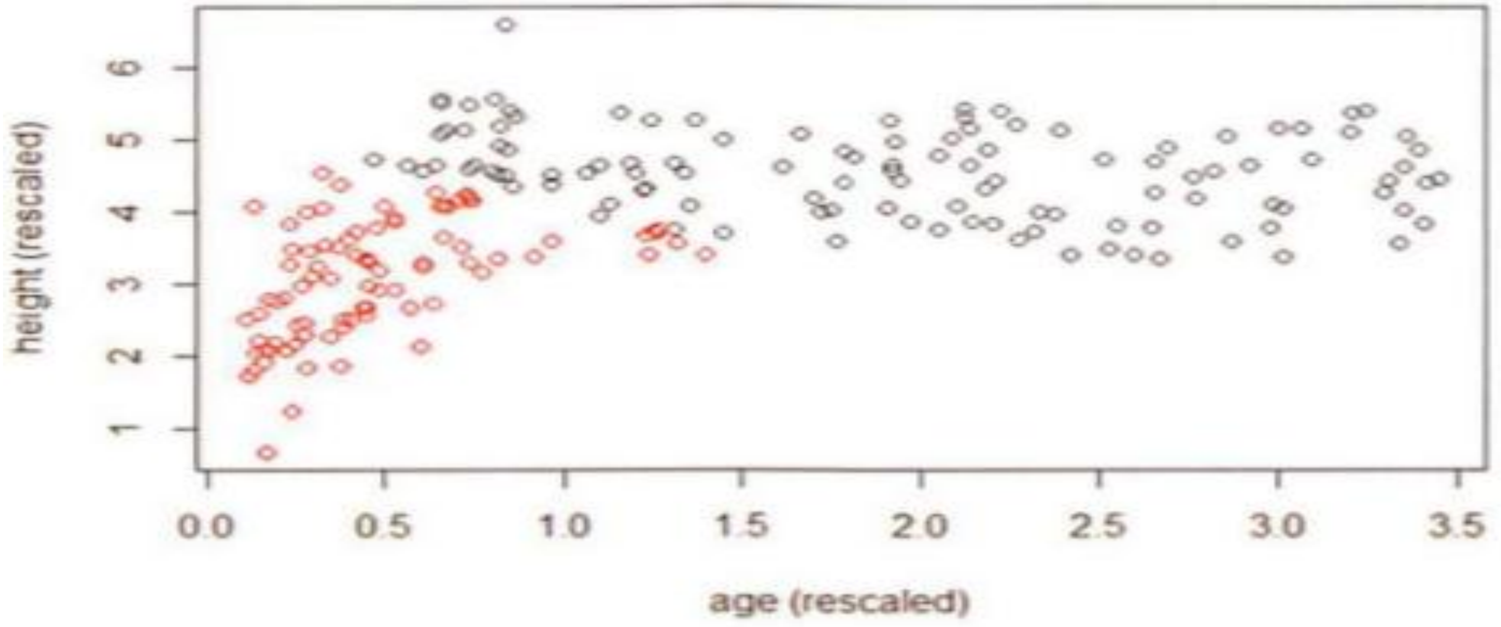
Rescaling → Do the attributes need to be rescaled so that **one attribute does not have a disproportionate effect on the results?**

- **Attributes can differ in magnitude from the other attributes**. (Height expressed in centimeter behave differently than the height expressed in meters by K Means algorithm)
- **For example, if personal income is expressed in dollars and age is expressed in years. The income attribute, often exceeding $10,000 can easily dominate the distance calculation with ages** typically less than 100 years.
- Although **some adjustments could be made by expressing the income in thousands of dollars** (for example, 10 for $10,000), a **more straightforward method is to divide each attribute by the attribute's standard deviation.**

Reasons to Choose and Cautions K-means- Rescaling

Rescaling

- **For example for the age and height, the standard deviations are 23.1 years and 36.4**, respectively. **Dividing each attribute value by the appropriate standard deviation and performing the k-means analysis yields the result shown as shown in figure.**



- **With the rescaled attributes for age and height, the borders of the resulting clusters now fall somewhere between the two earlier clustering analyses.**

Reasons to Choose and Cautions K-means- Additional Considerations

Additional Considerations→ What other considerations might apply?

- Here, **discussed k-means algorithm uses Euclidean distance function to assign the points to the closest centroids.**

- Other possible function choices include the **cosine similarity and the Manhattan distance functions**.

- The **cosine similarity function is often chosen to compare two documents based on the frequency of each word that appears in each of the documents**.

- For two points p and q at (P_1, P_2,… P_n) and (Q_1, Q_2,… Q_n), respectively, the Manhattan distance d1 between p and q is expressed as shown in the below equation.

$$d_1(p,q)=\sum_{i=1}^{n}\left|p_i-q_i\right|$$

Reasons to Choose and Cautions K-means- Additional Considerations

Additional Considerations→ What other considerations might apply?

- Using the above equation, the distance from (1, 1) to (4, 5) would be (1 – 4) + (1 – 5) = 7.

- From an **optimization perspective, if there is a need to use the Manhattan distance for a clustering analysis, the median is a better choice for the centroid than use of the mean**.

- **K-means clustering is applicable to objects that can be described by attributes that are numerical**. with a meaningful distance measure.

- However, **k-means does not handle categorical variables well**.

Reasons to Choose and Cautions K-means- Additional Considerations

Additional Considerations→ What other considerations might apply?

- For example, **suppose a clustering analysis is to be conducted on new car sales**. Among other attributes, **such as the sale price, the color of the car is considered important**.

- Although **one could assign numerical values to the color such as red = 1, yellow = 2, and green = 3, it is not useful to consider that yellow is as close to red than yellow is to green from a clustering perspective.**

- **In such cases, it may be necessary to use an alternative clustering methodology**.

Regression

- **Regression Analysis is an advanced analytic technique that attempts to explain the influence that a set of variables has on the outcome of another variable** of interest.

For Eg: 1) Relationship between experience and salary. Predicting salary of an employee based on his experience

2) Relationship between income and happiness of a person.

- **The outcome variable is called a dependent variable** because the outcome depends on the other variables.

- **These additional variables that have the greatest statistical influence on the outcome are** sometimes **called the Input variables** or the **Independent variables.** (Variable that has influence on other variable→ Independent Variable)

Regression

- Mainly there are **two types of regression analysis**
  - **Linear regression**
  - **Logistic regression**
- Regression analysis is useful for answering the following kinds of questions:
  - What is a person's expected income? (Predicted based on the sources→ Linear Regression)
  - What is the probability that an applicant will default on a loan?
- **Linear regression is a useful tool for answering the first question**, and **logistic regression is a popular method for addressing the second**.

Linear Regression

- **Linear regression is an analytical technique used to model the relationship between** several **input variables** and a continuous **outcome variable**. (Build model)

- A **key assumption is that the relationship between an input variable** and **the outcome variable is linear.**

- The **physical sciences have well-known linear models**, such as **Ohm's Law**, which states that the **electrical current flowing through a resistive circuit is linearly proportional to the voltage applied to the circuit.** Such a model is considered deterministic in the sense that **if the input values are known, the value of the outcome variable is precisely determined**.

Linear Regression

- A **linear regression model is a probabilistic** (Not deterministic) one that accounts for the randomness that can affect any particular outcome.

- **Based on known input values, a linear regression model provides the expected value of the outcome variable**, but **some uncertainty may remain in predicting** any particular outcome.

- Thus, **linear regression models are useful in physical and social science applications where there may be considerable variation in a particular outcome** based on a given set of input values.

Linear Regression: Use Cases

- **Linear regression is often used in business, government, and other scenarios**. Some common practical applications of linear regression in the real world include the following:

1) Real Estate:

➢ **A simple linear regression analysis can be used to model residential home prices as a function of the home's living area.** Such a model helps set or evaluate the list price of a home on the market.

➢ **The model could be further improved by including other input variables such as number of bathrooms, number of bed rooms, lot size, school district ran kings, crime statistics, and property taxes.**

Linear Regression: Use Cases

2) Demand Forecasting

- **Businesses and governments can use linear regression models to predict demand for goods and services.**

- **For example, restaurant chains** can appropriately prepare for the predicted type and **quantity of food that customers will consume based upon the weather, the day of the week, whether an item is offered as a special, the time of day**, **and the reservation volume.**

Linear Regression: Use Cases

3) Medical:

- **A linear regression model can be used to analyze the effect of a proposed radiation treatment on reducing tumor sizes.**

- **Input variables might include duration of a single radiation treatment, frequency of radiation treatment, and patient attributes such as age or weight.**

Linear Regression: Model Description

- As the name of this technique suggests, the **linear regression model assumes that there is a linear relationship between the input variables and the outcome variable**.

- This relationship can be expressed as shown in below equation.

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_{p-1} x_{p-1} + \varepsilon$$

where:

y is the outcome variable

x_j are the input variables, for $j = 1, 2, \ldots, p - 1$

β_0 is the value of y when each x_j equals zero

β_j is the change in y based on a unit change in x_j, for $j = 1, 2, \ldots, p - 1$

ε is a random error term that represents the difference in the linear model and a particular observed value for y

Linear Regression: Model Description

For E.g. Suppose it is desired to build a linear regression model that estimates a person's annual income as a function of two variables-age and education-both expressed in years.

- In this case, **income is the outcome variable**, and **the input variables are age and education**.
- However, **it is also obvious that there is considerable variation in income levels for a group of people with identical ages and years of education. This variation is represented by ε in the model**.
- So, in this example, the model would be expressed as shown in below equation.

$$Income = \beta_0 + \beta_1 Age + \beta_2 Education + \varepsilon$$

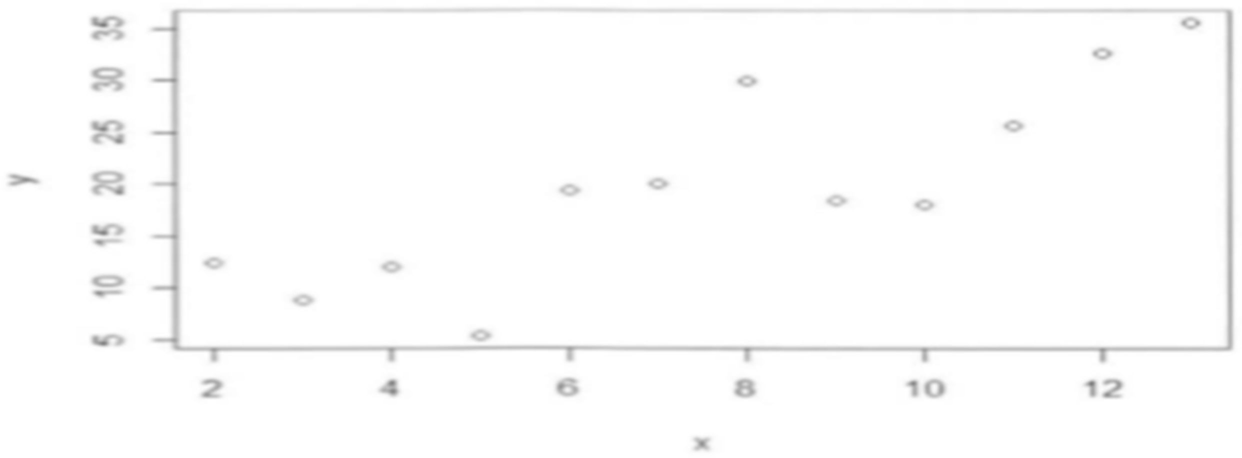
Linear Regression: Model Description

- In the linear model, the β_j's epresent the unknown p parameters.

- The estimates for these **unknown parameters are chosen so that, on average, the model provides a reasonable estimate of a person's income based on age and education.**

- **Ordinary least Squares (OLS) is a common technique to estimate the parameters**.

- To **illustrate how OLS works, suppose there is only one input variable, x, for an outcome variable y**. Furthermore, **n observations of { x, y} are obtained and plotted in shown in figure**.



Linear Regression: Model Description

- The **goal is to find the line that best approximates the relationship between the outcome variable and the input variables.**

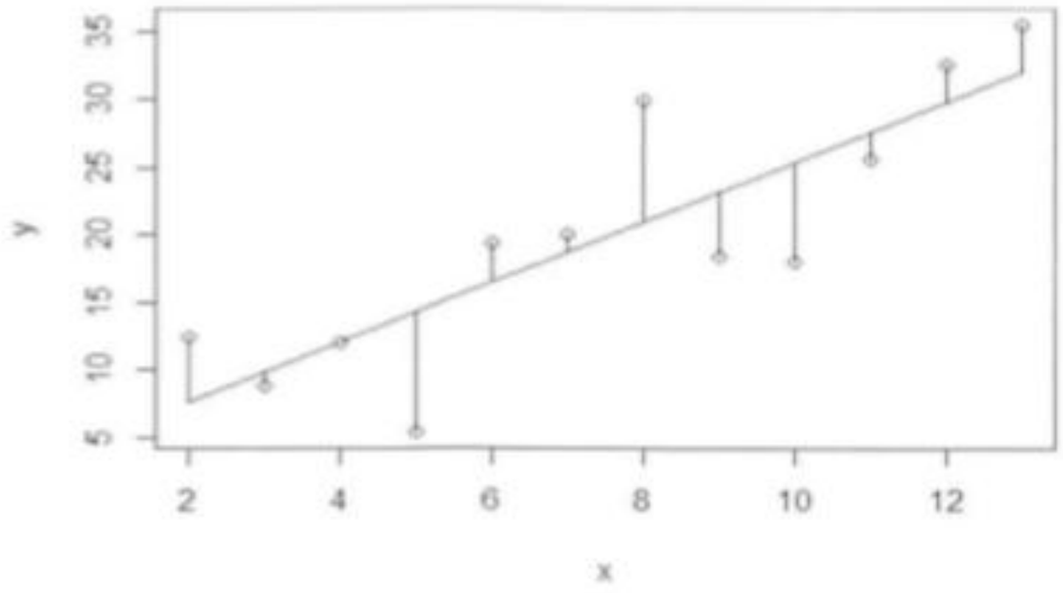
- **With OLS, the objective is to find the line through these points that minimizes the sum of the squares of the difference between each point and the line in the vertical direction**. I

- **In other words, find the values of** β_0 and β_1 **, such that the summation shown in below equation is minimized.**

$$\sum_{i=1}^{n}[y_i-(\beta_0+\beta_1 x_i)]^2$$

Linear Regression: Model Description

- The **n individual distances to be squared and then summed are illustrated in as shown below figure**. The **vertical lines represent the distance between each observed y value and the line** $y = \beta_0 + \beta_1 x$.



Linear Regression Model (with Normally Distributed Errors)

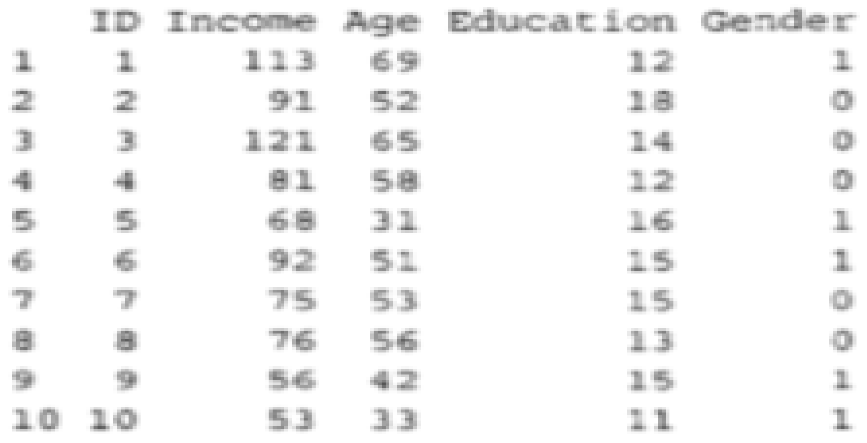
Linear Regression: Example in R

Consider the previously discussed Income example.

- In addition to the **variables age** and **education**, the **person's gender: female or male** is considered an **input variable**.
- The following **code reads a comma-separated-value** (CSV) **file of 1,500 people's incomes, ages, years of education, and gender**. The first 10 rows are displayed:

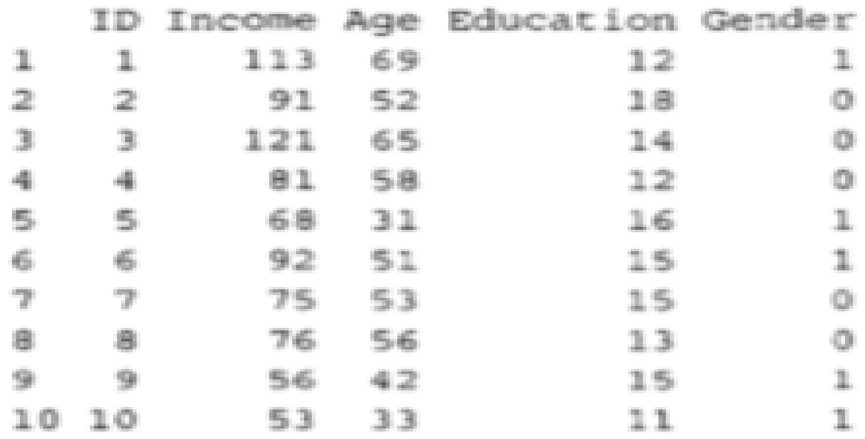
```
income_input = as.data.frame( read. csv ( *C: /data/income. csv'‘*) )

income_input[1:10,]
```



```
   ID Income Age Education Gender
1   1    113  69        12      1
2   2     91  52        18      0
3   3    121  65        14      0
4   4     81  58        12      0
5   5     68  31        16      1
6   6     92  51        15      1
7   7     75  53        15      0
8   8     76  56        13      0
9   9     56  42        15      1
10 10     53  33        11      1
```

Linear Regression: Example in R



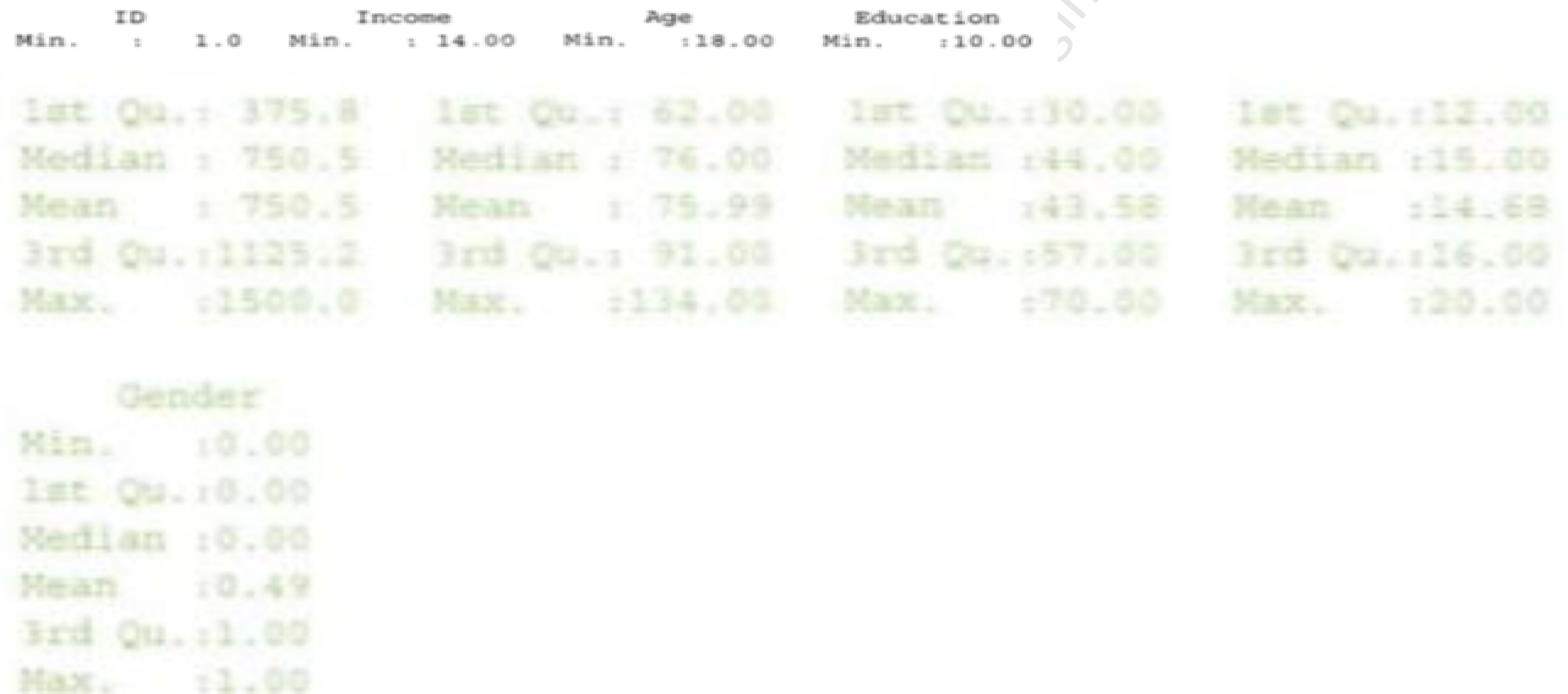
```
   ID Income Age Education Gender
1   1    113  69        12      1
2   2     91  52        18      0
3   3    121  65        14      0
4   4     81  58        12      0
5   5     68  31        16      1
6   6     92  51        15      1
7   7     75  53        15      0
8   8     76  56        13      0
9   9     56  42        15      1
10 10     53  33        11      1
```

- **Each person** in the sample has been **assigned an identification number: ID**.
- **Income is expressed in thousands of dollars**. (For example, 113 denotes $113,000.).
- **Age** and **Education** are expressed **in years**.
- For Gender, **a 0 denotes female** and **a 1 denotes male**.

Linear Regression: Example in R

- A **summary of the imported data reveals that the incomes vary from $14,000 to $134,000**. The **ages are between 18 and 70 years**. The **education experience** for each person varies **from a minimum of 10 years to a maximum of 20 years.**

summary(income_input)



```
       ID              Income              Age            Education
 Min.   :   1.0   Min.   : 14.00   Min.   :18.00   Min.   :10.00
 1st Qu.: 375.8   1st Qu.: 62.00   1st Qu.:30.00   1st Qu.:12.00
 Median : 750.5   Median : 76.00   Median :44.00   Median :15.00
 Mean   : 750.5   Mean   : 75.99   Mean   :43.58   Mean   :14.68
 3rd Qu.:1125.2   3rd Qu.: 91.00   3rd Qu.:57.00   3rd Qu.:16.00
 Max.   :1500.0   Max.   :134.00   Max.   :70.00   Max.   :20.00

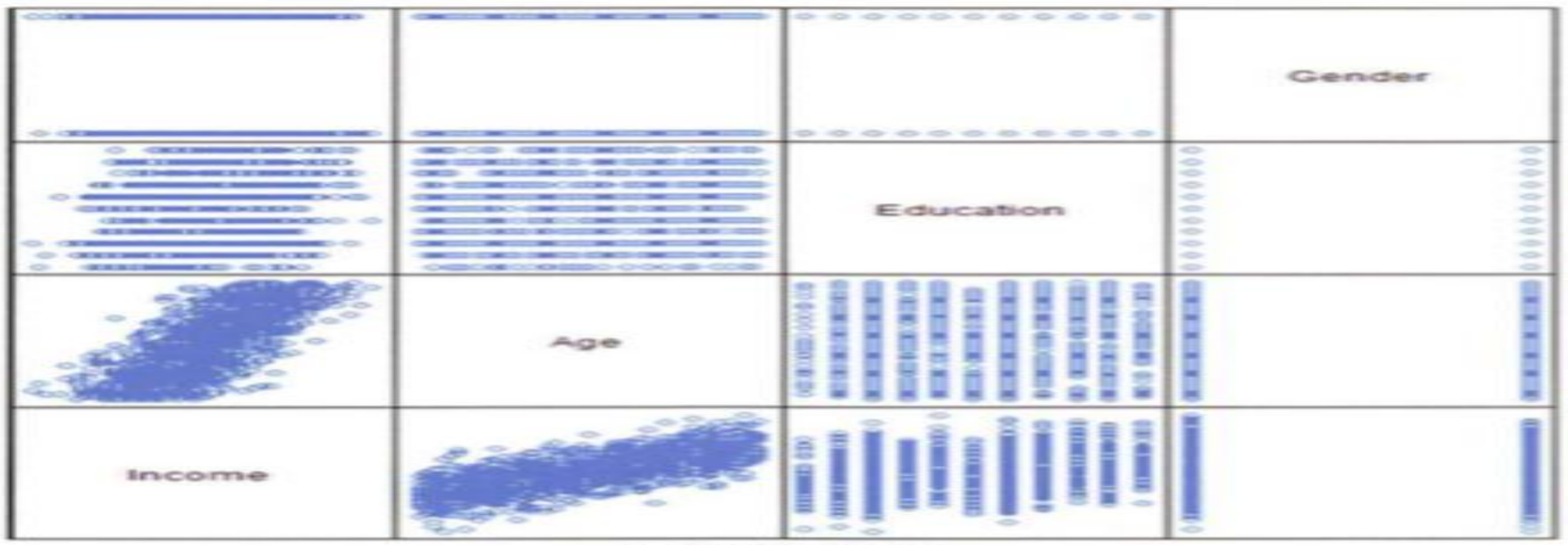
     Gender
 Min.   :0.00
 1st Qu.:0.00
 Median :0.00
 Mean   :0.49
 3rd Qu.:1.00
 Max.   :1.00
```

Linear Regression: Example in R

- A **scatterplot matrix is an informative tool to view the pair-wise relationships** of the variables.
- The basic assumption of a linear regression model is that there is a linear relationship between the outcome variable and the input variables.
- Using the **lattice package in R, the scatterplot matrix** as shown in below figure is generated with the following R code:

```
library(lattice)
splom(~income_input[c(2:5)], groups=NULL, data=income_input, axis.line.tck=0, axis.text.alpha = 0)
```

Linear Regression: Example in R



Scatter Plot Matrix

- Because the **dependent variable is typically plotted along the y-axis**, **examine the set of scatterplots along the bottom of the matrix.**
- A **strong positive linear trend is observed for Income as a function of Age**.
- **Against Education, a slight positive trend may exist**, but the trend is **not quite as obvious** as is the case with the Age variable.
- Lastly, there is **no observed effect on Income based on Gender**.

Linear Regression: Example in R

- With this **qualitative understanding of the relationships between Income and the input variables**, it seems reasonable to quantitatively evaluate the linear relationships of these variables.

- Now, the **proposed linear regression model is shown** in the below equation.

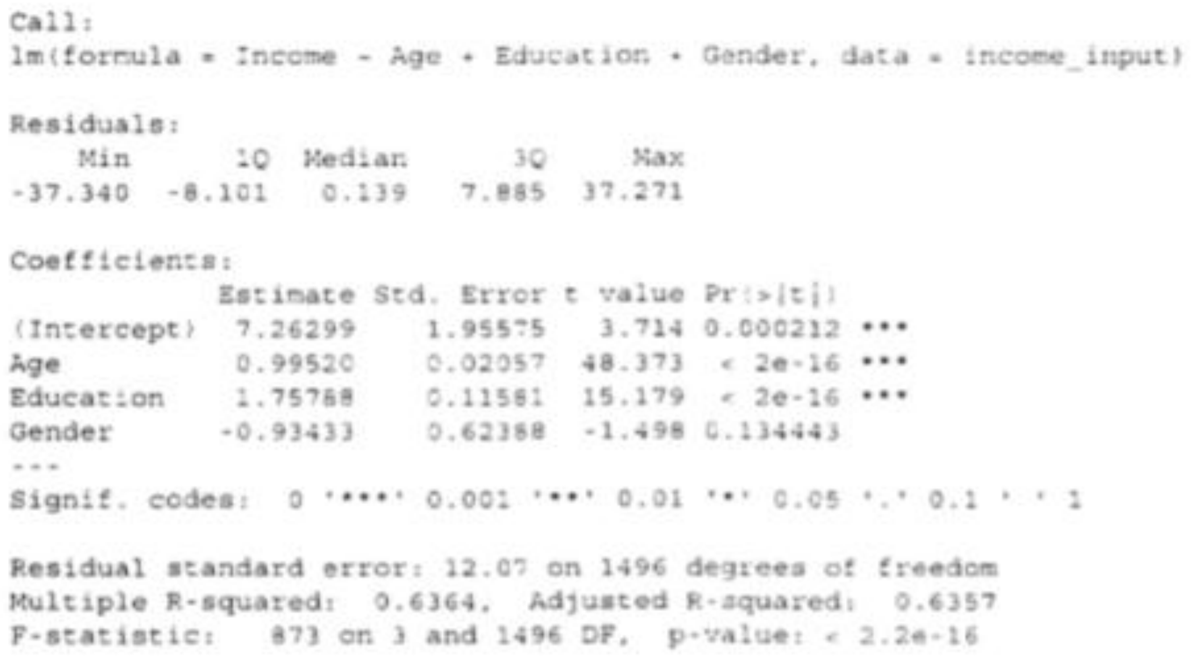
$$Income = \beta_0 + \beta_1 Age + \beta_2 Education + \beta_3 Gender + \varepsilon$$

- Using the **linear model function lm( ) in R**, the income model can be applied to the data as follows:

```
results <- lm(Income~Age + Education + Gender, income_input)

summary(results)
```

Linear Regression: Example in R



```
Call:
lm(formula = Income ~ Age + Education + Gender, data = income_input)

Residuals:
    Min      1Q  Median      3Q     Max
-37.340  -8.101   0.139   7.885  37.271

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.26299    1.95575   3.714 0.000212 ***
Age          0.99520    0.02057  48.373  < 2e-16 ***
Education    1.75788    0.11581  15.179  < 2e-16 ***
Gender      -0.93433    0.62388  -1.498 0.134443
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

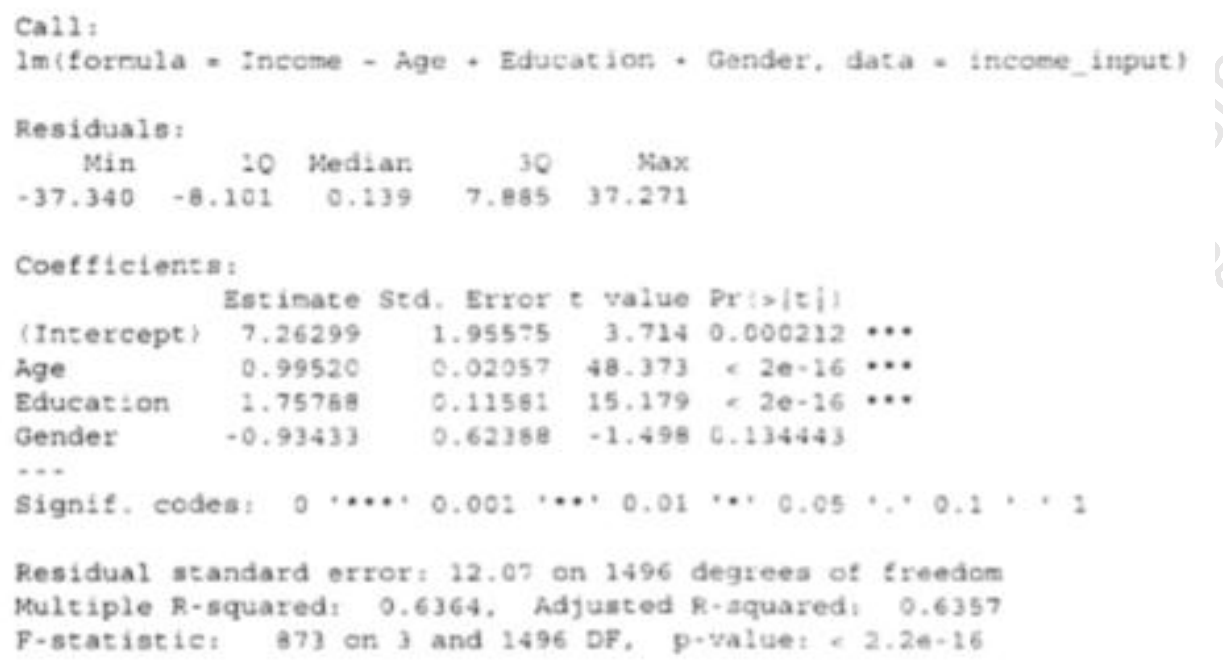
Residual standard error: 12.07 on 1496 degrees of freedom
Multiple R-squared:  0.6364,  Adjusted R-squared:  0.6357
F-statistic:   873 on 3 and 1496 DF,  p-value: < 2.2e-16
```

-

- The **lm () function performs the parameter estimation for the parameters** β_j $(j = 0, 1, 2, 3)$ **using ordinary least squares** and provides several useful calculations and **results that are stored in the variable called results in this example.**

- From the R output, **the residuals vary from approximately -37 to +37, with a median close to 0**. (A **residual** is the vertical distance between a data point and the **regression** line. Each data point has one **residual**. Each data point has one residual. They are positive if they are above the regression line and negative if they are below the regression line. If the regression line actually passes through the point, the residual at that point is zero).

Linear Regression: Example in R



```
Call:
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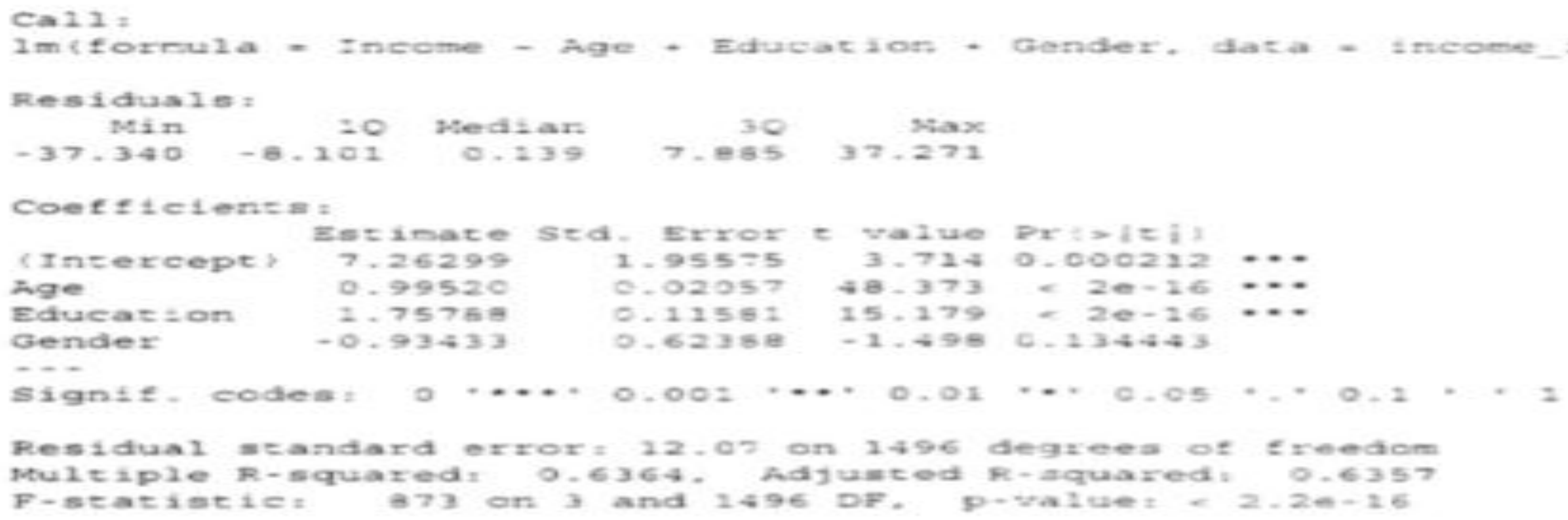
```

- The **output provides details about the coefficients**. The column **Estimate provides the OLS estimates of the coefficients** in the fitted linear regression model.
- In general, **the (Intercept) corresponds to the estimated response variable when all the input variables equal zero**. In this example, the intercept corresponds to an estimated income of $7,263 for a new born female with no education.

Linear Regression: Example in R



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Call:
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---
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F-statistic:   873 on 3 and 1496 DF,  p-value: < 2.2e-16
```

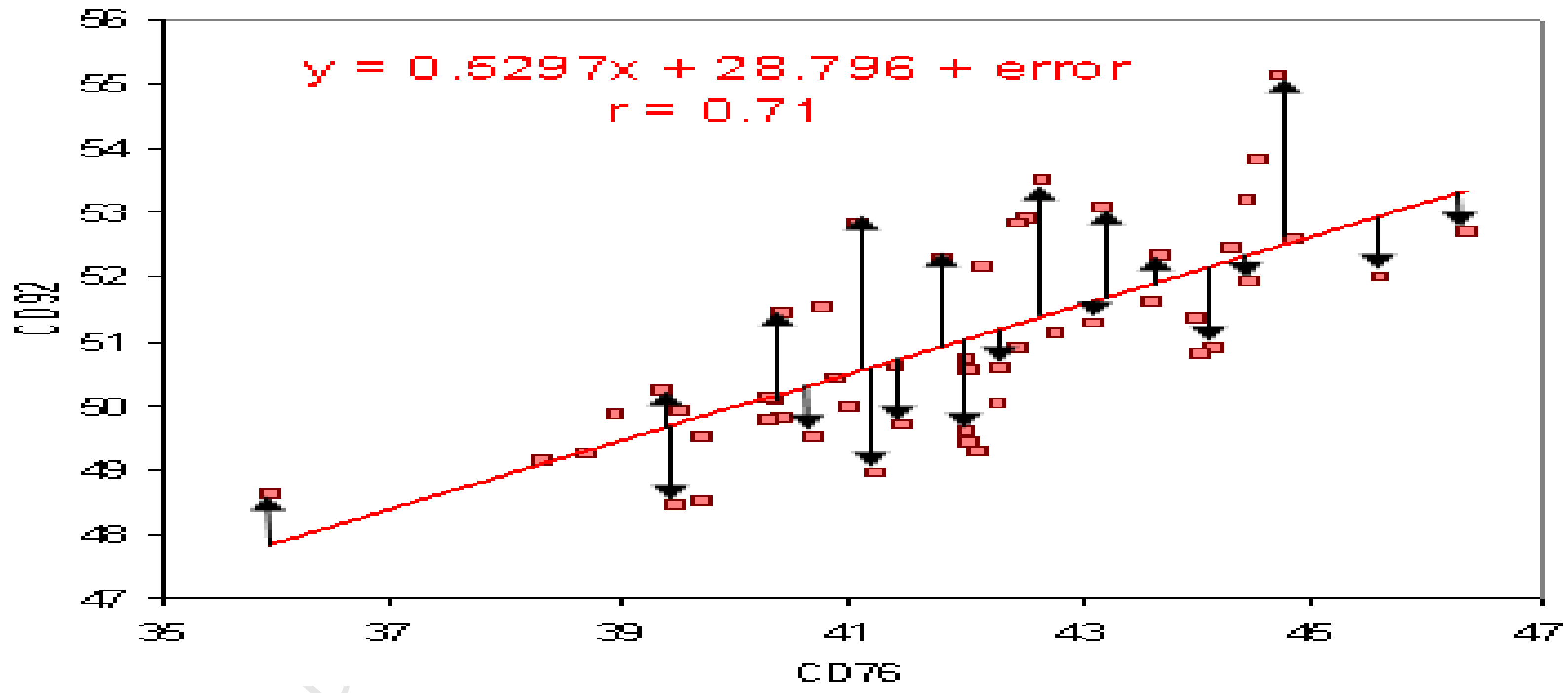
- The **coefficient for Age is approximately equal to one**. This coefficient is interpreted as follows: For **every one unit increase in a person's age, the person's income is expected to increase by $995**. Similarly, **for every unit increase in a person's years of education, the person's income is expected to increase by about $1,758.**

- **Interpreting the Gender coefficient is slightly different**. **When Gender is equal to zero, the Gender coefficient contributes nothing to the estimate of the expected income**. When **Gender is equal to one, the expected Income is decreased by about $934**.

Linear Regression: Model Description

Linear Regression: Model Description

Example in R A **residual** is the vertical distance between a data point and the **regression** line. Each data point has one **residual**. Each data point has one residual. They are positive if they are above the regression line and negative if they are below the regression line. If the regression line actually passes through the point, the residual at that point is zero.



- As residuals are the difference between any data point and the regression line, they are sometimes called “**errors**.” Error in this context doesn’t mean that there’s something wrong with the analysis; it just means that there is some unexplained difference. In other words, the residual is the error that isn’t explained by the regression line.
- **Residual = Observed value – predicted value**
  $e = y - \hat{y}$
- mean = the sum of the residuals / the number of items.

Logistic Regression

- **Linear regression** is an analytical technique used **to model the relationship between several input variables and a continuous outcome variable**, where a **relationship is linear**.

  For E.g.: 1) Predicting salary of an employee based on his experience.

  2) linear regression can be used to model the relationship between age and education to income.

- **Suppose a person's actual income was not of interest, but rather whether someone was wealthy or poor.**

  For E.g.: What is the probability that an applicant will default on a loan?

- **In such a case, when the outcome variable is categorical in nature, logistic regression can be used to predict the likelihood of an outcome based on the input variables.**

Logistic Regression

For example:

- **A logistic regression model can be built to determine if a person will or will not purchase a new automobile in the next 12 months.**

- **The training set could include input variables for a person's age, income, and gender as well as the age of an existing automobile. The training set would also include the outcome variable on whether the person purchased a new automobile over a 12-month period.**

- **The logistic regression model provides the likelihood or probability of a person making a purchase in the next 12 months.**

Logistic Regression: Use Cases

- The **Logistic Regression model is applied to a variety of situations** in both the public and the private sector.
- Some common ways that the **logistic regression model is used** include the following:

Medical

- **Develop a model to determine** the likelihood of a **patient's successful response to a specific medical treatment or procedure**.
- **Input variables** could include **age, weight, blood pressure and cholesterol levels**.

Finance

- Using a loan **applicant's credit history** and the **details on the loan**, **determine the probability that an applicant will default on the loan**.
- **Based on the prediction**, the **loan can be approved or denied**, or the terms can be modified.

Logistic Regression: Use Cases

Marketing

- **Determine a wireless customer's probability of switching carriers** (known as churning) **based on age, number of family members on the plan, months remaining on the existing contract, and social network contacts**.

- **With such insight**, target the high-probability **customers with appropriate offers to prevent churn**.

Engineering

- **Based on operating conditions** and **various diagnostic measurements, determine the probability of a mechanical part experiencing a malfunction or failure.**

- **With this probability estimation, schedule** the appropriate **preventive maintenance activity. (Servicing, Replacing etc)**

Logistic Regression: Model Description

- **Logistic regression is based on the logistic function f(y), as given in below Equation.**

$$f(y) = \frac{e^y}{1+e^y} \quad \text{for} -\infty < y < \infty$$

- ➢ **as y→∞, f(y) → 1 and**
- ➢ **as y →-∞ , f(y) → 0.**

- So, as figure illustrates, the **value of the logistic function f(y) varies from 0 to 1** as y increases.

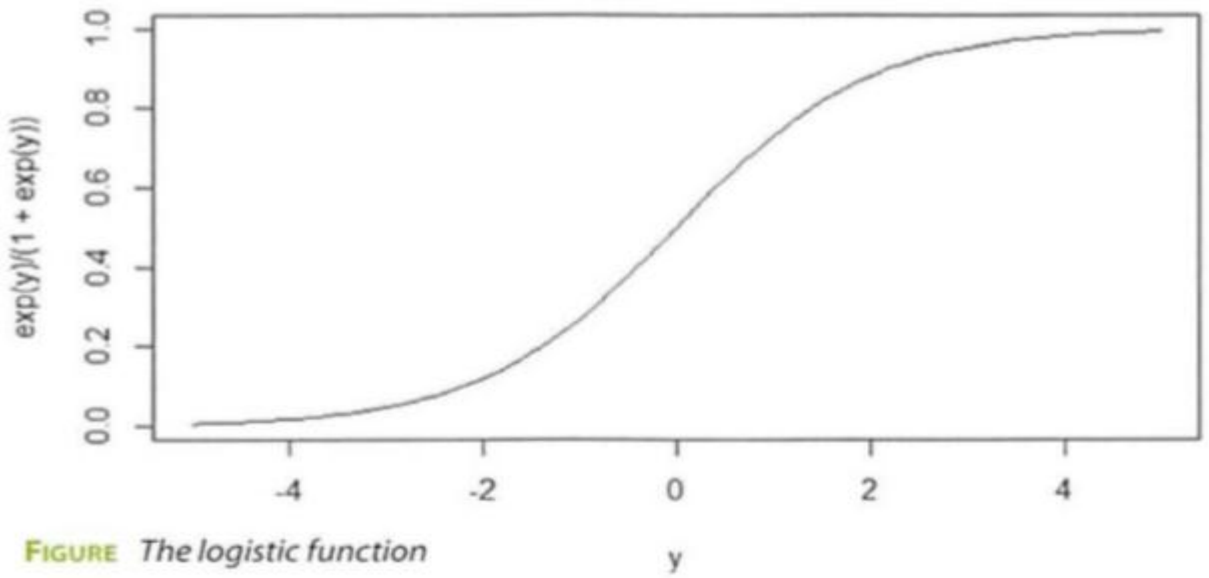


FIGURE *The logistic function*

Logistic Regression: Model Description

- Because **the range of f(y) is (0, 1), the logistic function appears to be an appropriate function to model the probability of a particular outcome occurring.**

- As the **value of y increases, the probability of the outcome occurring increases**. (probability of Outcome in categorical variable depends value of income variable y)

- In any proposed model, to predict the likelihood of an outcome, **y needs to be a function of the input variables.**

- In **Logistic Regression, y is expressed as a linear function of the input variables** as shown in below equation.

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 \ldots + \beta_{p-1} x_{p-1}$$

- Then, based on the input variables $x_1, x_2 \ldots, x_{p-1}$, the probability of an event is shown in below equation

$$p(x_1, x_2, \ldots, x_{p-1}) = f(y) = \frac{e^y}{1+e^y} \quad \text{for} -\infty < y < \infty$$

Logistic Regression: Model Description

- **Logistic Regression equation is comparable to Linear Regression equation** used in linear regression modeling.

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_{p-1} x_{p-1} + \varepsilon$$

- **However, one difference is that the values of y are not directly observed. Only the value of f(y) in terms of success or failure (typically expressed as 1 or 0, respectively) is observed.**

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 \ldots + \beta_{p-1} x_{p-1}$$

$$p(x_1, x_2, \ldots, x_{p-1}) = f(y) = \frac{e^y}{1+e^y} \quad \text{for} -\infty < y < \infty$$

Logistic Regression: Model Description

Customer Churn Example

- A **wireless telecommunications company wants to estimate the probability that a customer will churn** (switch to a different company) **in the next six months**.
- With a reasonably accurate **prediction of a person's likelihood of churning**, the **sales and marketing groups can attempt to retain the customer by offering various incentives**.
- **Data on 8,000 current and prior customers was obtained.**

Logistic Regression: Model Description

- The variables collected for each customer follow:
  - **Age (years)**
  - **Married(true/false)**
  - **Duration as a customer (years)**
  - **Churned_ con tact s (count)**-Number of the customer's contacts that have churned (count)
  - **Churned (true/false)**-Whether the customer churned

- After **analyzing the data and fitting a logistic regression model**, **Age** and **Churned_ contacts** were **selected as the best predictor variables**. The below equation provides the estimated model parameters.

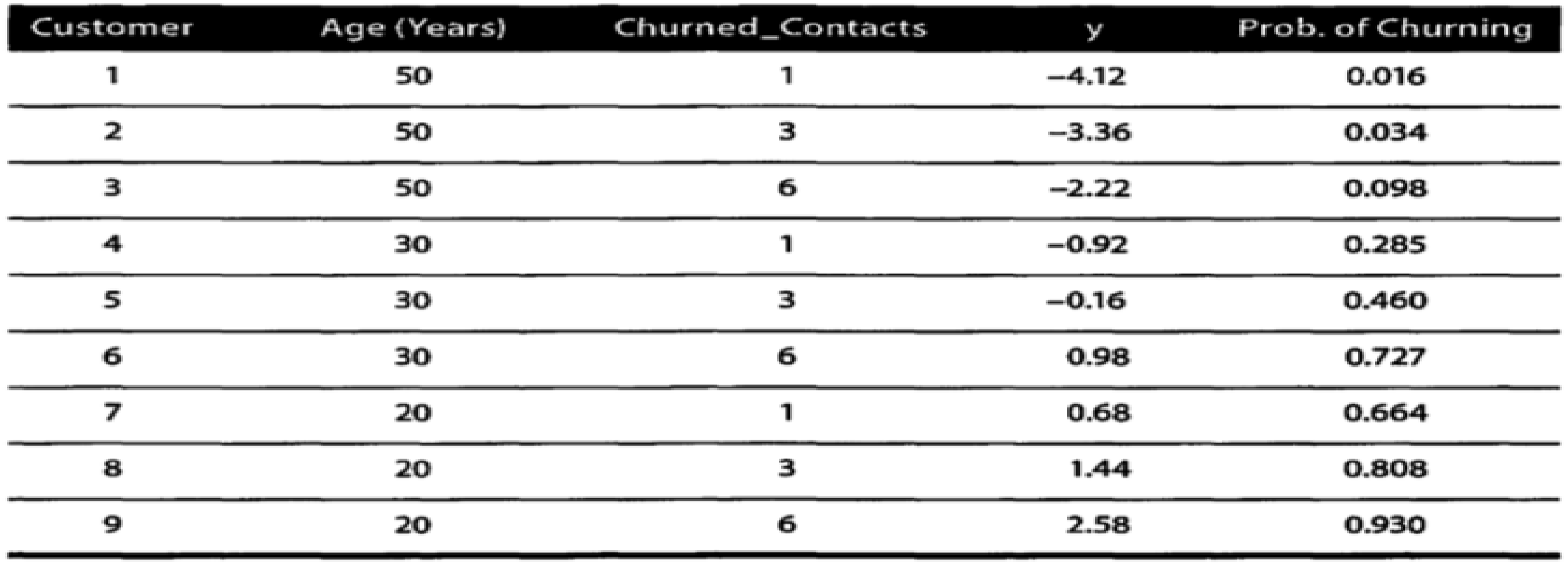
$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 \ldots + \beta_{p-1} x_{p-1}$$

y = 3.50 - 0.16 *Age + 0.38 *Churned_ contacts

Logistic Regression

- Using the fitted model from equation, below table provides the probability of a customer churning based on the customer's age and the number of churned contacts.

TABLE *Estimated Churn Probabilities*



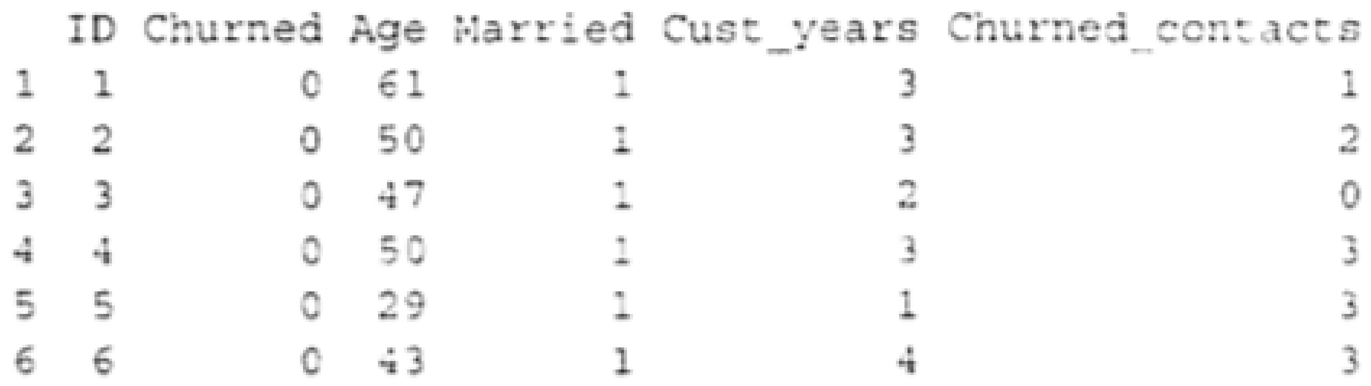
Customer	Age (Years)	Churned_Contacts	y	Prob. of Churning
1	50	1	−4.12	0.016
2	50	3	−3.36	0.034
3	50	6	−2.22	0.098
4	30	1	−0.92	0.285
5	30	3	−0.16	0.460
6	30	6	0.98	0.727
7	20	1	0.68	0.664
8	20	3	1.44	0.808
9	20	6	2.58	0.930

- Based on the fitted model, there is a 93% chance that a 20-year-old customer who has had six contacts churn will also churn.
- Examining the **sign and values of the estimated coefficients in equation** , it is observed that **as the value of Age increases, the value of y decreases.**
- Thus, the **negative Age coefficient indicates that the probability of churning decreases for an older customer**.

Logistic Regression: Diagnostics

- Take for example, the **churn_ input data frame** (A **wireless telecommunications company wants to estimate the probability that a customer will churn** (switch to a different company) **in the next six months. churn_ input includes 8000 current and prior customers data)**

head(churn_input)



```
  ID Churned Age Married Cust_years Churned_contacts
1  1       0  61       1          3                1
2  2       0  50       1          3                2
3  3       0  47       1          2                0
4  4       0  50       1          3                3
5  5       0  29       1          1                3
6  6       0  43       1          4                3
```

- A **Churned value of 1 indicates that the customer churned**. A **Churned value of 0 indicates that the customer remained as a subscriber**.

- Out of the **8,000 customer records in this dataset, 1,743 customers (-22%) churned**.

sum(churn_input$Churned)

1743

Logistic Regression : Diagnostics

- Using the **Generalized Linear Model function, glm ()**,in R and the **specified family/link**, a **logistic regression model can be applied to the variables in the dataset** as follows:

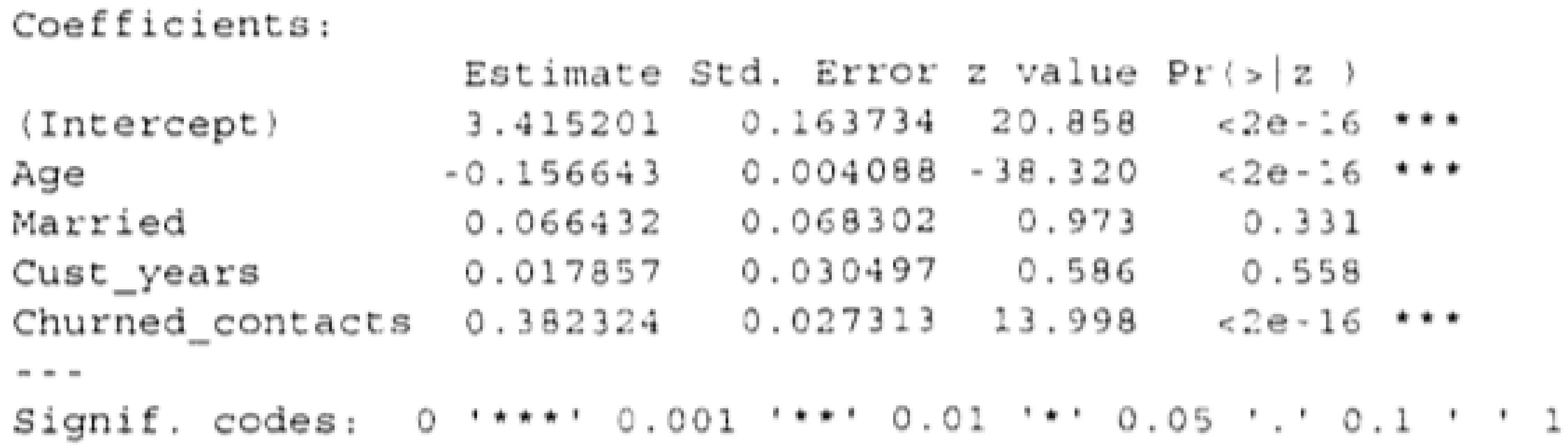
Churn_logistic1 <- glm (Churned ˜ Age + Married + Cust_years + Churned_contacts, data=churn_input, family=binomial(link="logit"))

- ➢ Family objects provide a convenient way to specify the details of the models used by functions such as glm().
- ➢ binomial(link = "logit") →binomial is type of family used to specify the details of the logistic regression model, where reponse from the model to be binary type either 0 or 1, yes/no,pass/fail,defaulter/non-defaulter.
- ➢ link="logit" means use logistic function to fit the model $\mathbf{e^y/(1+ e^y)}$
- ➢ gaussian(link = "identity") → similarly for other type of models

summary(Churn_logisticl)

Logistic Regression : Diagnostics

summary(Churn_logistic1)



```
Coefficients:
                    Estimate Std. Error z value Pr(>|z )
(Intercept)         3.415201   0.163734  20.858   <2e-16 ***
Age                -0.156643   0.004088 -38.320   <2e-16 ***
Married             0.066432   0.068302   0.973    0.331
Cust_years          0.017857   0.030497   0.586    0.558
Churned_contacts    0.382324   0.027313  13.998   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 \ldots + \beta_{p-1} x_{p-1}$ $\quad$ $p(x_1 x_2, \ldots, x_{p-1}) = f(y) = \frac{e^y}{1+e^y} \quad \text{for} -\infty < y < \infty$

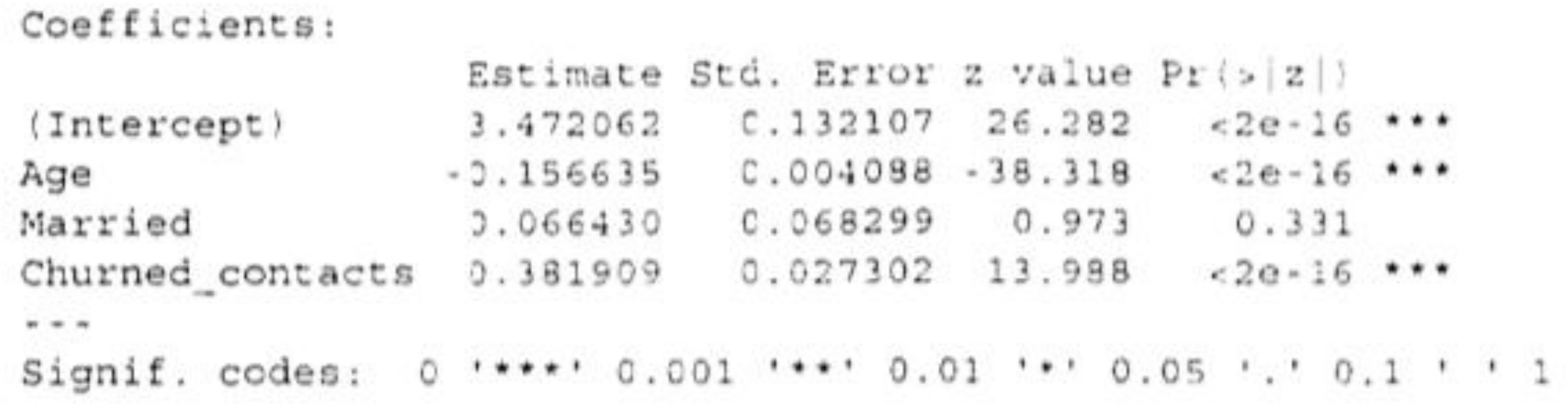
- Such **significant coefficients correspond to small values of Pr (> I z I),** which denote the p-value for the hypothesis test to determine if the estimated model parameter is significantly different from zero.
- **Lowest p-value suggesting a strong association of corresponding input variable.**
- Rerunning this analysis without the **Cust_years variable, which had the largest corresponding p-value**, yields the following result:

Logistic Regression : Diagnostics

- Rerunning this analysis without the **Cust_years variable, which had the largest corresponding p-value**, yields the following result:

Churn_logistic2 <- glm (Churned ~ Age + Married + Churned_contacts, data=churn_input, family=binomial(link="logit"))

summary(Churn_logistic2)



```
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       3.472062   0.132107  26.282   <2e-16 ***
Age              -0.156635   0.004088 -38.318   <2e-16 ***
Married           0.066430   0.068299   0.973    0.331
Churned_contacts  0.381909   0.027302  13.988   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

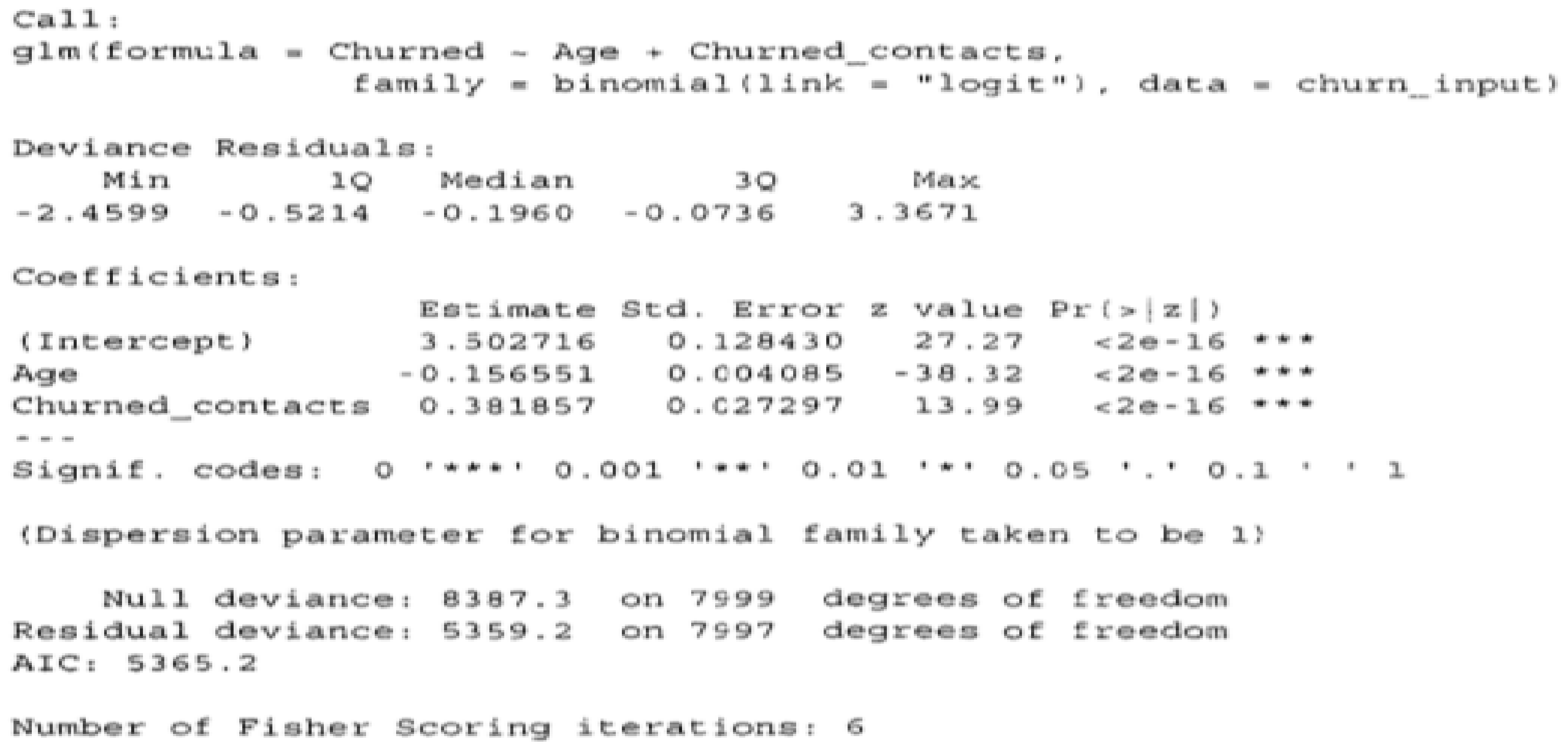
- Because the **p-value for the Married coefficient remains quite large**, the **Married variable is dropped from the model** (means Married field not much associated with the output). So remove Married field.

Logistic Regression : Diagnostics

- The **following R code provides the third and final model**, which **includes only the Age and Churned_ contacts variables**:

```
Churn_logistic3 <- glm (Churned ~ Age + Churned_contacts, data=churn_input,
family=binomial(link="logit"))

summary(Churn_logistic3)
```



```
Call:
glm(formula = Churned ~ Age + Churned_contacts,
               family = binomial(link = "logit"), data = churn_input)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.4599  -0.5214  -0.1960  -0.0736   3.3671

Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       3.502716   0.128430   27.27   <2e-16 ***
Age              -0.156551   0.004085  -38.32   <2e-16 ***
Churned_contacts  0.381857   0.027297   13.99   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 8387.3  on 7999  degrees of freedom
Residual deviance: 5359.2  on 7997  degrees of freedom
AIC: 5365.2

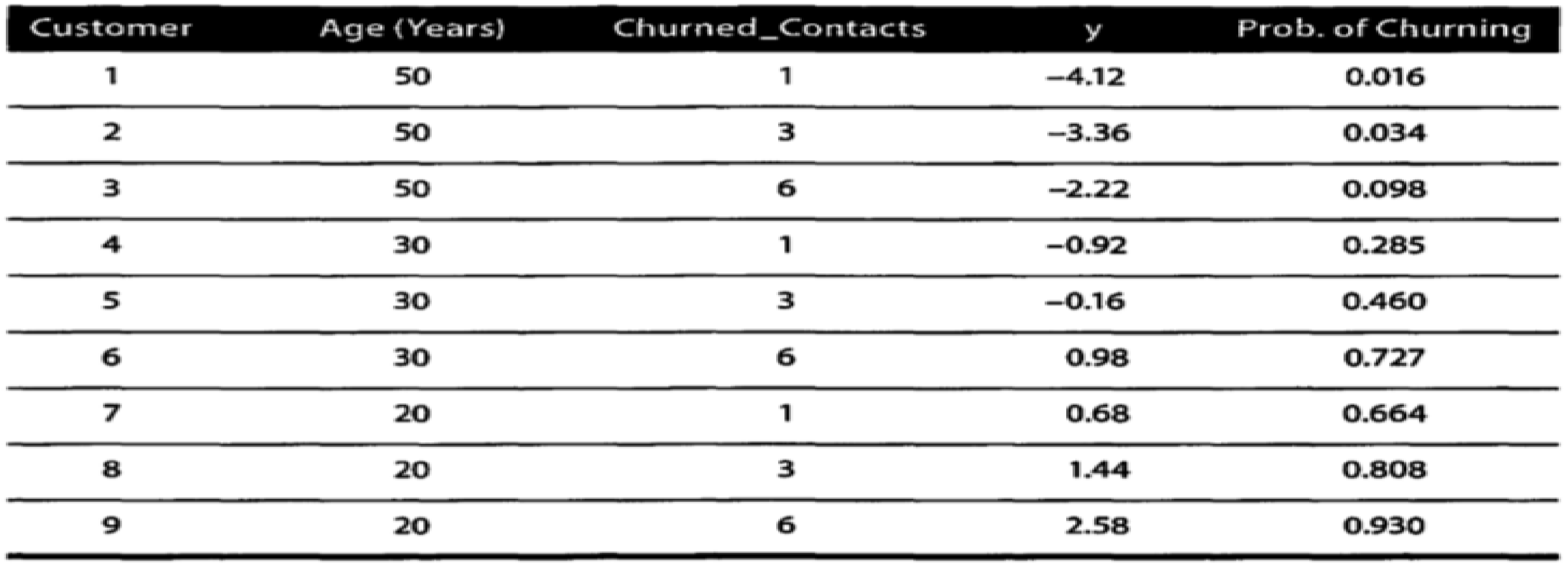
Number of Fisher Scoring iterations: 6
```

Logistic Regression

- The **output offers several values that can be used to evaluate the fitted model**.
- It should be noted that the model parameter estimates correspond to the values provided in Equation 6-11 that were used to construct Table 6-1.

y = 3.50 - 0.16 *Age + 0.38 *Churned_ contacts

TABLE *Estimated Churn Probabilities*



Customer	Age (Years)	Churned_Contacts	y	Prob. of Churning
1	50	1	−4.12	0.016
2	50	3	−3.36	0.034
3	50	6	−2.22	0.098
4	30	1	−0.92	0.285
5	30	3	−0.16	0.460
6	30	6	0.98	0.727
7	20	1	0.68	0.664
8	20	3	1.44	0.808
9	20	6	2.58	0.930

- Based on the fitted model, there is a 93% chance that a 20-year-old customer who has had six contacts churn will also churn.

Receiver Operating Characteristic (ROC) Curve

- **Logistic regression is often used as a classifier to assign class labels to a person, item, or transaction based on the predicted probability** provided by the model.

- In the **Churn example, a customer can be classified with the label called Churn if the logistic model predicts a high probability that the customer will churn. Otherwise**, a **Remain label is assigned to the customer.**

- Commonly, **0.5 is used as the default probability threshold** to distinguish between any two class labels.

- However, **any threshold value can be used depending on the preference to avoid false positives** (for example, to predict Churn when actually the customer will Remain) **or false negatives** (for example, to predict Remain when the customer will actually Churn).

Receiver Operating Characteristic (ROC) Curve

- In general, for two class labels: C and ¬C, , where ¬C, denotes "not C," some working definitions and formulas follow:

  - **True Positive:** predict C, when actually C
  - **True Negative:** predict ¬C, when actually ¬C
  - **False Positive:** predict C, when actually ¬C
  - **False Negative:** predict ¬C, when actually C

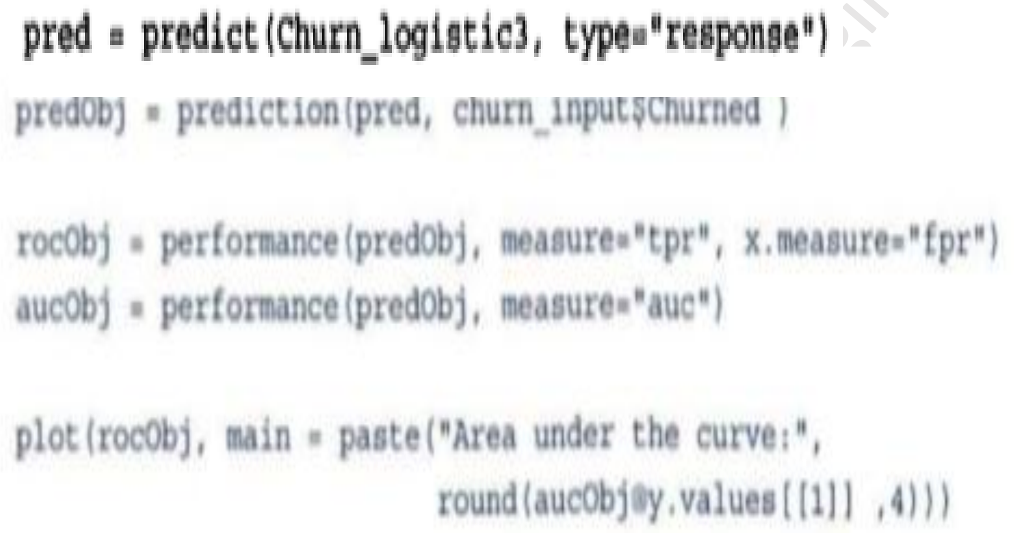
$$\text{False Positive Rate (FPR)} = \frac{\textit{\# of false positives}}{\textit{\# of negatives}}$$

$$\text{True Positive : Rate (TPR)} = \frac{\textit{\# of true positives}}{\textit{\# of positives}}$$

Receiver Operating Characteristic (ROC) Curve

- The plot of the True Positive Rate (TPR) against the False Positive Rate (FPR) is known as the **Receiver Operating Characteristic (ROC) curve**.

- Using the ROCR package, the following R commands generate the ROC curve for the Churn example:



```
pred = predict(Churn_logistic3, type="response")
predObj = prediction(pred, churn_input$Churned )

rocObj = performance(predObj, measure="tpr", x.measure="fpr")
aucObj = performance(predObj, measure="auc")

plot(rocObj, main = paste("Area under the curve:",
                          round(aucObj@y.values[[1]] ,4)))
```

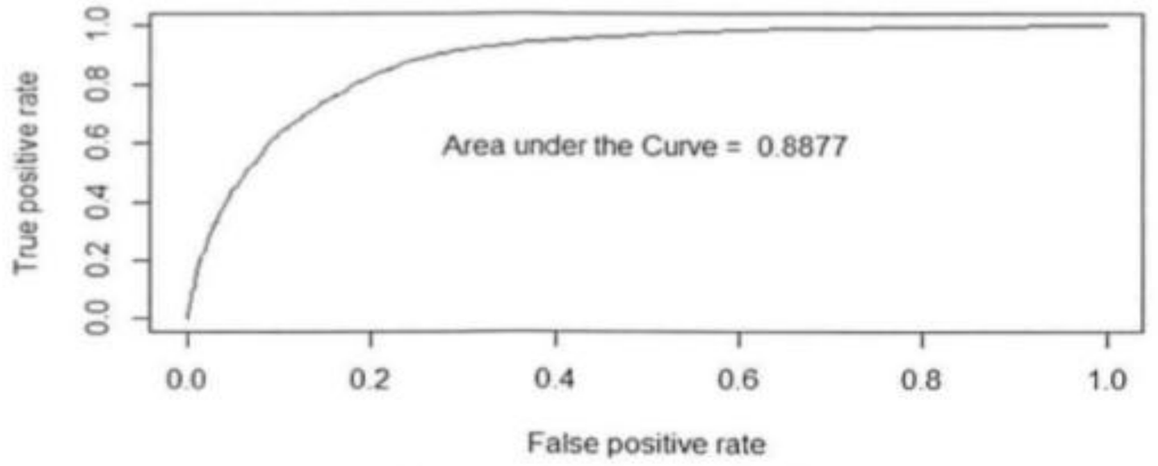
Receiver Operating Characteristic (ROC) Curve

- The **usefulness of this plot** as shown in below figure is that **the preferred outcome of a classifier is to have a low FPR and a high TPR.**

- So, **when moving from left to right on the FPR axis**, a good model/ classifier has the **TPR rapidly approach values near 1, with only a small change in FPR**.

- The closer the ROC curve tracks along the vertical axis and approaches the upper-left hand of the plot, near the point (0,1), the better the model/classifier performs.

- Thus, **a useful metric is to compute the area under the ROC curve (AUC).**



ROC curve for the churn example

Text analysis

- **Text analysis**, sometimes called **Text Analytics**, refers to the **representation**, **processing**, and **modeling** of **textual data** to **derive useful insights**.

- An **important component of text analysis is text mining**, the process of **discovering relationships** and **interesting patterns in large text collections**.

- **Text analysis is suffers** from the curse of **high dimensionality**.

For E.g.

- **Popular children's book Green Eggs and Ham. Author Theodor Geisel was challenged to write an entire book with just 50 distinct words.**

- **He responded with the book Green Eggs and Ham, which contains 804 total words, only 50 of them distinct.**

- **There's a substantial amount of repetition in the book. Yet, as repetitive as the book is, modeling it as a vector of counts, or features, for each distinct word still results in a 50-dimension problem.**

Text analysis

- Text analysis often deals with **textual data that is far more complex**.

  For E.g.

  - **Google n-gram** corpus contains **one trillion words from publicly accessible web pages**.
  - **Out of the one trillion words** in the Google n-gram corpus, there **might be one million distinct words**, which would **correspond to one million dimensions**.

- The **high dimensionality of text is an important issue**, and it has a direct impact on the **complexities of many text analysis tasks**.

- **Another major challenge with text analysis is** that most of the time the **text is not structured**.

- This may include **unstructured data (Text), semi-structured (HTML page) or quasi-structured (Server Log, which web pages visited, in what order, how long or reviews about a specific product)**.

Text Analysis Steps

- A **Text Analysis problem usually consists of three important steps**

  - **Parsing**
  - **Search and Retrieval**
  - **Text Mining**

Parsing

- **Parsing is the process that takes unstructured text** and **imposes a structure for further analysis**.
- The **unstructured text** could be a **plain text file**, a **weblog**, an **Extensible Markup Language (XML) file**, a **HyperText Markup Language (HTML) file**, or a **Word document**. (XML is a markup language which is designed to store data. HTML is the markup language which helps you to create and design web content.)
- **Parsing deconstructs the provided text** and **renders it in a more structured way for the subsequent steps.**

Text analysis

Search and Retrieval

- **Search and Retrieval is the identification of the documents in a corpus** that contain search items such as **specific words, phrases, topics, or entities like people or organizations**. (Filtering→ taking required documents)
- These **search items are generally** called **key terms**.

Text Mining

- **Text mining** uses the terms and indexes produced by the prior two steps to **discover meaningful insights pertaining to domains or problems of interest.**
- With the proper representation of the text, **many of the techniques such as clustering and classification**, can be adapted to text mining.
- For example, the **k-means can be modified to cluster text documents into groups, where each group represents a collection of documents with a similar topic.** (Clustering customers review documents based on region)

Text Analysis Steps

- **Classification tasks such as sentiment analysis and spam filtering are prominent use cases for the naive Bayes classifier.** (Classify based on sentimental keywords)
- Note that, **in reality, all three steps do not have to be present in a text analysis project**.
- **If the goal is to construct a corpus** or **provide a catalog service** (just preprocessing→ prepare structured catalog, converting one sentence into other forms for further analysis), for example, the focus would be the **parsing task using one or more text preprocessing techniques**, such as **part-of-speech (POS) tagging**, named entity recognition, **lemmatization, or stemming.**
- Furthermore, the **three tasks do not have to be sequential**. Sometimes their orders might **even look like a tree**. For example, one could use **parsing to build a data store** and **choose to either search and retrieve** the related documents or **use text mining on the entire data store to gain insights**.

Text Analysis Steps

Part-of-Speech (POS) Tagging, Lemmatization, and Stemming

- The **goal of POS tagging is to build a model whose input is a sentence**, such as:

  he saw a fox

- and whose output is a tag sequence. Each tag marks the POS for the corresponding word, such as:

  PRP VBD DT NN

- according to the Penn Treebank POS tags.
- Therefore, the **four words are mapped to pronoun (personal), verb (past tense). determiner, and noun (singular), respectively**.

Text Analysis Steps

Part-of-Speech (POS) Tagging, Lemmatization, and Stemming

- **Both lemmatization and stemming are techniques to reduce the number of dimensions** and **reduce inflections or variant forms to the base form** to more accurately measure the number of times each word appears. (Lemma→remove inflectional endings only and to return the base or dictionary form of a word)

- With the use of a given dictionary, lemmatization finds the correct dictionary base form of a word. For example, given the sentence:

  obesity causes many problems

- the output of lemmatization would be:

  obesity cause many problem

Text Analysis Steps

Part-of-Speech (POS) Tagging, Lemmatization, and Stemming

- Different from lemmatization, **stemming refers to a crude process of stripping affixes based on a set of heuristics** with the hope of correctly achieving the goal **to reduce inflections or variant forms.** (Synonyms of a word→ all represents same stem, Eg: Happy→ Cheerful, Joyful→ convert to the same base or root word in dictionary. search engines treat words with the same stem as synonyms)
- After the process, **words are stripped to become stems**. A **stem is not necessarily an actual word defined in the natural language, but it is sufficient to differentiate itself from the stems of other words**.
- A well-known rule-based stemming algorithm is **Porter's stemming algorithm**. It **defines a set of production rules to iteratively transform words into their stems**. For the sentence shown previously:

  obesity causes many problems
- the **output of Porter's stemming algorithm** is:

  obes caus mani problem

A Text Analysis Example

- To describe the **three text analysis steps, consider the fictitious company ACME**, **maker of two products: bPhone and bEbook.**

- **ACME is in strong competition with other companies that manufacture and sell similar products**.

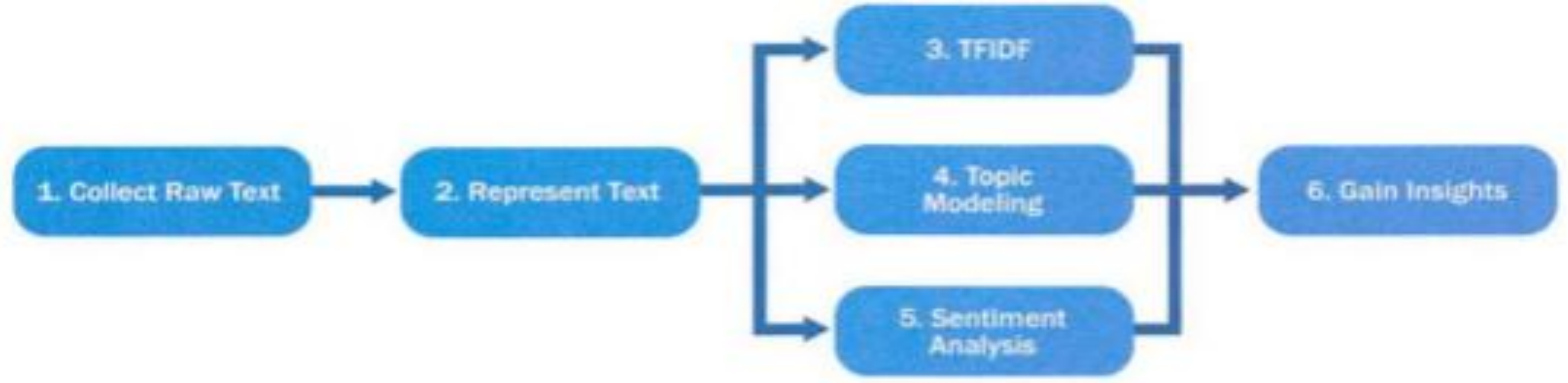
- **To succeed, ACME needs to produce excellent phones and eBook readers and increase sales**.

- One of the ways **the company does this is to monitor what is being said about ACME products in social media** such as **Twitter** and **Facebook**, and **popular review sites**, such as **Amazon** and **ConsumerReports**.

A Text Analysis Example

- It wants to answer questions such as these.
  - ➢ **Are people mentioning its products?**
  - ➢ **What is being said? Are the products seen as good or bad? If people think an ACME product is bad, why? For example, are they complaining about the battery life of the bPhone, or the response time in their bEbook?**

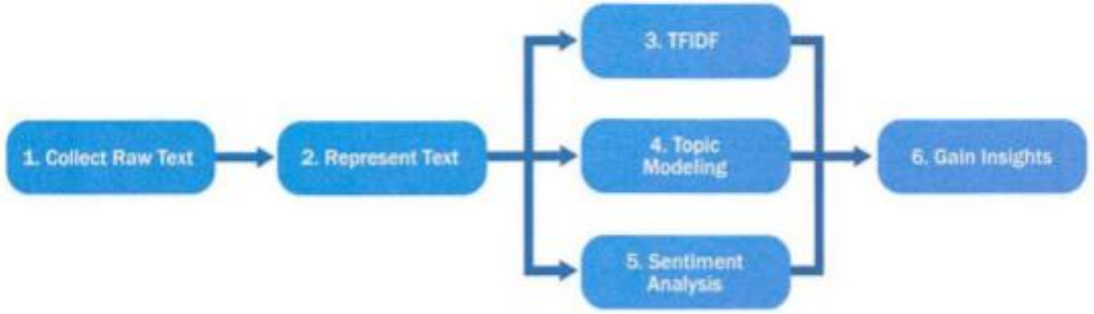
- **The text analysis process carrying out by the ACME company is as shown in the below figure**



ACME's Text Analysis Process

A Text Analysis Example

1) Collect Raw Text



ACME's Text Analysis Process

- **Collect raw text**. **This corresponds to Phase 1 and Phase 2 of the Data Analytic Lifecycle**.

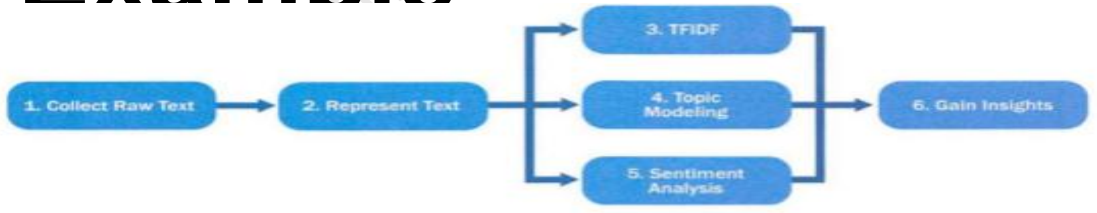
- In this step, the **Data Science team at ACME monitors websites** for references to specific products. The websites may include **social media and review sites.**

- The **team could interact with social network, use product names as keywords to get the raw data**. **Regular expressions are commonly used in this case to identify text** that matches certain patterns.(Use regular expression to identify sentences that includes product name)

- **Additional filters can be applied to the raw data for a more focused study**. **For E.g., only retrieving the reviews originating in New York instead of the entire United States would allow ACME to conduct regional studies on its products.**

A Text Analysis Example

2) Represent Text

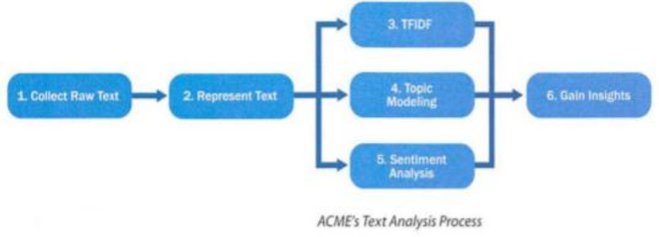


ACME's Text Analysis Process

- **Convert each review into a suitable document** representation **with proper indices**, and **build a corpus based on these indexed reviews**.

- **This step corresponds to Phases 2 and 3 of the Data Analytic Lifecycle**.

A Text Analysis Exampl



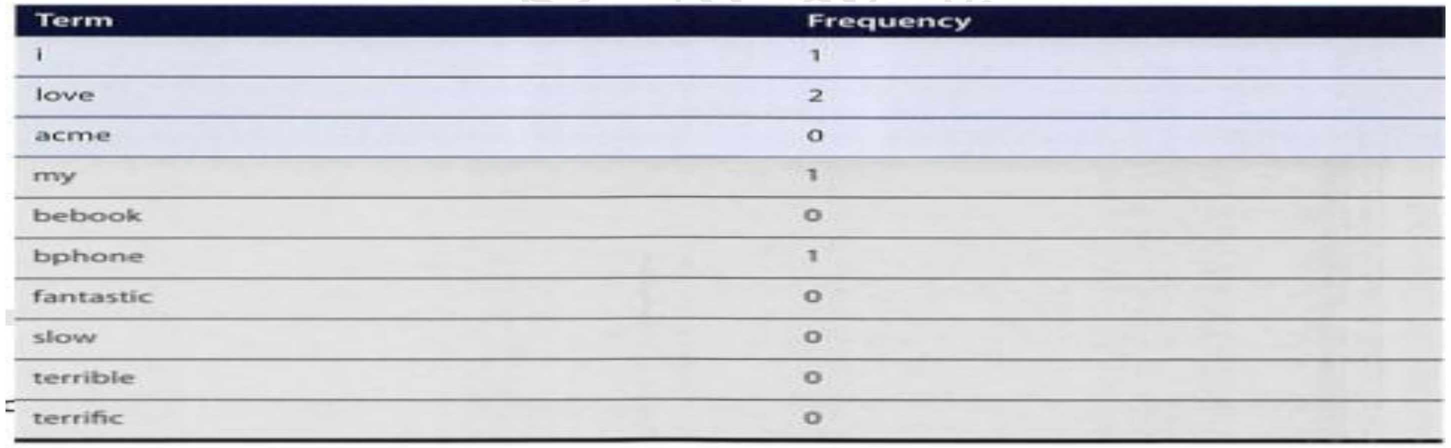
ACME's Text Analysis Process

3) TFIDF (Term Frequency-Inverse Document Frequency)

- **Compute the usefulness of each word in the reviews using methods such as TFIDF.**
- **To understand how the term frequency is computed, consider a bag-of-words vector space of 10 words:**

  i, love, acme, my, bebook, bphone, fantastic, slow, terrible, and terrific.

- **Given the text "I love LOVE my bPhone" extracted from the RSS feed.** **(Detail explanation abt TFIDF in section 9.5→not in syllabus)**
- **Below table shows its corresponding term frequency vector after case folding and tokenization.**

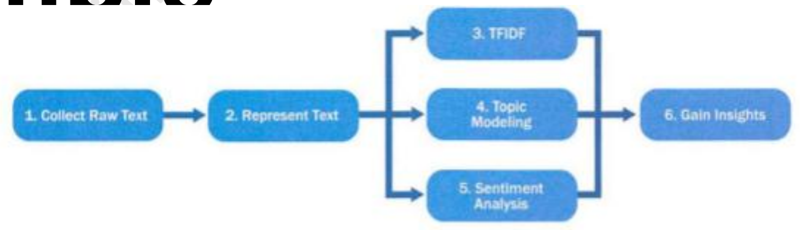


Term	Frequency
i	1
love	2
acme	0
my	1
bebook	0
bphone	1
fantastic	0
slow	0
terrible	0
terrific	0

- **This and the following two steps correspond to Phases 3 through 5 of the Data Analytic Lifecycle.**

A Text Analysis Example

4) Topic Modeling



ACME's Text Analysis Process

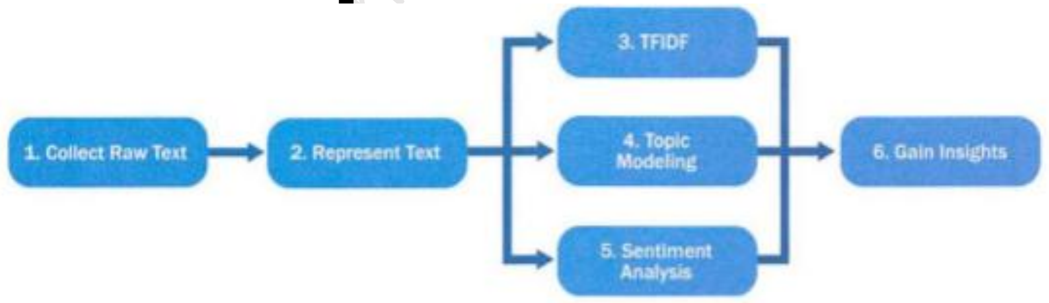
- **Categorize documents by topics.**
- **This can be achieved through topic models (such as latent Dirichlet allocation).**

5) Sentimental Analysis

- Many product **review sites provide ratings of a product with each review**. If **such information is not available, techniques like sentiment analysis can be used on the textual data to infer the underlying sentiments.**
- **Determine sentiments of the reviews**.
- **Identify whether the reviews are positive or negative**.
- **People can express many emotions**. To keep the process simple, **ACME considers sentiments as positive, neutral, or negative.**

A Text Analysis Example

6) Gain Insights



ACME's Text Analysis Process

- **Review the results and gain greater insights**.
- **This step corresponds to Phase 5 and 6 of the Data Analytic Lifecycle**.
- **Find out what exactly makes people love or hate a product**.
- Use **one or more visualization techniques to report the findings**. (how many positive, how many negative, how many neutral)
- Test the soundness of the **conclusions** and **operationalize the findings if applicable**.

Collecting Raw Text

- **Data Science team starts collecting the data for data analysis.**
- The **user-generated contents being collected could be related articles** from
  - **Social Media Posts**
  - **News Portals and Blogs**
  - **Online Shops or Reviews Sites**
- **Regardless of where the data comes from**, it's likely that the **team would deal with semi-structured data such as HTML web pages, Really Simple Syndication (RSS) feeds, XML, or JavaScript Object Notation (JSON) files.**

Collecting Raw Text

Social Media Posts

- **Many websites and services offer public APIs for third-party developers to access their data**. For example, the **Twitter API allows developers to retrieve public Twitter posts that contain the keywords bPhone or bEbook.**

- The fetched **tweets are in the JSON format**.

News Portals and Blogs

- Many **news portals and blogs provide data feeds that are in an open standard format, such as RSS or XML.**

Collecting Raw Text

Online Shops or Reviews Sites

- **If the plan is to collect user comments on ACME's products from online shops and review sites where APIs or data feeds are not provided**, the **team may have to write web scrapers to parse web pages** and automatically **extract the interesting data from those HTML files**.

- A **web scraper is a software program** (bot) that **systematically browses the World Wide Web, downloads web pages, extracts useful information, and stores it somewhere for further study**. (in data store for further analysis)

- **Unfortunately, it is nearly impossible to write a one-size-fits-all web scraper**. This is **because websites like online shops and review sites have different structures.**

- It is common to **customize a web scraper for a specific website**. In addition, the **website formats can change over time, which requires the web scraper to be updated every now and then**.

Collecting Raw Text

- It is common to **customize a web scraper for a specific website**. In addition, the **website formats can change over time, which requires the web scraper to be updated every now and then**.

- **To build a web scraper for a specific website, one must study the HTML source code of its web pages** (HTML format followed by the website) to find patterns before extracting any useful content.

- The **team can then construct the web scraper** based on the identified patterns. The **scraper can use the curl tool** to fetch **HTML source code given specific URLs**, use **XPath** and **regular expressions to select and extract the data that match the patterns**, and **write them into a data store**.

Representing Text

- Read from text book

UNIT-4

Multiple Plots in One Window

- It is **sometimes useful to create several graphs in one Window**.
- This **could be because they are closely related** and you **want to display them together**.
- We can **split a graphical window into sections** and **draw the graph into the sections directly from R**.
- **Plot window can be split into equal sections using the following commands**

mfrow() and mfcol()

- The **mfrow()** and **mfcol() instruction requires two values**, the **number of rows and number of columns** required

mfrow=c(nrows,ncols)

mfcol=c(nrows,ncols)

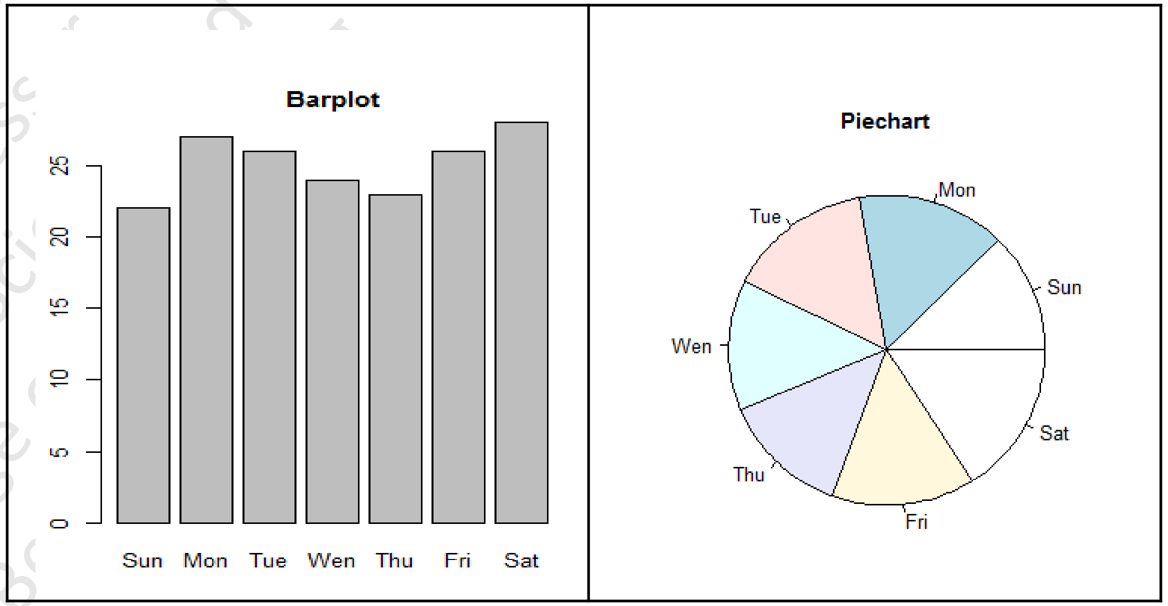
Multiple Plots in One Window

- We **can put multiple graphs in a single plot window** by setting some graphical parameters **with the help of par() function. The par() function includes mfrow( ) or mfcol( ) as a parameter.**

For Eg:

>max.temp # a vector used for plotting

Sun	Mon	Tue	Wed	Thu	Fri	Sat
22	27	26	24	23	26	28



par(mfrow=c(1,2)) # set the plotting area into a 1*2 array

barplot(max.temp, main="Barplot")

pie(max.temp, main="Piechart", radius=1)

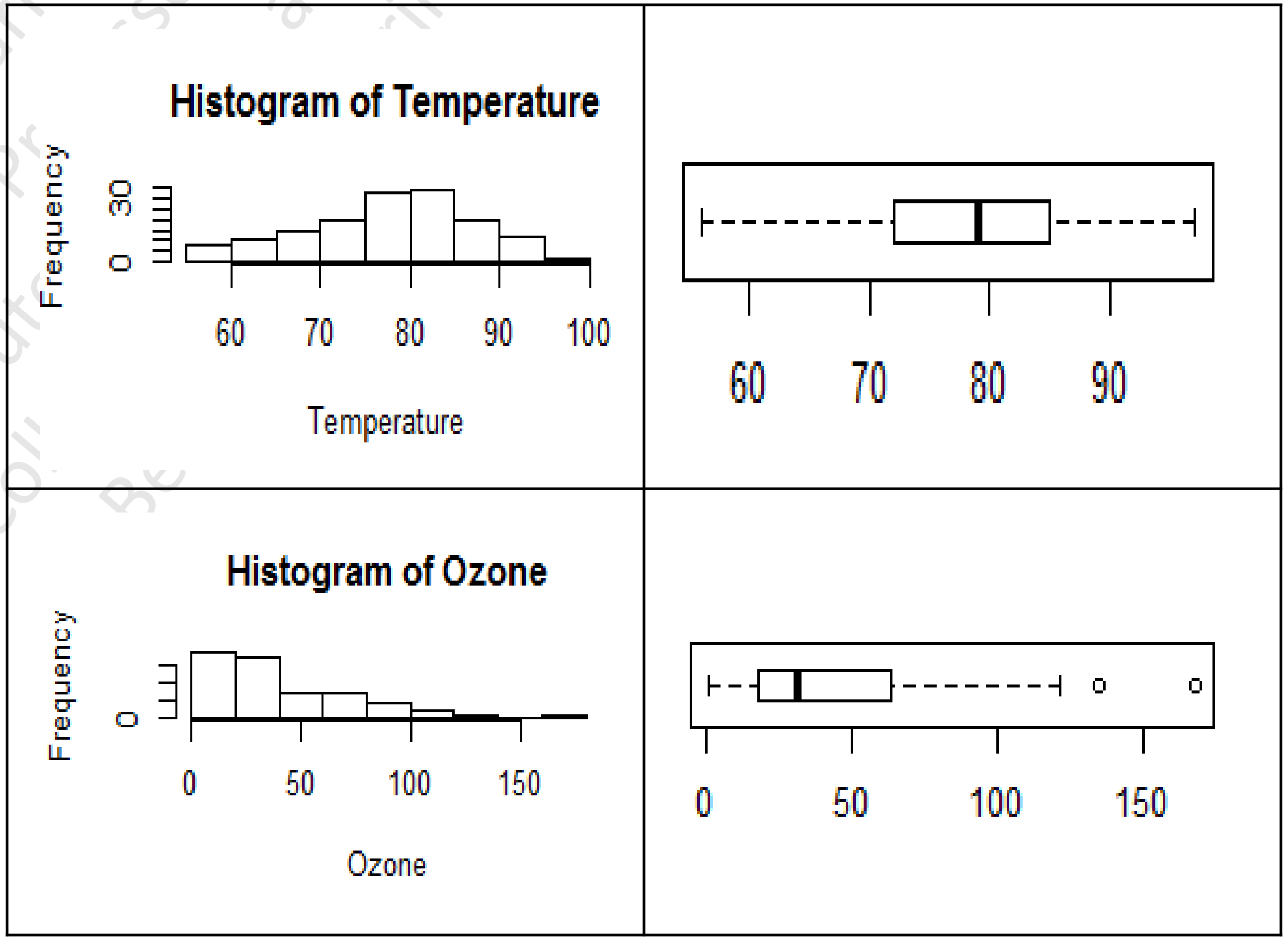
Multiple Plots in One Window

- This **same phenomenon can be achieved with the graphical parameter mfcol( ).**

- **mfrow fills in the subplot region with the graphs row wise and mfcol fills in the subplot region with the graphs column wise**.

For Eg:

```
Temperature <- airquality$Temp
Ozone <- airquality$Ozone
par(mfrow=c(2,2))
hist(Temperature)
boxplot(Temperature, horizontal=TRUE)
hist(Ozone)
boxplot(Ozone, horizontal=TRUE)
```



Multiple Plots in One Window

Same **plot with the change par(mfcol = c(2, 2))** would look as follows. Note that only the ordering of the subplot is different.

For Eg:

```
Temperature <- airquality$Temp

Ozone <- airquality$Ozone

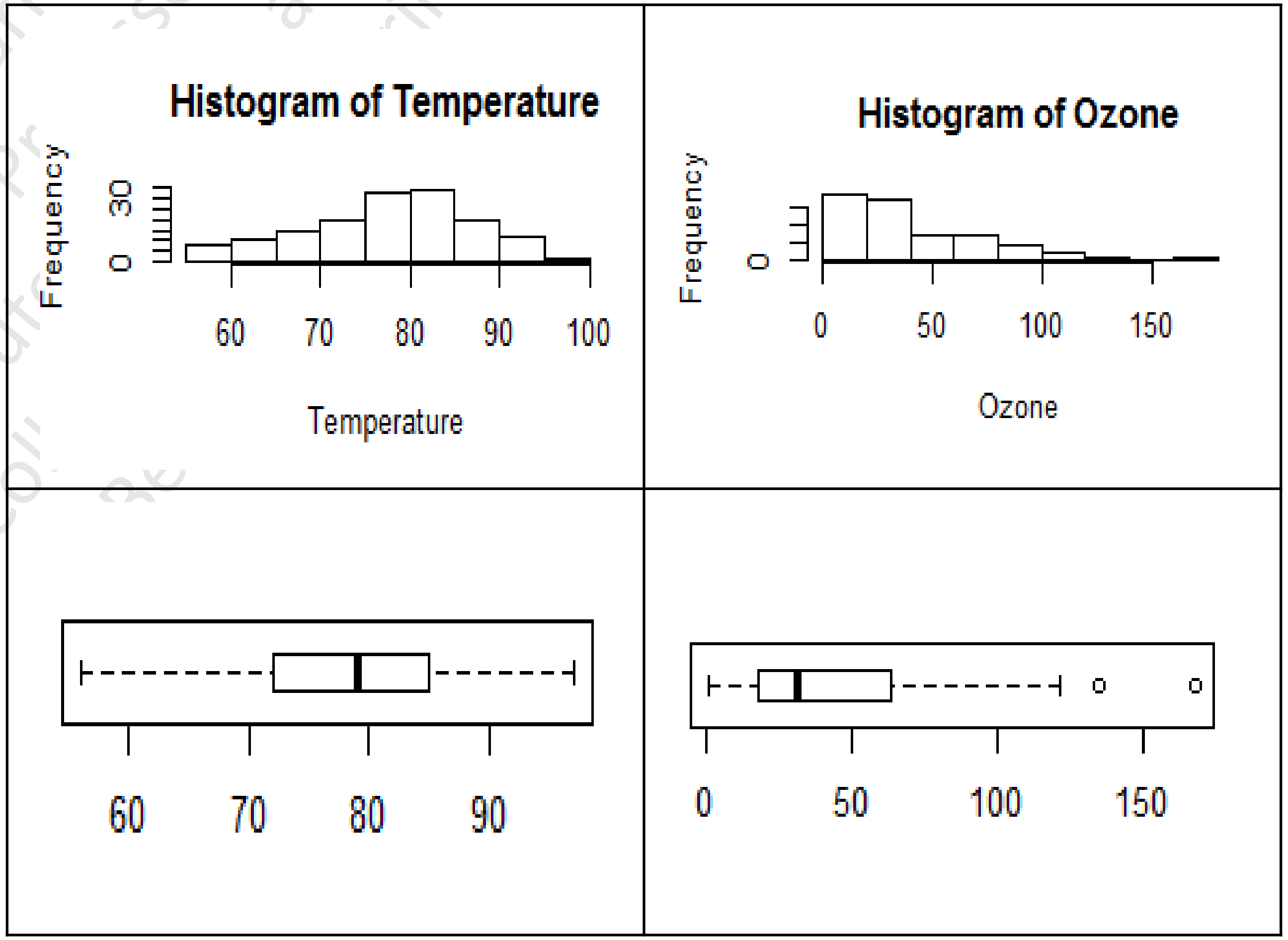
par(mfcol=c(2,2))

hist(Temperature)

boxplot(Temperature, horizontal=TRUE)

hist(Ozone)

boxplot(Ozone, horizontal=TRUE)
```



Multiple Plots in One Window

- We can **combine multiple plots into one overall graph using another function layout( ).**
- **The layout( ) function has the form:**

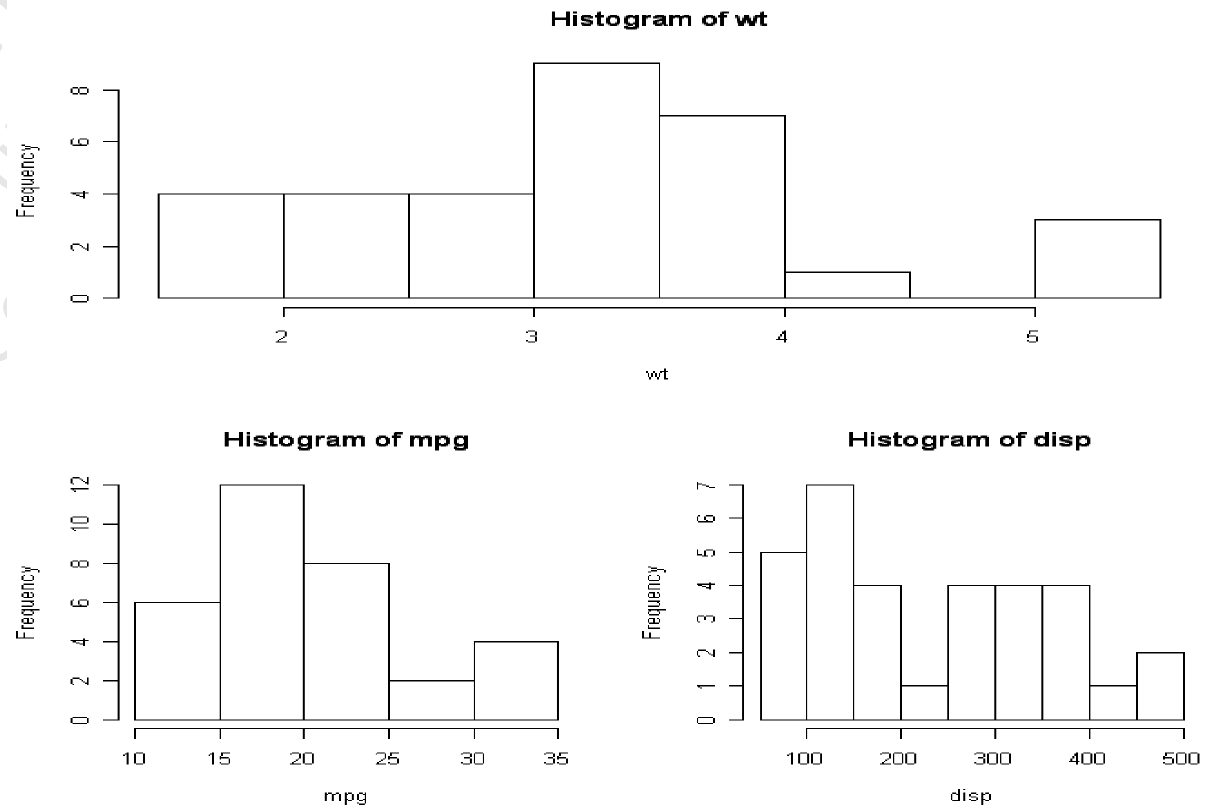
layout(mat)

Where mat is a matrix object specifying the location of the N figures to plot.

For Eg:

# One figure in row 1 and two figures in row 2

```
attach(mtcars)
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE))
hist(wt)
hist(mpg)
hist(disp)
```



Multiple Plots in One Window

- Optionally, **we can include widths= and heights= options in the layout( ) function to control the size of each figure** more precisely. These options have the form

  widths= a vector of values for the widths of columns

  heights= a vector of values for the heights of rows.

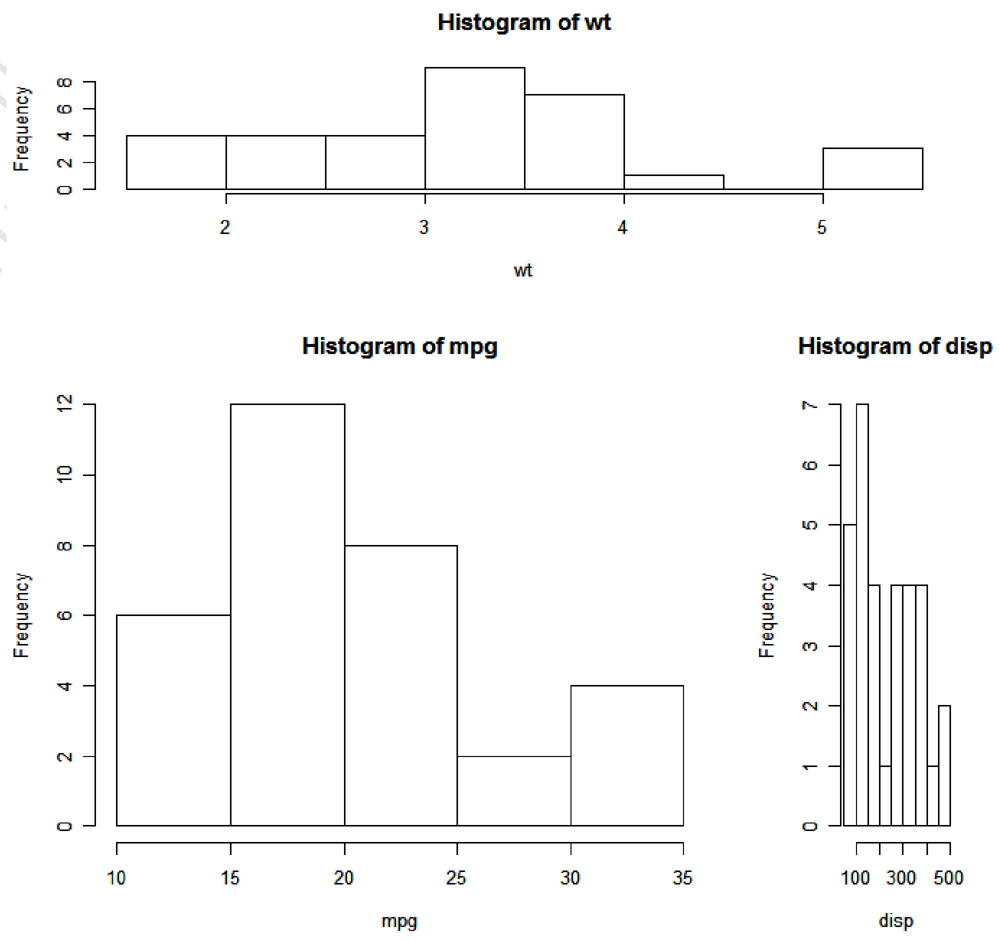
  For Eg:

2 Rows and 2 Columns→ One figure in row 1 and two figures in row 2

# row 1 is 1/3 the height of row 2

# column 2 is 1/4 the width of the column 1

```
attach(mtcars)
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE),
widths=c(3,1), heights=c(1,2)) ; (3/4+1/4) (1/3+2/3)
hist(wt)
hist(mpg)
hist(disp)
```



Multiple Plots in One Window

To skip a plot in par()

- **While plotting multiple plots using par(),** sometimes we want to **skip a plot in the matrix and leave a blank space in its location**.
- This can be achieved using the call to **plot.new()** function.

For Eg:

- In a **2x3 matrix of plots**, if we want to **skip the 5th plot** and **leave a blank** there, **call the 4 plots** as usual, and **during fifth plot, just call the plot.new() function**. After this, **plot the sixth graph**. This **leaves a blank at the position of fifth plot**.
- **In the following example, we set the window to four sections and draw plots by column.**

```
opt=par(mfcol=c(2,2))
plot(Length~BOD,data=mf, main='plot1')
plot.new()
plot.new()
plot(Length~No3,data=mf, main='plot4')
par(opt)
```

Multiple Plots in One Window

Example Program for multiple plots in one window

```
Length<-c(20,21,22,23,21,20)

Speed<-c(12,14,12,16,20,21)

Algae<-c(40,45,45,80,75,65)

NO3<-c(2.25,2.15,1.75,1.95,1.95,2.75)

BOD<-c(200,180,135,120,110,120)

mf<-data.frame(Length,Speed,Algae,NO3,BOD)

mf

Opt=par(mfrow=c(2,2))

plot(Length ~ BOD,data=mf,main='plot1')

plot(Length ~ Algae,data=mf,main='plot2')

plot(Length ~ Speed,data=mf, main='plot3')

plot(Length ~ NO3,data=mf,main='plot4')
```

Matrix Plot

- **Matrix plot plots the columns of a matrix against other columns**.
- **Matplot() function** in R can be used **for quickly plotting multiple sets of observations from the same object**, particularly from a **matrix**, on the same graph. i.e, Matplot( ) function plots the columns of a matrix individually as a function of x.

For E.g.: Consider a Matrix containing four sets of random draws, each with a different mean as given below

```
xmat <- cbind(rnorm(100, -3), rnorm(100, -1), rnorm(100, 1), rnorm(100, 3))
head(xmat)
#           [,1]        [,2]       [,3]     [,4]
# [1,] -3.072793 -2.53111494  0.6168063 3.780465
# [2,] -3.702545 -1.42789347 -0.2197196 2.478416
# [3,] -2.890698 -1.88476126  1.9586467 5.268474
# [4,] -3.431133 -2.02626870  1.1153643 3.170689
# [5,] -4.532925  0.02164187  0.9783948 3.162121
# [6,] -2.169391 -1.42699116  0.3214854 4.480305
```

Matrix Plot

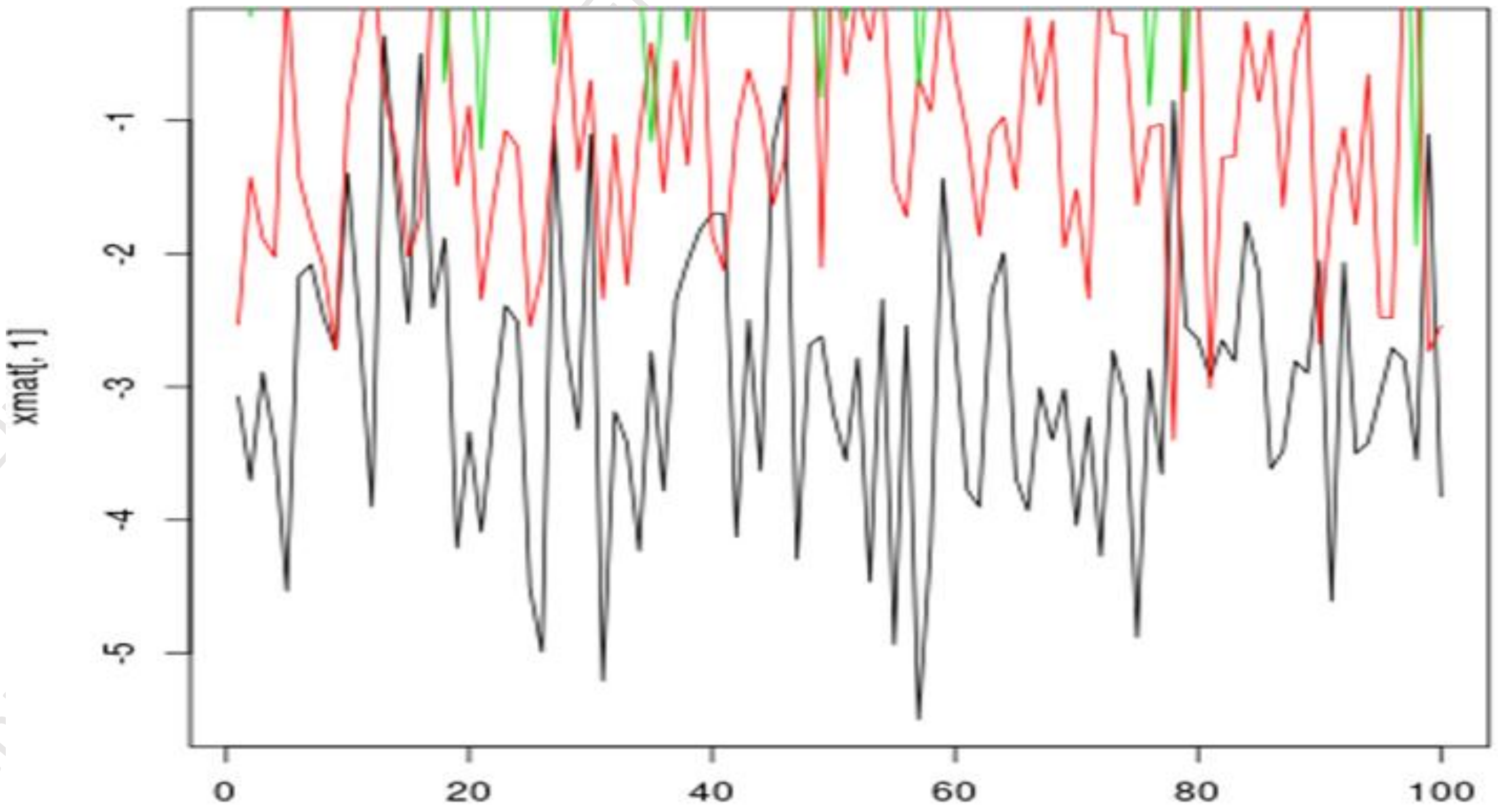
- One way to plot all of these observations on the same graph is to do **one plot( ) function call followed by three more points ( ) function calls** or **lines( ) function calls**.

```
plot(xmat[,1], type = 'l')

lines(xmat[,2], col = 'red')

lines(xmat[,3], col = 'green')

lines(xmat[,4], col = 'blue’)
```

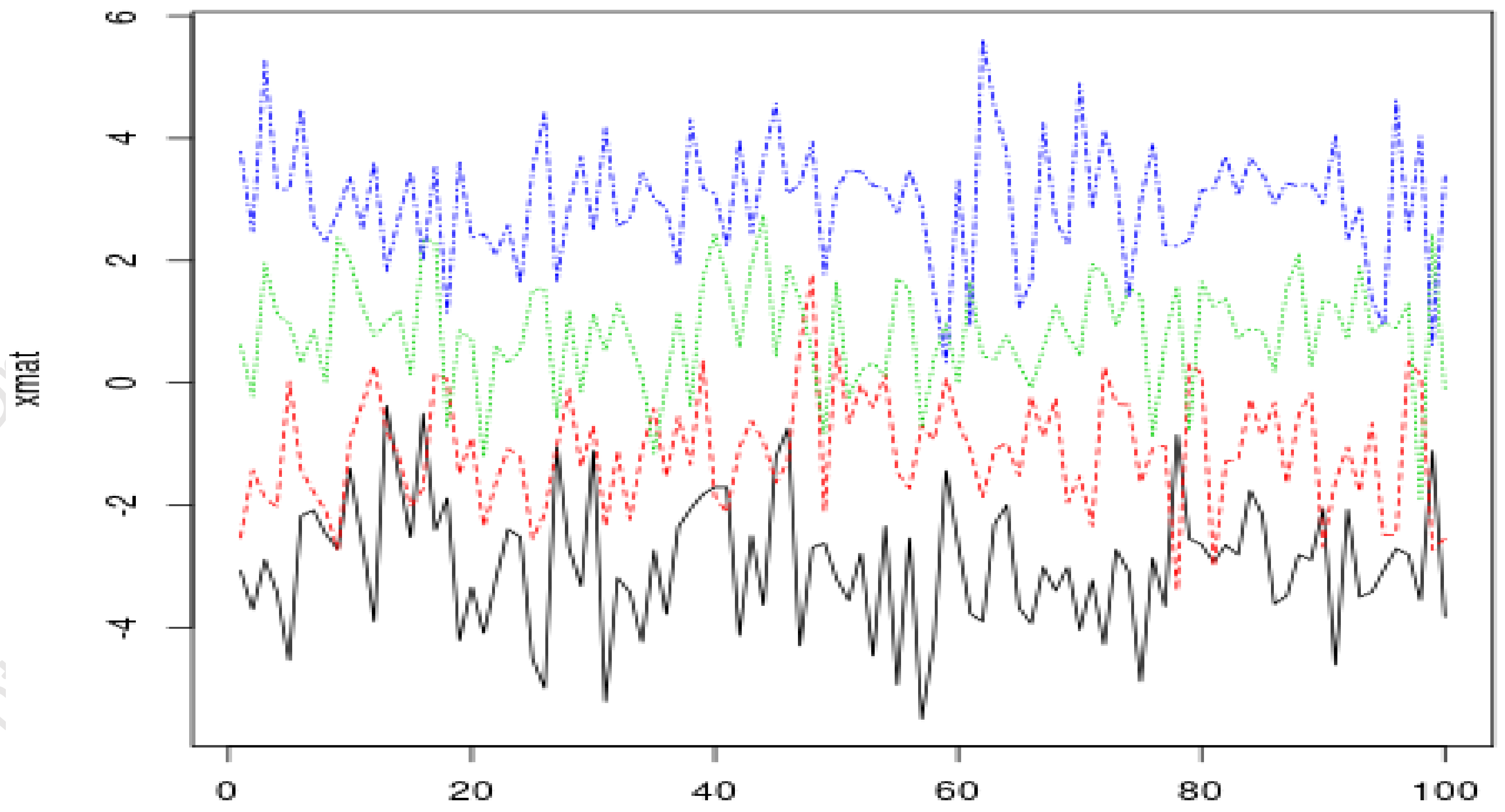


- This is **both tedious**, and **causes problems** because, among other things, **by default the axis limits are fixed by plot to fit only the first column.** (Observe in the graph→ Y-axis limits from -5 to -1 so, 4th column value in the matrix which contain positive values not able to see in the graph)

Matrix Plot

- **Much more convenient in this situation is to use the matplot( ) function**, which only **requires one call and automatically takes care of axis limits and changing the aesthetics for each column to make them distinguishable.**

matplot(xmat, type = 'l')

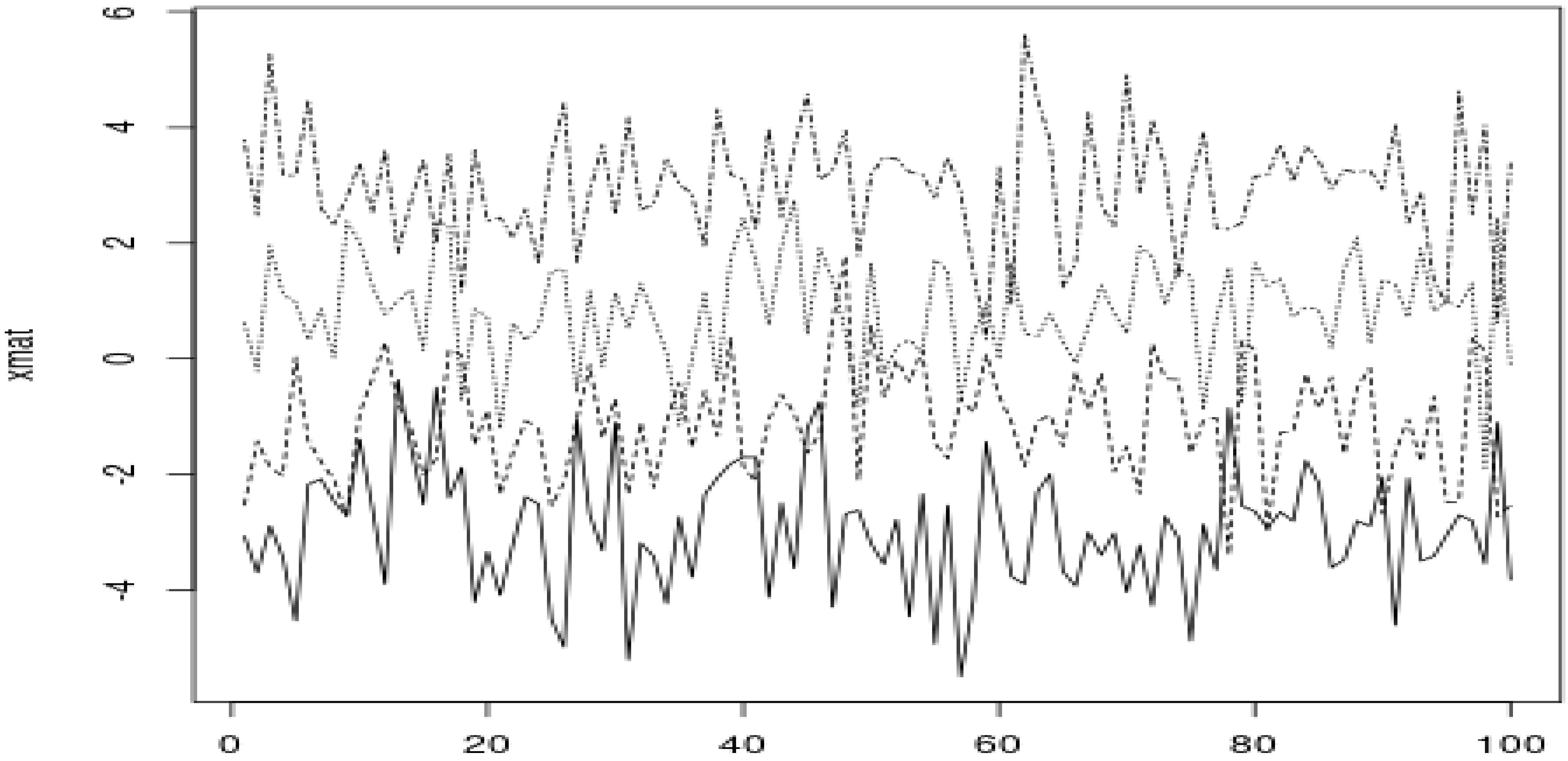


- Note that, **by default, matplot( ) function varies both color (col) and linetype (lty)**

Matrix Plot

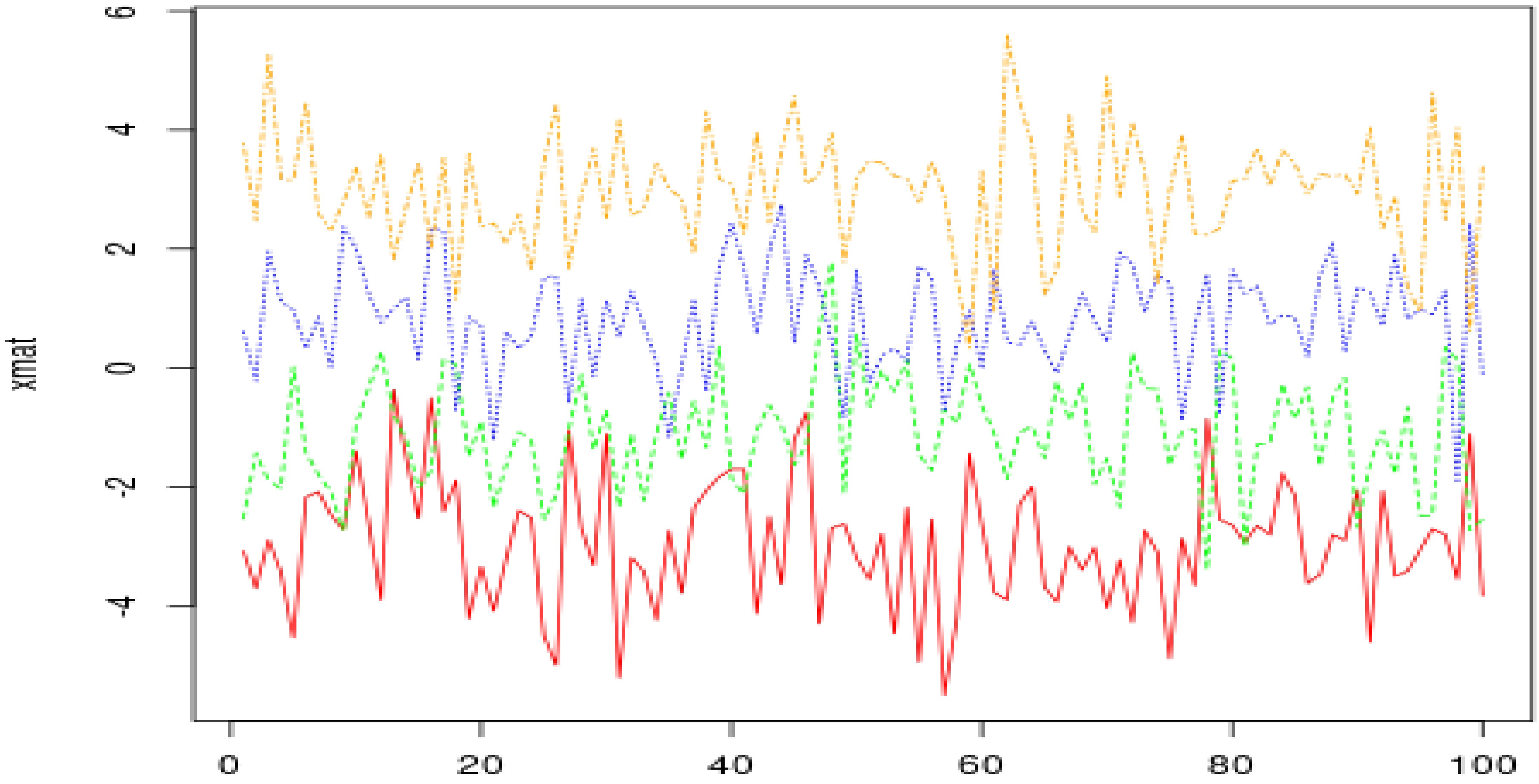
- However, **any (or both) of these aesthetics** (color and line type) **can be fixed to a single value.**

```
matplot(xmat, type = 'l', col = 'black’)
```



Matrix Plot

matplot(xmat, type = 'l', col = c('red', 'green', 'blue', 'orange'))



Matrix Plot

General Form

matplot(x, y, type = "p", lty = 1:5, lwd = 1, lend = par("lend"),

pch = NULL, col = 1:6, cex = NULL, bg = NA, xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,

log = "", ..., add = FALSE, verbose = getOption("verbose"))

Arguments
x,y

vectors or matrices of data for plotting. The number of rows should match. If one of them are missing, the other is taken as y and an x vector of 1:n is used. Missing values (NAs) are allowed. Since R 4.0.0, class(.)es of x and y such as "Date" are typically preserved.

type

character string (length 1 vector) or vector of 1-character strings indicating the type of plot for each column of y, see plot for all possible types. The first character of type defines the first plot, the second character the second, etc. Characters in type are cycled through; e.g., "pl" alternately plots points and lines.

lty,lwd,lend

vector of line types, widths, and end styles. The first element is for the first column, the second element for the second column, etc., even if lines are not plotted for all columns. Line types will be used cyclically until all plots are drawn.

Matrix Plot

pch

character string or vector of 1-characters or integers for plotting characters, see points for details. The first character is the plotting-character for the first plot, the second for the second, etc. The default is the digits (1 through 9, 0) then the lowercase and uppercase letters.

col

vector of colors. Colors are used cyclically.

cex

vector of character expansion sizes, used cyclically. This works as a multiple of par("cex"). NULL is equivalent to 1.0.

bg

vector of background (fill) colors for the open plot symbols given by pch = 21:25 as in points. The default NA corresponds to the one of the underlying function plot.xy.

xlab, ylab

titles for x and y axes, as in plot.

xlim, ylim

ranges of x and y axes, as in plot.

Matrix Plot

log

Graphical parameters (see par) and any further arguments of plot, typically plot.default, may also be supplied as arguments to this function; even panel.first etc now work. Hence, the high-level graphics control arguments described under par and the arguments to title may be supplied to this function.

add

logical. If TRUE, plots are added to current one, using points and lines.

verbose

logical. If TRUE, write one line of what is done.

Matrix Plot

Example Program for Matrix Plot

MATPLOT PROGRM (Lab Program)

```
sfly<-c(26,23,33,6,3,4,20,2)

mfly<-c(4,5,12,9,15,10,8,22)

speed<-c(3,4,4,5,6,7,7,9)

ivert<-cbind(sfly,mfly)

dim(ivert)

spd<-cbind(speed)

spd

dim(spd)

ivert

matplot(spd,ivert,type='b',pch=1:2,col=2,lty=2:3,xlab='Speed',ylab='Invertebrate')+legend(x
='topright',legend=c('Stonefly','MayFly'),col=1,pch=1:2,lty=2:3)
```

Using Graphics Parameters

https://www.mscs.dal.ca/Splus/parameters.html

- The following is a list of arguments available to control the appearance of graphs.
- The following arguments can be specified within any graphical function to specify titles, where string is the title inserted in quotes, or a character vector containing the title:

main="string“ **//main title, above plot, in enlarged characters**

sub="string“ **//sub-title for bottom of plot**

main="# of chin ups \n Females“ **//for titles and sub-titles to run over more than one line, use \n in the character string to start a new line**

- The **following parameters may only be used in high-level graphical functions** (those that set up **coordinate systems**, e.g., plot, qqplot).

xlab="string", ylab="string“ **//labels for the x an y axes**

Using Graphics Parameters

axes= logical flag //specifying axes=F forces Splus to omit drawing the axes

xlim=, ylim=vectors //giving the min and max values for the x and y axes

log= //specifies the axes to be logarithmic (ie.: log="xy")

type=type of plot //"p" points, "l" lines, "b" both, "o" both – overstruck, "h" high density, "n" null (no data plotted)

- The **function par() can be used to set graphical parameters which stay in effect throughout all plotting until they are reset in another call to par** or by invoking a new graphic device.

Using Graphics Parameters

par(mfrow=c(2,3))

it is possible to **specify the number and arrangement of graphs on a page using the mfrow= option.** **mfrow=c(2,3) allows 6 plots to appear on a page** (2 rows and 6 columns section → one plot at each section). because the **mfrow argument was used within the par function, the set up will stay in effect for all subsequent graphs.**

par(mfrow=c(1,1))

restores the normal one-graph-per-page form * this could also be done by invoking a new graphic device

X11()
par(mfcol=c(3,2))

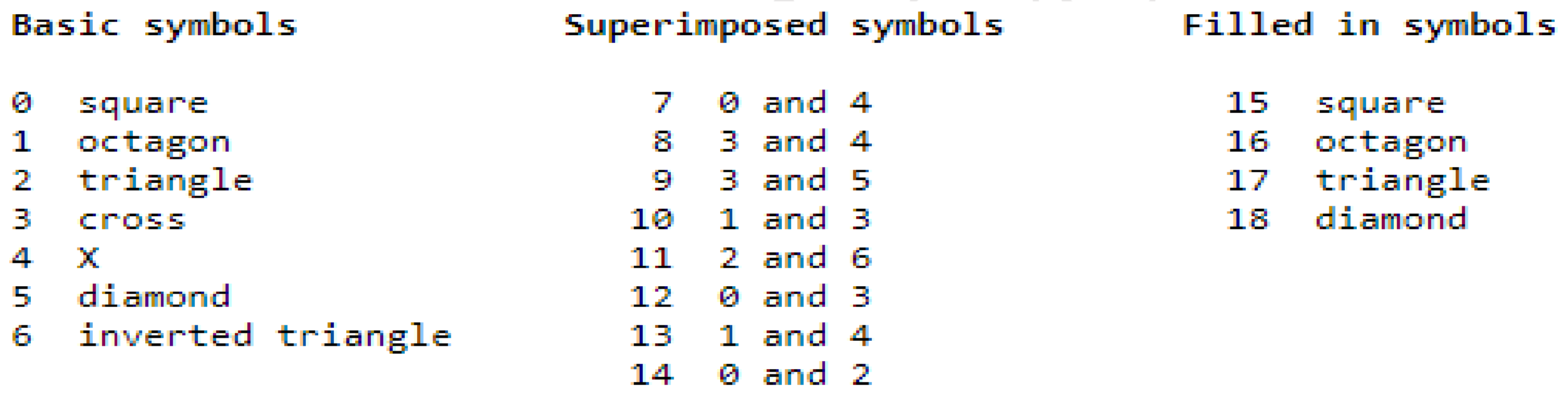
the page is set up as above except that the graphs are printed column wise, mfrow prints graphs row by row

Using Graphics Parameters

- The **following arguments can be specified either by the par() function or within a graphics function**

pch= plotting character

the default is pch="*“. It is possible to specify either a character, using quotes, or a numeric value.



```
Basic symbols              Superimposed symbols      Filled in symbols

0   square                    7   0 and 4              15   square
1   octagon                   8   3 and 4              16   octagon
2   triangle                  9   3 and 5              17   triangle
3   cross                    10   1 and 3              18   diamond
4   X                        11   2 and 6
5   diamond                  12   0 and 3
6   inverted triangle        13   1 and 4
                             14   0 and 2
```

cex= character expansion. **//cex=0.5 gives half the standard character size**

lty=line type **//a value of 1 gives solid lines, values of 2,3... will select a non-solid line type**

lwd= line width **//the default value is 1. Increasing values produce thicker lines**

col= numeric color specification (default is 1)

Using Graphics Parameters

adj= string justification **// 0→left justify 1→right justify 0.→centre or any other fraction**

ask= logical value **// ask=T means graphical device will prompt before going to the next page/screen of output** (prevents plots from being erased before they are studied)

las= type of axis labels **//0 parallel to axis, 1 horizontal, 2 perpendicular to axis**

Multiple Plots in One Window

Exporting Graph

All the old-style graphics windows have the following export options in the toolbar:

Export as PDF

Export as GIF

and additionally, the Export menu contains:

Export as Encapsulated PostScript

Export as Gzipped Encapsulated PostScript

Export as JPEG

Export as PNG

These can be used to export the currently visible plot to an external graphics format for later use.

Documentation and Deployment

(Once discover the drawback or loopholes with the existing model, collection data from the users, cleaning, conditioning, model planning, model building, train the model, test the model with the test data. If it finds model is good, need to produce technical document and present it in front of stat holders, project managers, project sponsors, users etc. How they produce technical document and present will discuss here)

knitr

- **knitr is an R package that allows the inclusion of text, R code and results inside documents.** (allows to produce a document where explanation abt the model, technical details, code, results/graphs in a single document)
- Using Knitr, **allows to create a document where text, code, analysis, results and discussion are all in one place.**
- In practice **we maintain a master file that contains both user readable documentation and chunks of program source code.**
- when **processed through knitr, the function takes an input file, extracts the R code in it** according to a list of patterns, **evaluates the code, the code is replaced by the results and writes the output in another file.**

Documentation and Deployment

- The **document types supported by knitr include LaTeX, Markdown, and HTML.** (Output file from the function)

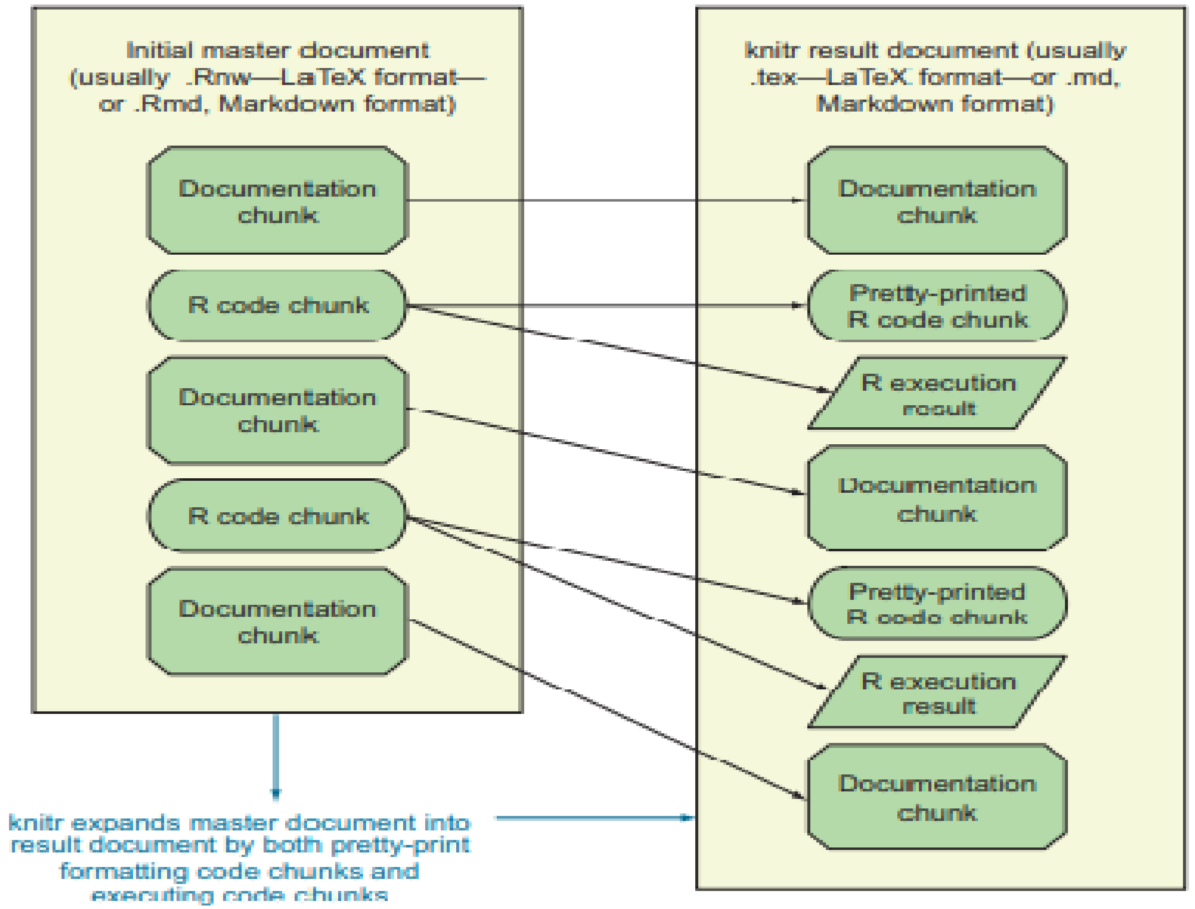
  - **LaTeX format** is a good choice **for detailed typeset technical documents.**

  - **Markdown format** is a good choice **for online documentation** and wikis. (The text will be converted into mark up language with .md extension. if we want to upload in some blog post web sites. It takes .md file and convert it into specific HTML file through a markdown app)

  - **Direct HTML format** may be appropriate **for some web applications.** (if you are creating web site and psot the document, can use this .html file)

Documentation and Deployment

- **knitr extracts and executes all of the R code and then builds a new result document that assembles the contents of the original document plus pretty-printed code and results.**
- The below figure **demonstrates the knitr process**

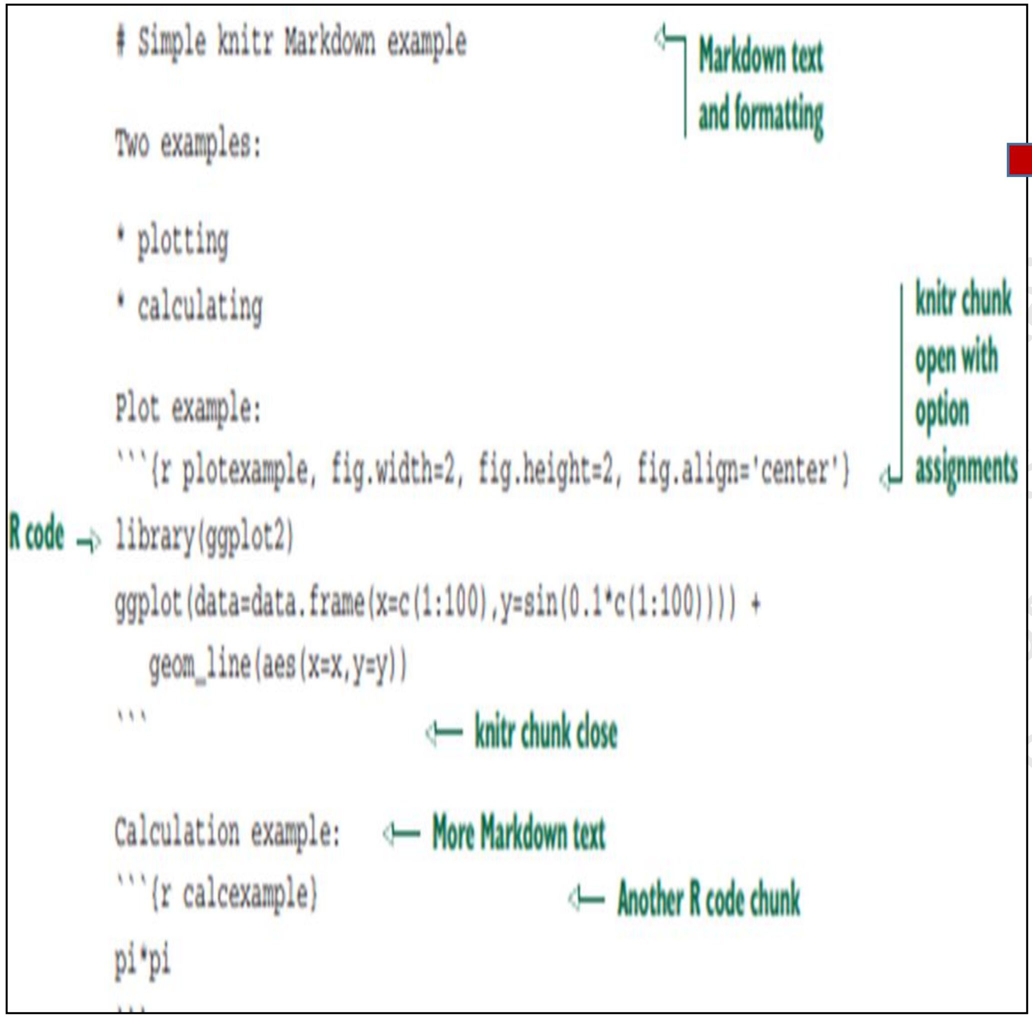

Initial master document (usually .Rnw—LaTeX format— or .Rmd, Markdown format)
Documentation chunk
R code chunk
Documentation chunk
R code chunk
Documentation chunk
knitr result document (usually .tex—LaTeX format—or .md, Markdown format)
Documentation chunk
Pretty-printed R code chunk
R execution result
Documentation chunk
Pretty-printed R code chunk
R execution result
Documentation chunk
knitr expands master document into result document by both pretty-print formatting code chunks and executing code chunks

knitr process schematic

Documentation and Deployment

A SIMPLE KNITR MARKDOWN EXAMPLE

- The following listing shows a simple Markdown document with knitr annotation blocks denoted with ```
- This document is saved in a file named simple.Rmd. In R we'd process this as shown next:



~~~
# Simple knitr Markdown example

Two examples:

* plotting
* calculating

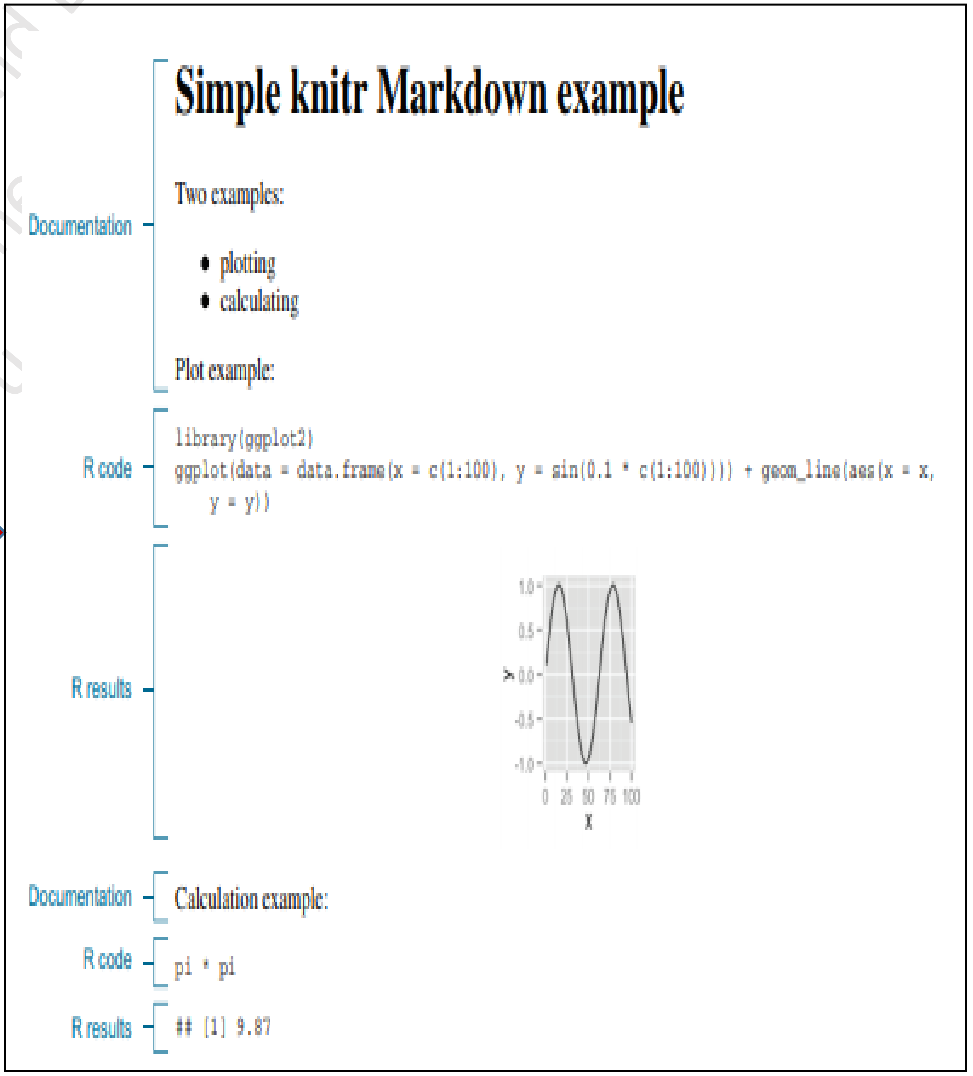
Plot example:
```{r plotexample, fig.width=2, fig.height=2, fig.align='center'}
library(ggplot2)
ggplot(data=data.frame(x=c(1:100),y=sin(0.1*c(1:100)))) +
  geom_line(aes(x=x,y=y))
```

Calculation example:
```{r calcexample}
pi*pi
```
~~~

Markdown text and formatting
knitr chunk open with option assignments
R code
knitr chunk close
More Markdown text
Another R code chunk

```
library(knitr)
knit('simple.Rmd')
```

This produces the new file simple.md, which is in Markdown format and appears as



Simple knitr Markdown example

Two examples:

- plotting
- calculating

Plot example:

```
library(ggplot2)
ggplot(data = data.frame(x = c(1:100), y = sin(0.1 * c(1:100)))) + geom_line(aes(x = x,
    y = y))
```

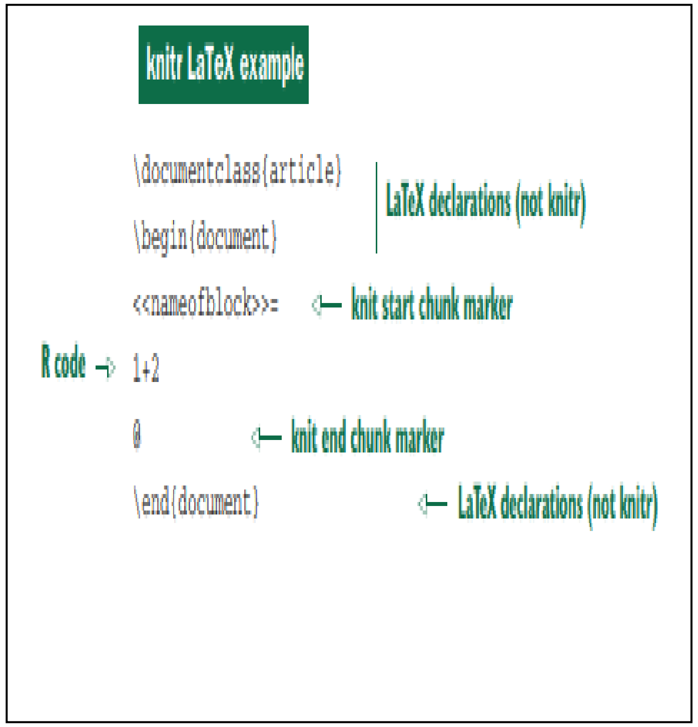
Calculation example:

```
pi * pi
## [1] 9.87
```

Documentation and Deployment

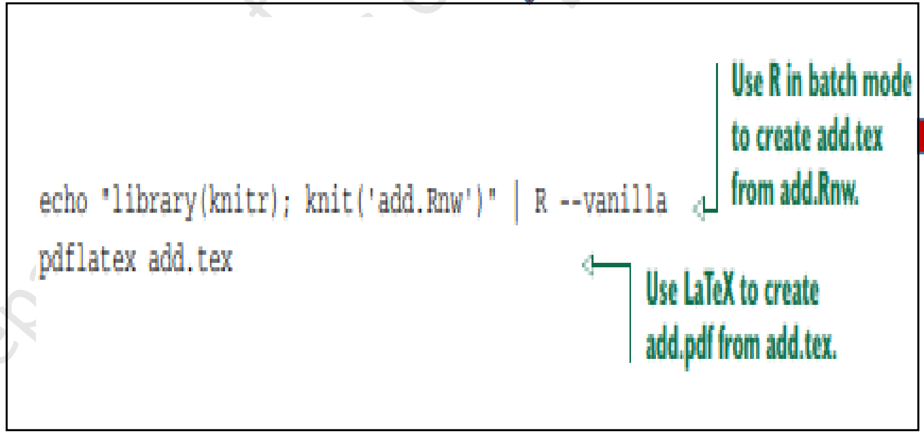
A SIMPLE KNITR LATEX EXAMPLE

- **LaTeX is a powerful document preparation system** suitable for publication-quality typesetting both for **articles** and **entire books.**
- The **main new feature is that in LaTeX, code blocks are marked with << and @ instead of ```**



```
\documentclass{article}
\begin{document}
<<nameofblock>>=
1+2
@
\end{document}
```

The content is saved into a file named **add.Rnw** and then run R in batch to produce the file add.tex. At a shell prompt, then run LaTeX to create the final add.pdf file:

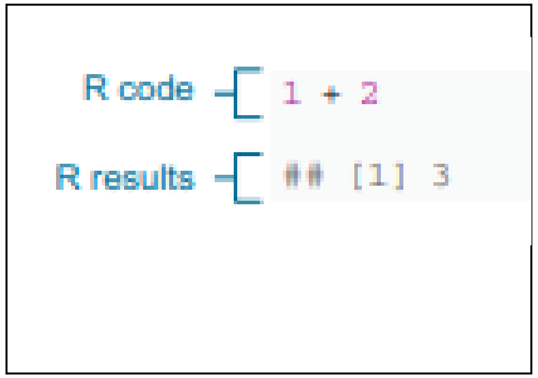


```
echo "library(knitr); knit('add.Rnw')" | R --vanilla
pdflatex add.tex
```

Use R in batch mode to create add.tex from add.Rnw.

Use LaTeX to create add.pdf from add.tex.

This produces the PDF as

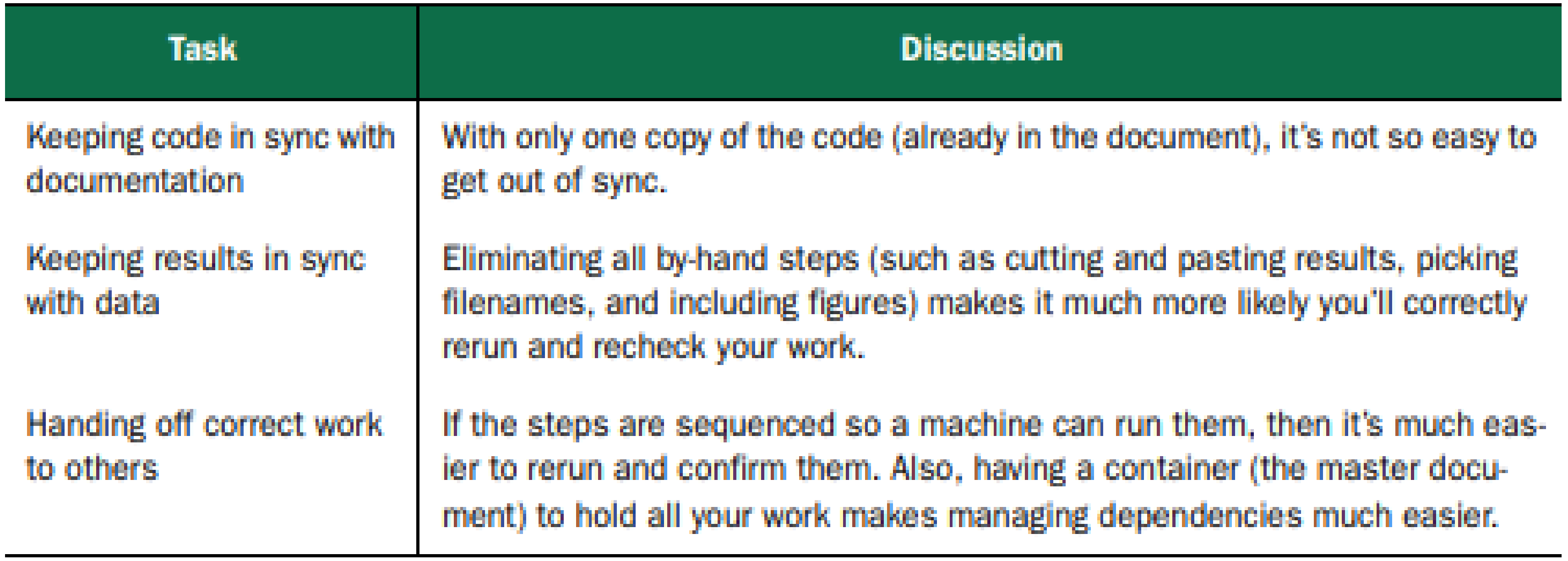


```
1 + 2
## [1] 3
```

PURPOSE OF KNITR

- **The purpose of knitr is to produce reproducible work.(Replicate work)**
- When we **distribute our work in knitr format, anyone can download** our work and, without great effort, **rerun it to confirm they get the same results we did.**
- This is the **ideal standard of scientific research**, **but** is rarely met, as **scientists usually are deficient in sharing all of their code, data, and actual procedures.**

Maintenance tasks made easier by knitr



Task	Discussion
Keeping code in sync with documentation	With only one copy of the code (already in the document), it's not so easy to get out of sync.
Keeping results in sync with data	Eliminating all by-hand steps (such as cutting and pasting results, picking filenames, and including figures) makes it much more likely you'll correctly rerun and recheck your work.
Handing off correct work to others	If the steps are sequenced so a machine can run them, then it's much easier to rerun and confirm them. Also, having a container (the master document) to hold all your work makes managing dependencies much easier.

knitr Technical Details

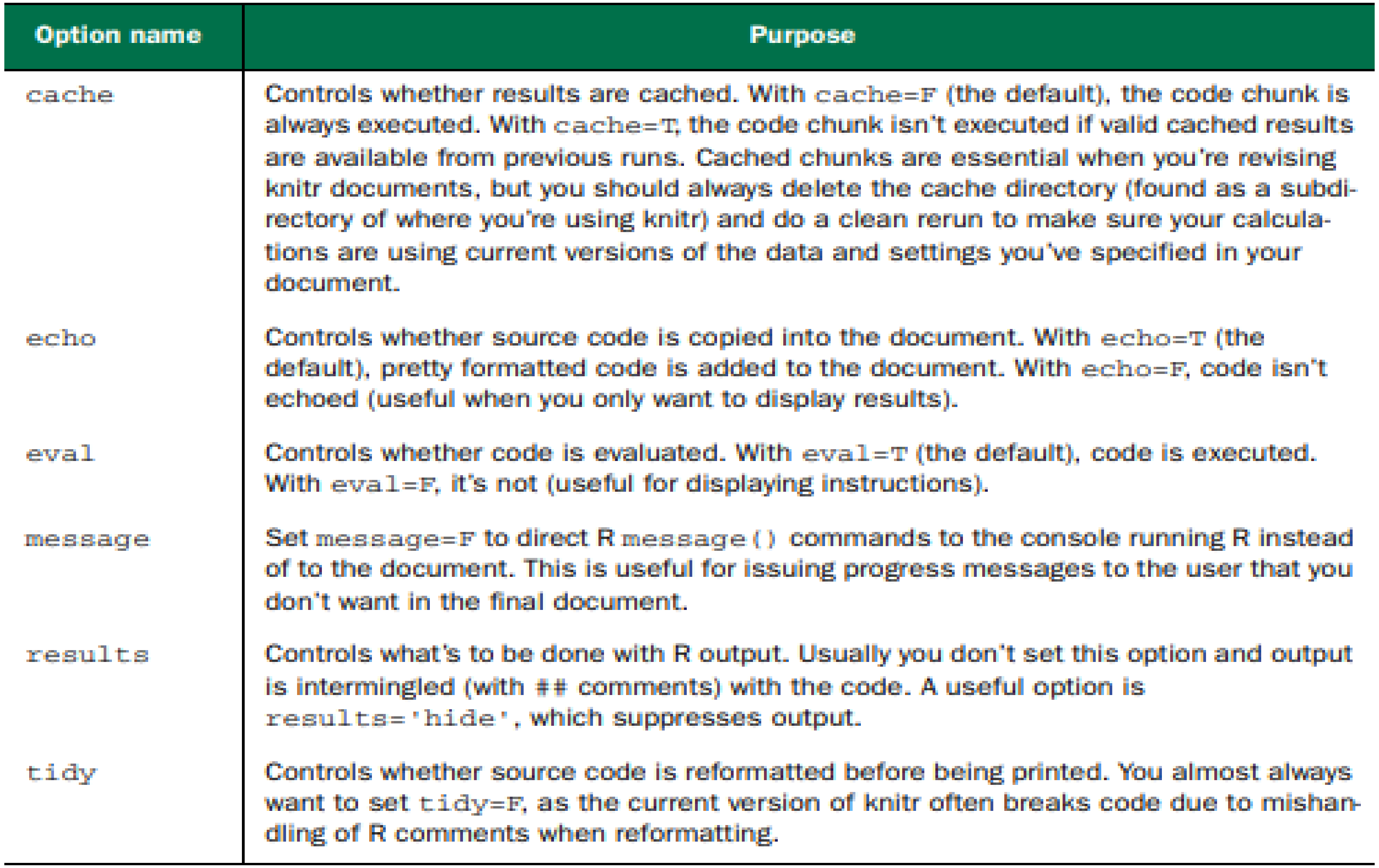
KNITR BLOCK DECLARATION FORMAT

- **A knitr code block starts with the block declaration** (**``` in Markdown and << in LaTeX**).
- The **first string is the name of the block** (must be unique across the entire project). **After that, a number of comma-separated option=value chunk option assignments are allowed**.

knitr Technical Details

KNITR CHUNK OPTIONS

- **A sampling of useful option assignments is given in the below table.**



Option name	Purpose
`cache`	Controls whether results are cached. With `cache=F` (the default), the code chunk is always executed. With `cache=T`, the code chunk isn't executed if valid cached results are available from previous runs. Cached chunks are essential when you're revising knitr documents, but you should always delete the cache directory (found as a subdirectory of where you're using knitr) and do a clean rerun to make sure your calculations are using current versions of the data and settings you've specified in your document.
`echo`	Controls whether source code is copied into the document. With `echo=T` (the default), pretty formatted code is added to the document. With `echo=F`, code isn't echoed (useful when you only want to display results).
`eval`	Controls whether code is evaluated. With `eval=T` (the default), code is executed. With `eval=F`, it's not (useful for displaying instructions).
`message`	Set `message=F` to direct R `message()` commands to the console running R instead of to the document. This is useful for issuing progress messages to the user that you don't want in the final document.
`results`	Controls what's to be done with R output. Usually you don't set this option and output is intermingled (with `##` comments) with the code. A useful option is `results='hide'`, which suppresses output.
`tidy`	Controls whether source code is reformatted before being printed. You almost always want to set `tidy=F`, as the current version of knitr often breaks code due to mishandling of R comments when reformatting.

knitr Technical Details

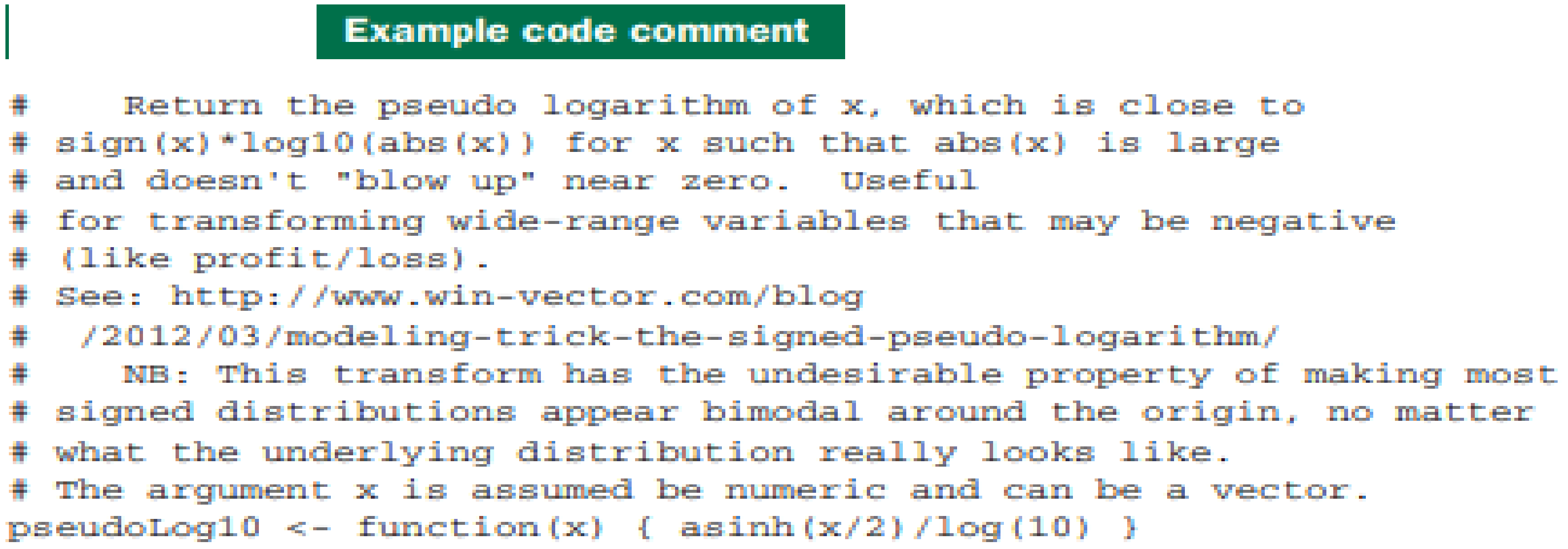
KNITR TAKEAWAY

- The **key point is that because we took the extra effort to do this work in knitr, we have the following**:
  - ➢ **Nicely formatted documentation (buzz.md and buzz.pdf)**
  - ➢ **Shared executable code (buzz.Rmd and buzz.Rnw)**
- This makes **debugging** (which usually involves **repeating and investigating earlier work**), **sharing, and documentation much easier and more reliable.**

Using Comments and Version Control for Running Documentation

Writing effective comments

- **R's comment style is simple: everything following a # until the end of a line is a comment and ignored by the R interpreter.**
- The following is an example of a well-commented block of R code.



Example code comment

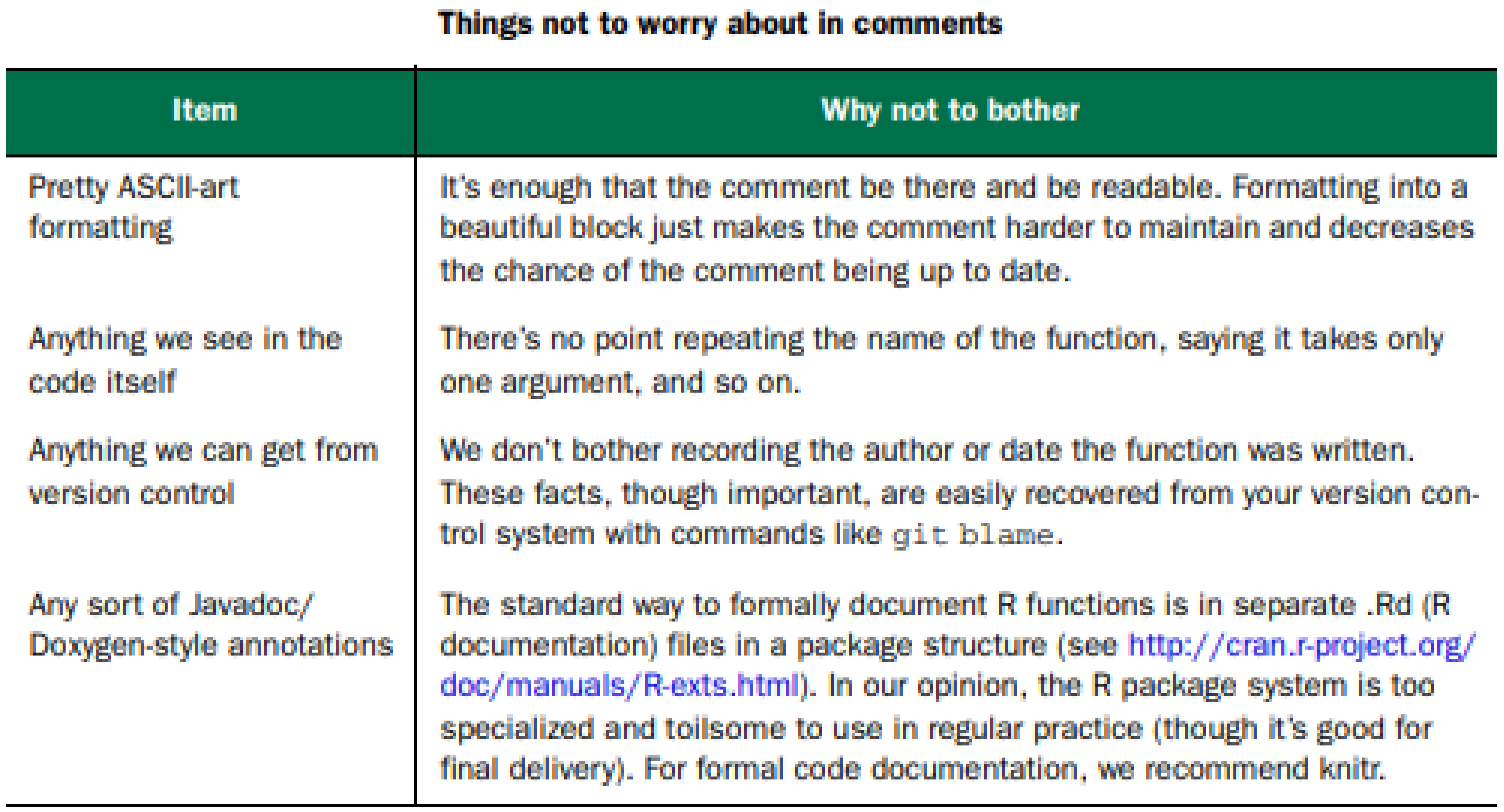
```
#    Return the pseudo logarithm of x, which is close to
# sign(x)*log10(abs(x)) for x such that abs(x) is large
# and doesn't "blow up" near zero.  Useful
# for transforming wide-range variables that may be negative
# (like profit/loss).
# See: http://www.win-vector.com/blog
#  /2012/03/modeling-trick-the-signed-pseudo-logarithm/
#    NB: This transform has the undesirable property of making most
# signed distributions appear bimodal around the origin, no matter
# what the underlying distribution really looks like.
# The argument x is assumed be numeric and can be a vector.
pseudoLog10 <- function(x) { asinh(x/2)/log(10) }
```

- **Good comments** include **what the function does, what types arguments are expected to be, limits of domain, why we should care about the function, and where it's from.**

Using Comments and Version Control for Running Documentation

Writing effective comments

- It’s vastly more important to **document any unexpected features or limitations in the code than to try to explain** the obvious. (Explain in the document rather that comment)
- Note that in our comments we didn’t bother with anything listed in below table.



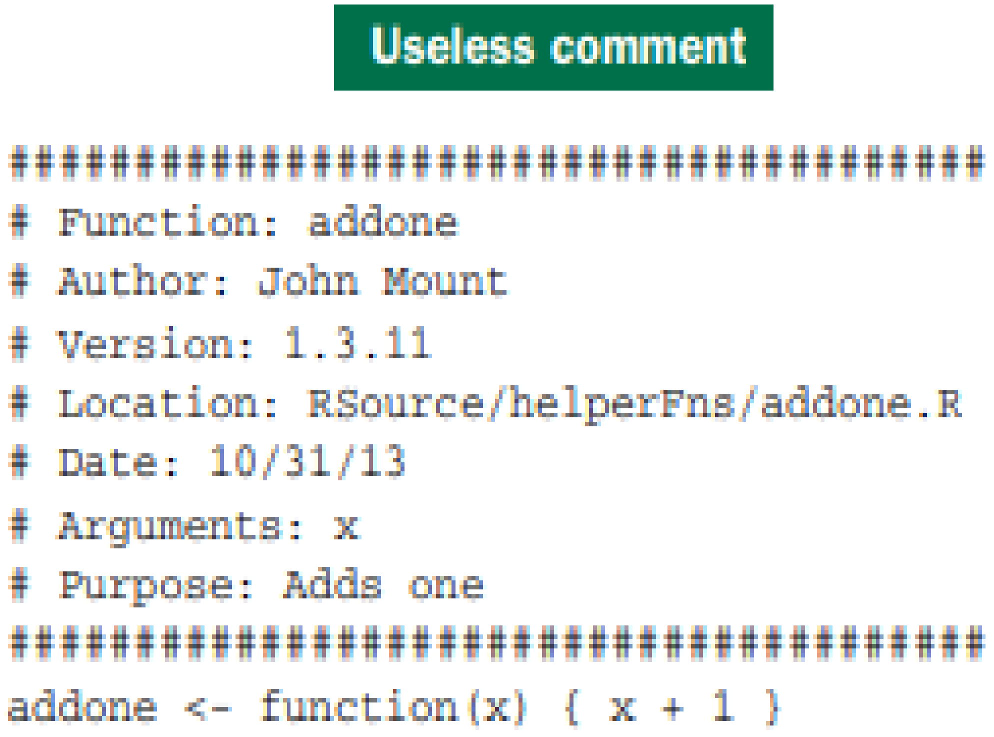
Things not to worry about in comments

Item	Why not to bother
Pretty ASCII-art formatting	It’s enough that the comment be there and be readable. Formatting into a beautiful block just makes the comment harder to maintain and decreases the chance of the comment being up to date.
Anything we see in the code itself	There’s no point repeating the name of the function, saying it takes only one argument, and so on.
Anything we can get from version control	We don’t bother recording the author or date the function was written. These facts, though important, are easily recovered from your version control system with commands like `git blame`.
Any sort of Javadoc/ Doxygen-style annotations	The standard way to formally document R functions is in separate .Rd (R documentation) files in a package structure (see http://cran.r-project.org/doc/manuals/R-exts.html). In our opinion, the R package system is too specialized and toilsome to use in regular practice (though it’s good for final delivery). For formal code documentation, we recommend knitr.

Using Comments and Version Control for Running Documentation

Writing effective comments

- Also, **avoid comments that add no actual content**, such as in the following table.



Useless comment

```
########################################
# Function: addone
# Author: John Mount
# Version: 1.3.11
# Location: RSource/helperFns/addone.R
# Date: 10/31/13
# Arguments: x
# Purpose: Adds one
########################################
addone <- function(x) { x + 1 }
```

Using Comments and Version Control for Running Documentation

Using version control to record history

- **Version control** also known as source control, **is a software that keeps track of every modification to the code in a special kind of database.**

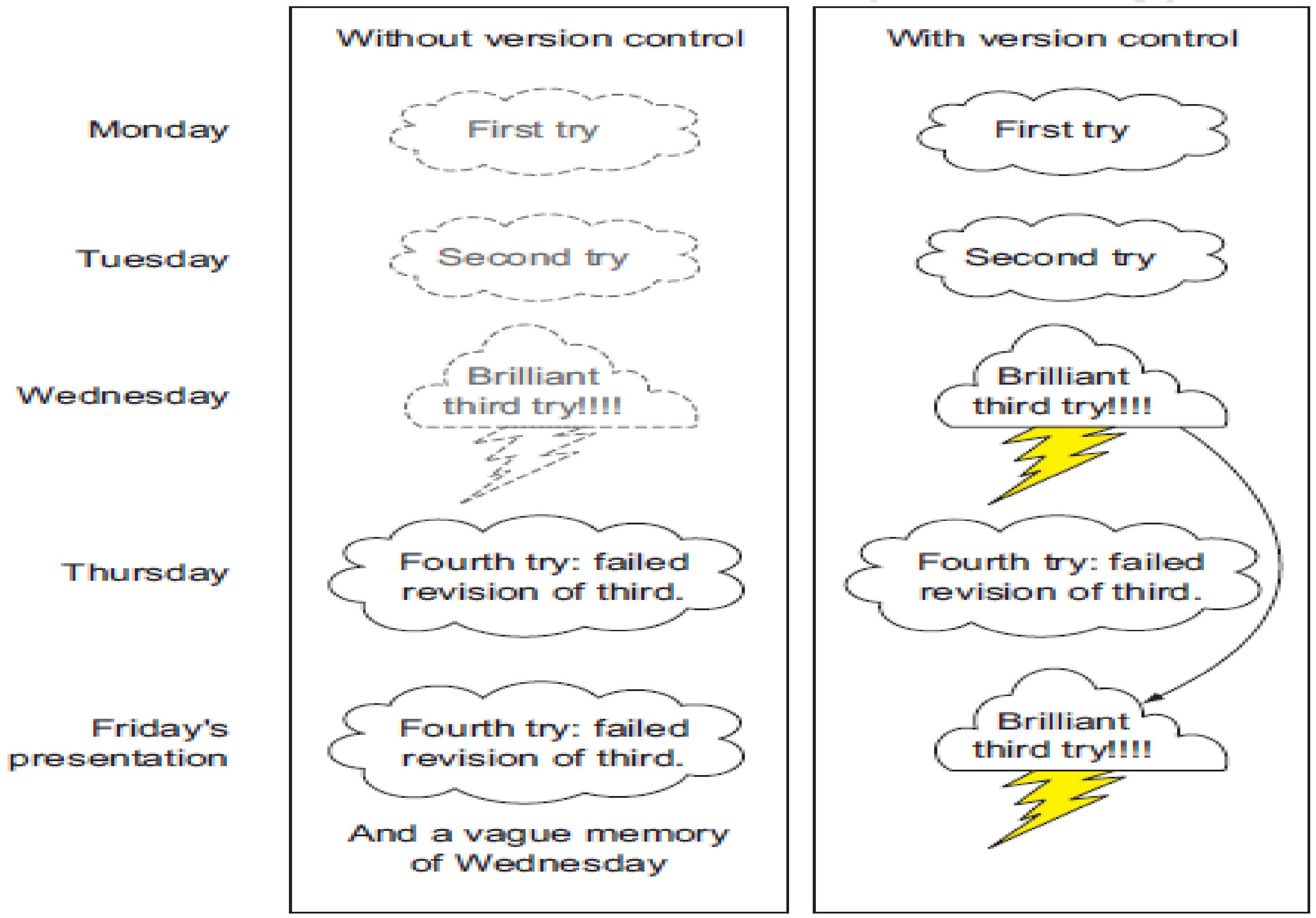
- We can **use version control software for all code, files, and assets that multiple team members will collaborate on.** It keep every **team member working off the latest version.**

- Version control can both **maintain critical snapshots of your work in earlier states** and produce running documentation of **what was done by whom and when in your project.**

Using Comments and Version Control for Running Documentation

Using version control to record history

- Figure shows a cartoon “**version control saves the day**” scenario that is in fact common.



Version control saving the day

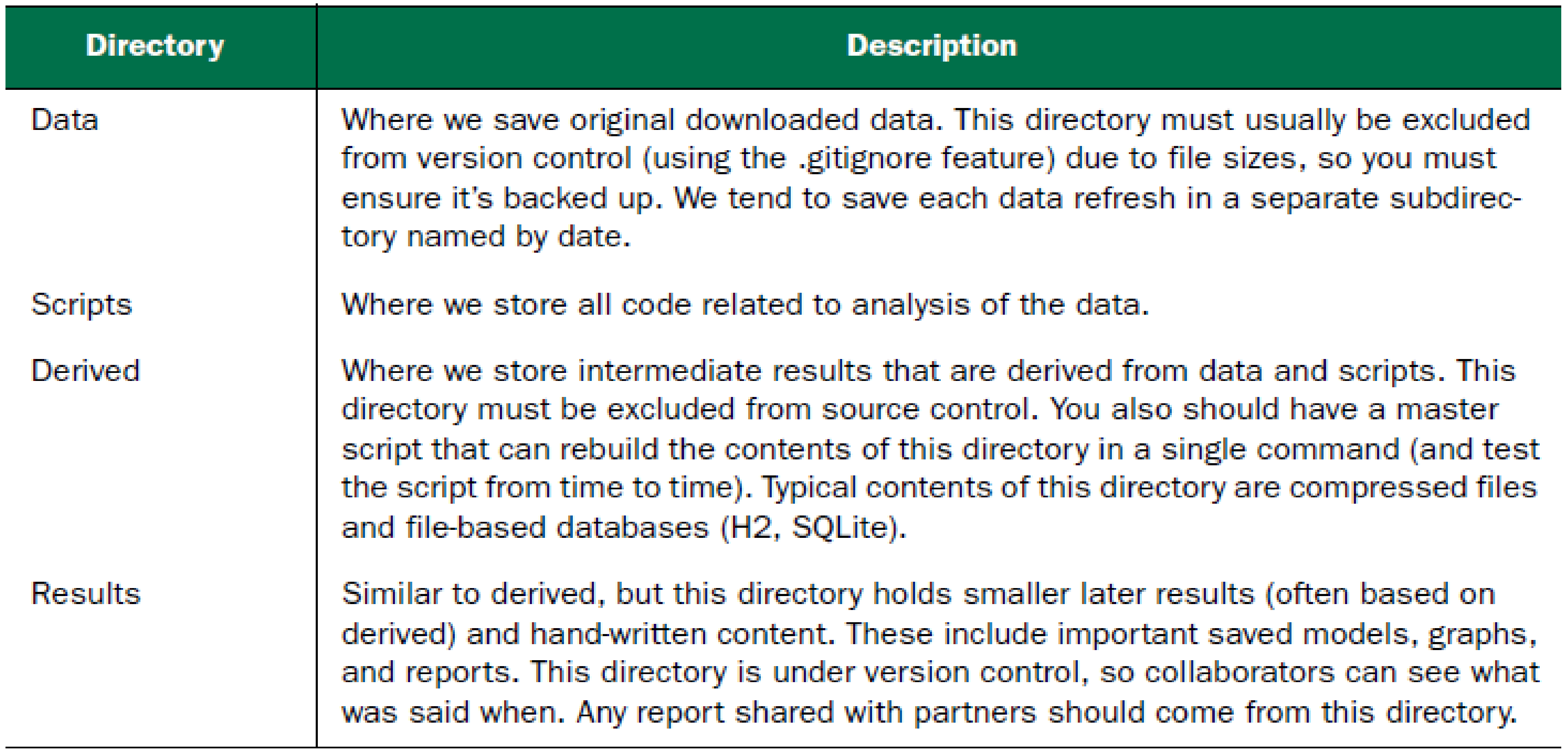
Using Comments and Version Control for Running Documentation

Using version control to record history

Choosing a Project Directory Structure

- **Before starting with source control**, it's important to settle on and document a good **project directory structure.**

A possible project directory structure



Directory	Description
Data	Where we save original downloaded data. This directory must usually be excluded from version control (using the .gitignore feature) due to file sizes, so you must ensure it's backed up. We tend to save each data refresh in a separate subdirectory named by date.
Scripts	Where we store all code related to analysis of the data.
Derived	Where we store intermediate results that are derived from data and scripts. This directory must be excluded from source control. You also should have a master script that can rebuild the contents of this directory in a single command (and test the script from time to time). Typical contents of this directory are compressed files and file-based databases (H2, SQLite).
Results	Similar to derived, but this directory holds smaller later results (often based on derived) and hand-written content. These include important saved models, graphs, and reports. This directory is under version control, so collaborators can see what was said when. Any report shared with partners should come from this directory.

Using Comments and Version Control for Running Documentation

Using version control to record history

Starting a Git Project using the Command Line

- When we've **decided on our directory structure** and want to **start a version controlled project**, do the following: **(Git is a type of version control system)**

  1) **Start the project in a new directory**. **Place any work either in this directory** or **in subdirectories**.

  2) **Move your interactive shell into this directory and type** **git init**. It's okay if we've already started working and there are already files present. (An **interactive shell** is simply any **shell** process that we can use to type commands, and get back output from those commands.)

  3) **Exclude any subdirectories** that we don't want under source control with **.gitignore** control files.

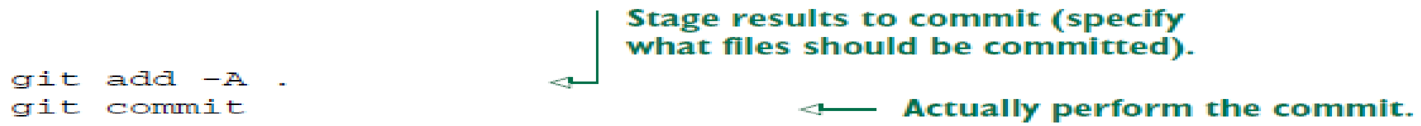
- The **init step sets up in the directory a single hidden file tree called .git** and prepares you to **keep extra copies of every file in the directory**

Using Comments and Version Control for Running Documentation

Using version control to record history

Starting a Git Project using the Command Line

- As often as practical, **enter the following two commands into an interactive shell in our project directory**:

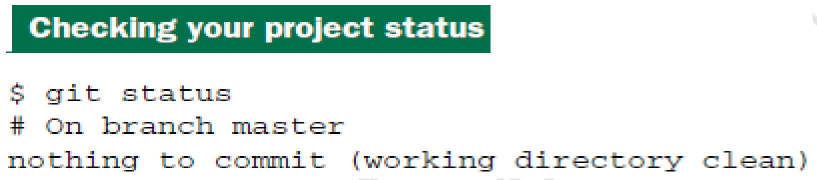


```
git add -A .
git commit
```

Stage results to commit (specify what files should be committed).

Actually perform the commit.

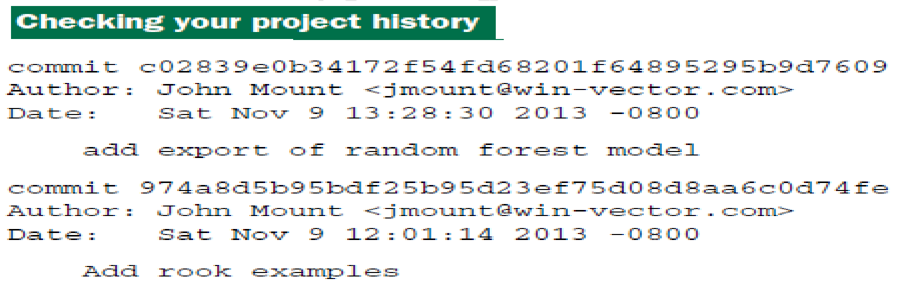
- **Checking in a file is split into two stages: add and commit.**
- **Run the add/commit pair of commands after every minor accomplishment on our project.**
- Any time we want to **know about our work progress, type command**
- **git status to see if there are any edits** you can put through the add/commit cycle.



Checking your project status

```
$ git status
# On branch master
nothing to commit (working directory clean)
```

- **git log to see the history of our work** (from the viewpoint of the add/commit cycles).



Checking your project history

```
commit c02839e0b34172f54fd68201f64895295b9d7609
Author: John Mount <jmount@win-vector.com>
Date:   Sat Nov 9 13:28:30 2013 -0800

    add export of random forest model

commit 974a8d5b95bdf25b95d23ef75d08d8aa6c0d74fe
Author: John Mount <jmount@win-vector.com>
Date:   Sat Nov 9 12:01:14 2013 -0800

    Add rook examples
```

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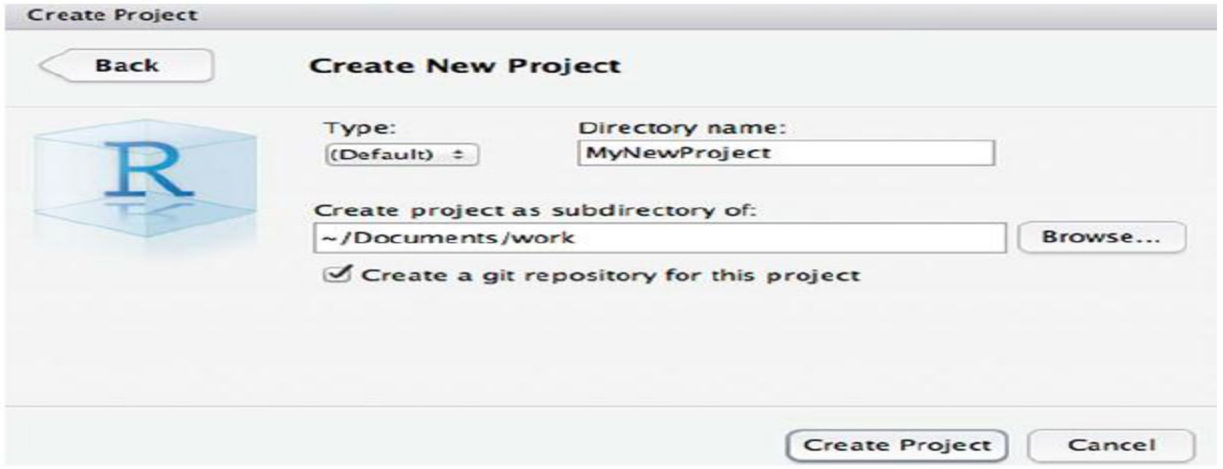
Using Git Through Rstudio

- The **RStudio IDE supplies a graphical user interface to Git that we can be perform add/commit cycle** as follows:

1. **Start a new project**. From the **RStudio command menu**, select **Project > Create Project**, and **choose New Project.** Then **select the name of the project**, what **directory to create the new project directory** in, leave the type as (Default), and **make sure create a Git repository for this project is checked**, click **Create Project**.



Create Project

Back — Create New Project

Type: (Default)

Directory name: MyNewProject

Create project as subdirectory of: ~/Documents/work — Browse...

☑ Create a git repository for this project

Create Project — Cancel

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Using Git Through Rstudio

2. **Do some work in the project. Create new files** by selecting **File > New > R Script. Type some R code (like 1/5)** into the editor pane and then **click the Save icon to save the file**. **When saving the file, be sure to choose project directory or a subdirectory of the project.**

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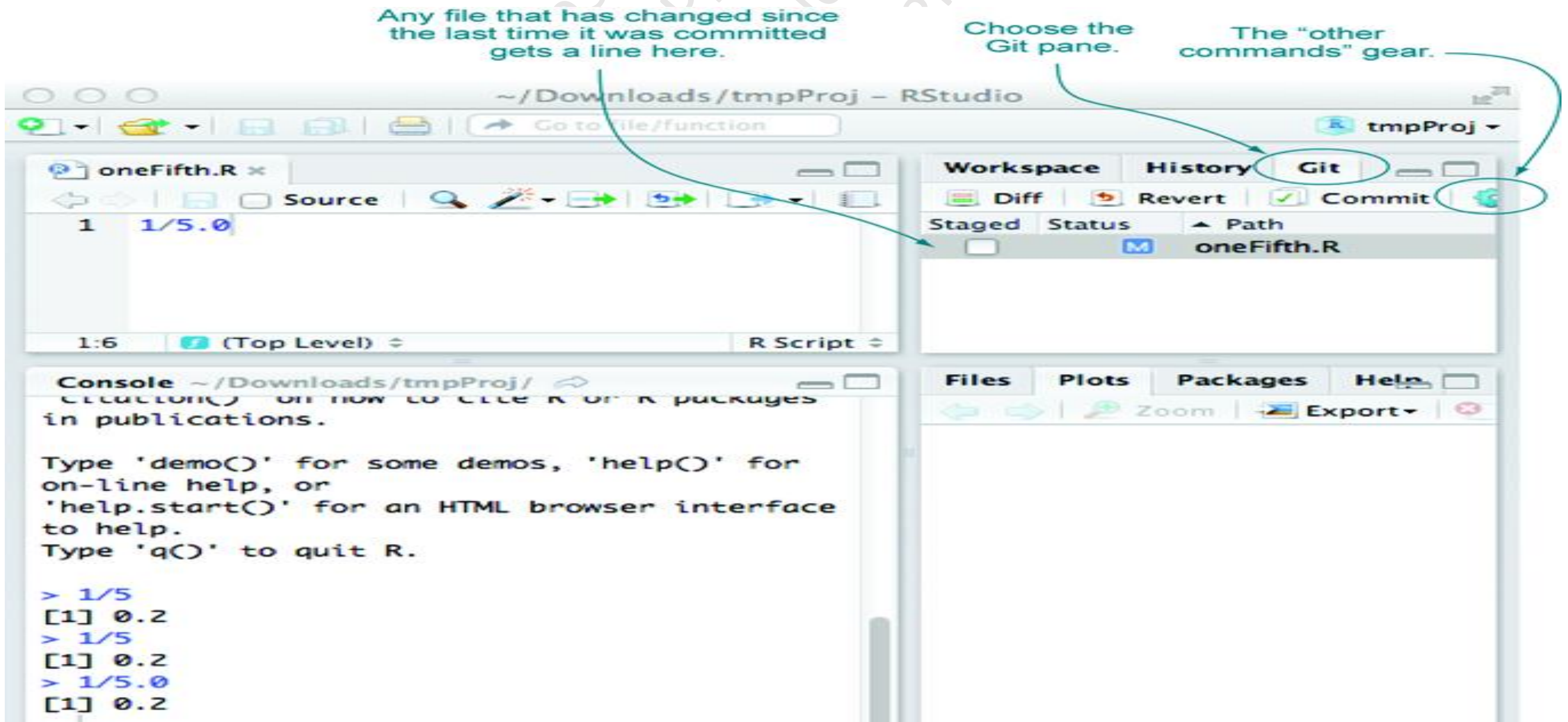
Using Git Through Rstudio

3. **Commit the changes to version control.** Below figure shows how to do this. Select the **Git control pane in the top right of RStudio. This pane shows all changed files as line items. Check the Staged check box for any files you want to stage for this commit. Then click Commit, and you're done.**



```
in publications.

Type 'demo()' for some demos, 'help()' for
on-line help, or
'help.start()' for an HTML browser interface
to help.
Type 'q()' to quit R.

> 1/5
[1] 0.2
> 1/5
[1] 0.2
> 1/5.0
[1] 0.2
```

Using Comments and Version Control for Running Documentation

Using version control to explore our project

- **If we add/commit often** enough, Git is ready to help us with any of the following tasks:
    - **Tracking our work over time**
    - **Recovering a deleted file**
    - **Comparing two past versions of a file**
    - **Finding when you added a specific bit of text**
    - **Recovering a whole file or a bit of text from the past (undo an edit)**
    - **Sharing files with collaborators**
    - **Publicly sharing our project** (à la GitHub at https://github.com/, or Bitbucket at https://bitbucket.org)
    - **Maintaining different versions (branches) of our work**

Using Comments and Version Control for Running Documentation

Using version control to share work

- **In addition to producing work, we must often share it with peers.**
- We advise using version control
- **to share work with peers. To do that effectively with Git, we need to start using additional commands such as git pull, git rebase, and git push.**
- The new Git commands are:
  - ➢ **git push** (usually used in the git push -u origin master variation)
  - ➢ **git pull** (usually used in the git fetch; git merge -m pull master origin/ master or git pull --rebase origin master variations)

Using Comments and Version Control for Running Documentation

Using version control to share work

- **Typically two authors may be working on different files in the same project at the sametime. As you can see in figure, the second author to push their results to the shared repository must decide how to specify the parallel work was performed.**

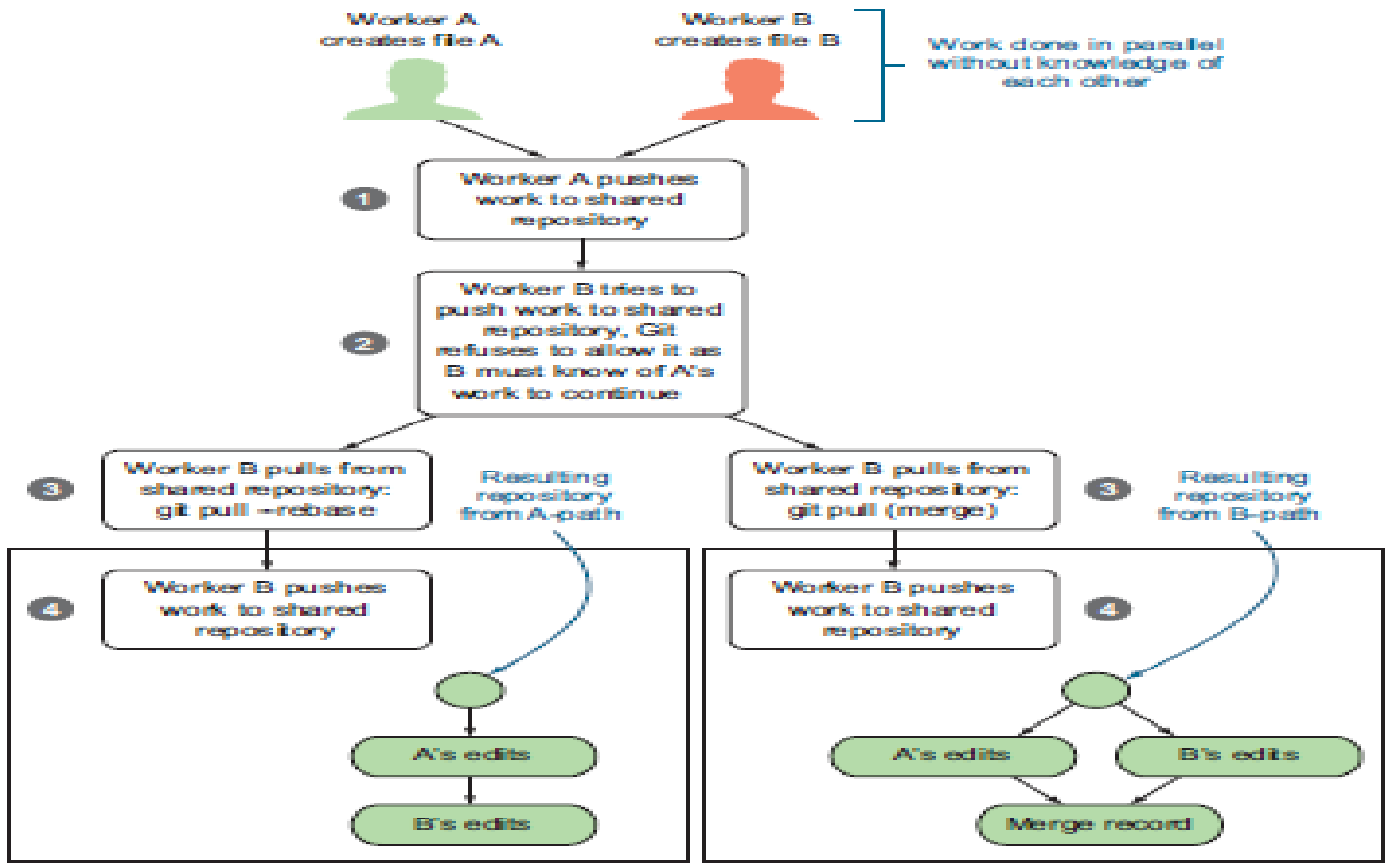

Worker A creates file A
Worker B creates file B
Work done in parallel without knowledge of each other
1
Worker A pushes work to shared repository
2
Worker B tries to push work to shared repository. Git refuses to allow it as B must know of A's work to continue
3
Worker B pulls from shared repository: git pull --rebase
Resulting repository from A-path
Worker B pulls from shared repository: git pull (merge)
3
Resulting repository from B-path
4
Worker B pushes work to shared repository
Worker B pushes work to shared repository
4
A's edits
B's edits
A's edits
B's edits
Merge record

Figure : `git pull: rebase versus merge`

Using Comments and Version Control for Running Documentation

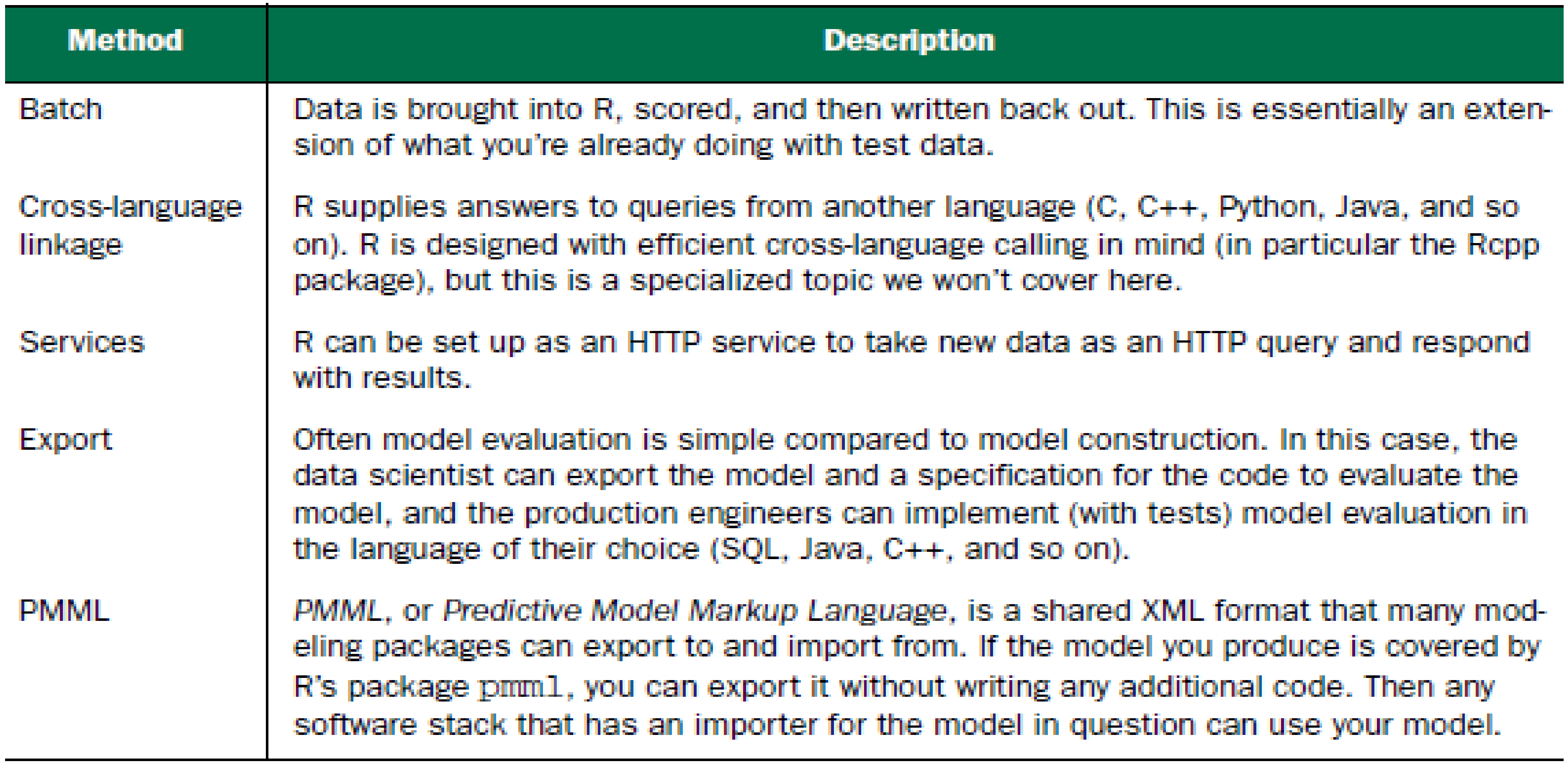
Using version control to share work

- Either they can say the work was truly in parallel (represented by two branches being formed and then a merge record joining the work), or they can rebase their own work to claim their work was done “after” the other’s work (preserving a linear edit history and avoiding the need for any merge records). Note: *before* and *after* are tracked in terms of arrows, not time.
- Merging is what’s really happening, but *rebase* is much simpler to read. The general rule is that you should only rebase work you haven’t yet shared (in our example, Worker B should feel free to rebase their edits to appear to be after Worker A’s edits, as Worker B hasn’t yet successfully pushed their work anywhere). You should avoidrebasing records people have seen, as you’re essentially hiding the edit steps they may be basing their work on (forcing them to merge or rebase in the future to catch up with your changed record keeping).

Deploying Models

- **Some deployment methods in listed in below table.**

Methods to demonstrate predictive model operation



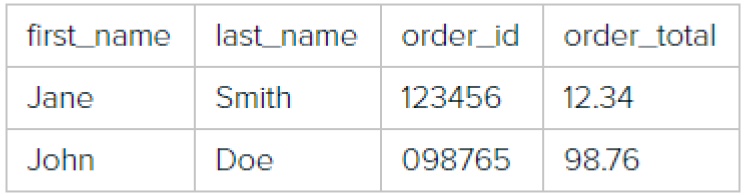
Method	Description
Batch	Data is brought into R, scored, and then written back out. This is essentially an extension of what you're already doing with test data.
Cross-language linkage	R supplies answers to queries from another language (C, C++, Python, Java, and so on). R is designed with efficient cross-language calling in mind (in particular the Rcpp package), but this is a specialized topic we won't cover here.
Services	R can be set up as an HTTP service to take new data as an HTTP query and respond with results.
Export	Often model evaluation is simple compared to model construction. In this case, the data scientist can export the model and a specification for the code to evaluate the model, and the production engineers can implement (with tests) model evaluation in the language of their choice (SQL, Java, C++, and so on).
PMML	*PMML*, or *Predictive Model Markup Language*, is a shared XML format that many modeling packages can export to and import from. If the model you produce is covered by R's package `pmml`, you can export it without writing any additional code. Then any software stack that has an importer for the model in question can use your model.

Producing Effective Presentation

Thank You

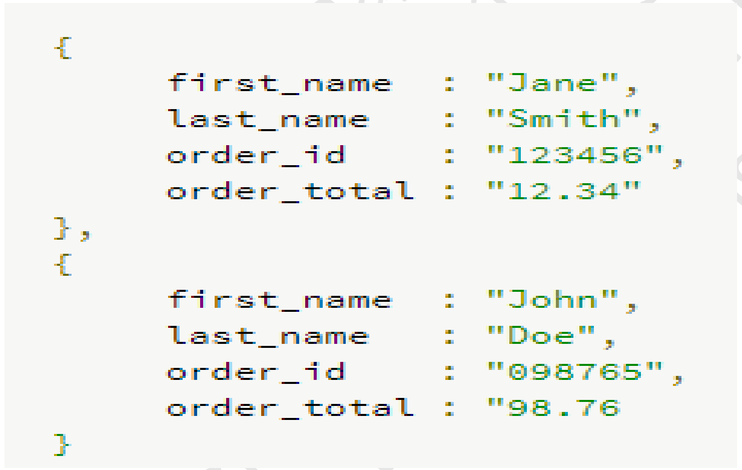
Text analysis (Example for different types of data formats)

- Structured data is highly organized data that is easy to search and is predictable.



first_name	last_name	order_id	order_total
Jane	Smith	123456	12.34
John	Doe	098765	98.76

- Semi structured data does not have the same level of organization and predictability of structured data.



```
{
        first_name  : "Jane",
        last_name   : "Smith",
        order_id    : "123456",
        order_total : "12.34"
},
{
        first_name  : "John",
        last_name   : "Doe",
        order_id    : "098765",
        order_total : "98.76
}
```

- Quasi(Self Styled) **Quasi-structured Data –** This type of **data** consists of textual content with erratic(irregular) **data** formats, and its formatted with effort, software system tools, and time. An example of **quasi-structured data** is the **data** about webpages a user visited and in what order.eg: **Webserver log**