



### **Canadian Bioinformatics Workshops**

### Introduction to R Programming for Bioinformatics

Day 1- Module 1B: Exploring your data in R

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# Why Explore Data?



Understand structure and types of variables

Detect missing or incorrect values early

Check for outliers and unusual patterns

Guide decisions about cleaning and analysis

Prevent errors in downstream analysis

# Key Tools in R for Data Exploration

- Preview your data
  - $\circ$  head()  $\rightarrow$  first few rows
  - $\circ$  tail()  $\rightarrow$  last few rows
- Inspect structure
  - $\circ$  str()  $\rightarrow$  data type & structure of each column
- Quick summary
  - o summary() → basic statistics for each variable
- Check dimensions
  - dim(), nrow(), ncol()
- Frequency counts
  - table() → frequency counts of categorical variables

> summary(df)

age name group
Min. :25.00 Length:2 Length:2
1st Qu.:26.25 Class :character Class :character

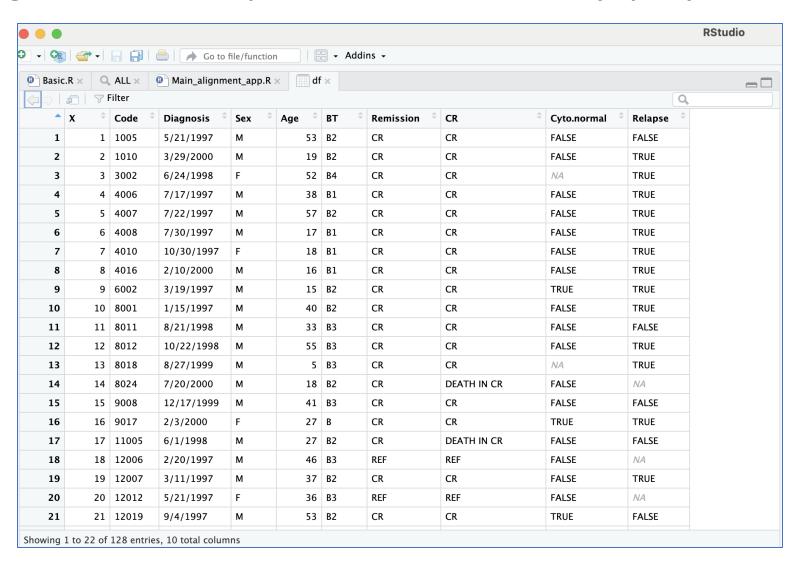
Median :27.50 Mode :character Mode :character

Mean :27.50 3rd Qu.:28.75

Max. :30.00

## Demo: Basic Data Inspections

Inspecting real life data of 128 patients of T- and B-cell Acute Lymphocytic Leukemia (ALL)



# Demo: Basic Data Inspections

#### The ALL dataset:

Microarray gene expression data from acute lymphoblastic leukemia (ALL) patients.

### Metadata includes patient-level information:

- o Code: patient ID
- Diagnosis: date of diagnosis
- Sex, Age: demographics
- o BT: B-cell tumor subtype (e.g., B1, B2, B3, B4)
- o Remission & CR: clinical outcomes (Complete Remission, Death in CR, etc.)
- Cyto.normal: cytogenetic normality (TRUE/FALSE)
- Relapse: indicator of relapse



### Key Learning Point:

Understanding the structure of your dataset is the first step before any analysis.

# Summarizing with Statistics

### Central tendency:

- o mean()
- o median()

### Variability:

- sd() standard deviation
- o var() variance

#### • Extremes:

- o min()
- o max()

### • Frequency counts:

- table() for categorical variables
- hist() for histogram creation
- o summary () Quick summary

```
# View patient metadata
data("ALL")
df2 <- pData(ALL)
# Quick summary
summary(pData(ALL)[, c("age", "sex", "BT", "relapse")])
# mean and median age
mn <- mean(df2$age) # this will return NA
md <- median(df2$age) # this will return NA
mn <- mean(df2$age, na.rm = TRUE) # this will work
md <- median(df2$age, na.rm = TRUE) # this will work
# standard deviation and variance
std <- sd(df2$age, na.rm = TRUE)
vr <- var(df2$age, na.rm = TRUE)</pre>
# Extremes
mxx \leftarrow max(df2\$age, na.rm = T)
mnn \leftarrow min(df2\$age, na.rm = T)
# Table and (Frequency)
age_dit <- table(df2$age)</pre>
# Quick summary
summary(df2[, c("age", "sex", "BT", "relapse")])
```

# Data Filtering

### • Filtering or Subsetting:

- Let us focus on specific patients or conditions of interest
- Help reduce complexity
- o Prepare data for analysis or visualization

### Common use cases (in the ALL example):

- Select patients above a certain age
- Select patients by tumor subtype (BT)
- o Identify patients who relapsed



# Data Filtering (Combining Conditions)

### We can apply multiple filters at once

- Real data is messy and multi-factorial.
  - o In bioinformatics, we rarely filter by just one variable. For example:
    - You might want patients older than 40 AND with relapse.
    - Or find females OR patients with subtype B2.
- Supports hypothesis-driven exploration.
  - Scientists often ask multi-dimensional questions like:
    - Do older male patients relapse more often?
    - Are remission rates different in B2 vs B3 subtypes, but only in females?

### • Use logical operators:

- $\circ$  & = AND
- | = OR
- ! = NOT



# Demo: Data Filtering (Combining Conditions)

- Subsetting
  - o subset()
- Indexing with [
  - o df[df\$Age > 40, ]
  - o df[df\$Age > 40 & df\$Relapse, ]
- Assignment with condition
  - o df <- df[df\$Sex == "F", ]</pre>
- cleaner syntax: with()
  - o with(df, df[Age > 40 & Relapse == TRUE, ])
  - o df[which(df\$Age > 40), ]
- Matching values
  - o match() / %in%
  - df[df\$BT %in% c("B2", "B3"), ]
- Logical indexing directly

```
o df[df$Relapse == TRUE | df$Sex == "F", ]
```

```
# Subsetting and Filtering
# subset()
subset(df2, Age > 40 & Relapse == TRUE)
# Indexing with [
df2 \lceil df2 \rangle Age > 40
                         # filter rows
df2[df2$Age > 40 & df2$Relapse, ] # multiple conditions (same as df$Relapse == T)
df2[, c("Age", "BT")]
                        # select columns
df \leftarrow df2 df$Sex == "F", ] # female patients only (#Assignment with condition)
# with()
with(df, df[Age > 40 & Relapse == TRUE, ]) #for cleaner syntax
df[which(df$Age > 40), ] # more cleanr syntax
#match() / %in% (matching values)
  df[df$BT %in% c("B2", "B3"), ]
# Logical indexing directly
  df[df$Relapse == TRUE | df$Sex == "F", ]
```

### Hands-on Practice: Subsetting the ALL Metadata

### Task 1 – Basic Filtering

Extract all patients who are younger than 20 years

### Task 2 – Single Condition + Column Selection

Get only Age and Sex for patients with BT = "B2"

### Task 3 – Combining Conditions

- Find male patients older than 40
- Get patients who are female OR had a relapse

### Mini-Challenge

Find all patients who are male, had relapse, and whose age is greater than 30. How many are there?

# THANK YOU





