MODULE 3: PROGRAMMING FOR BIOLOGICAL DATA

Session 4: Visualizing Clinical Data

Building Dashboards and QC Charts with ggplot2

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The "Black Box" Problem

The Table

10,000 rows of numbers.

Computers love it.

Humans cannot spot errors.

The Plot

Visual patterns.

Humans love it.

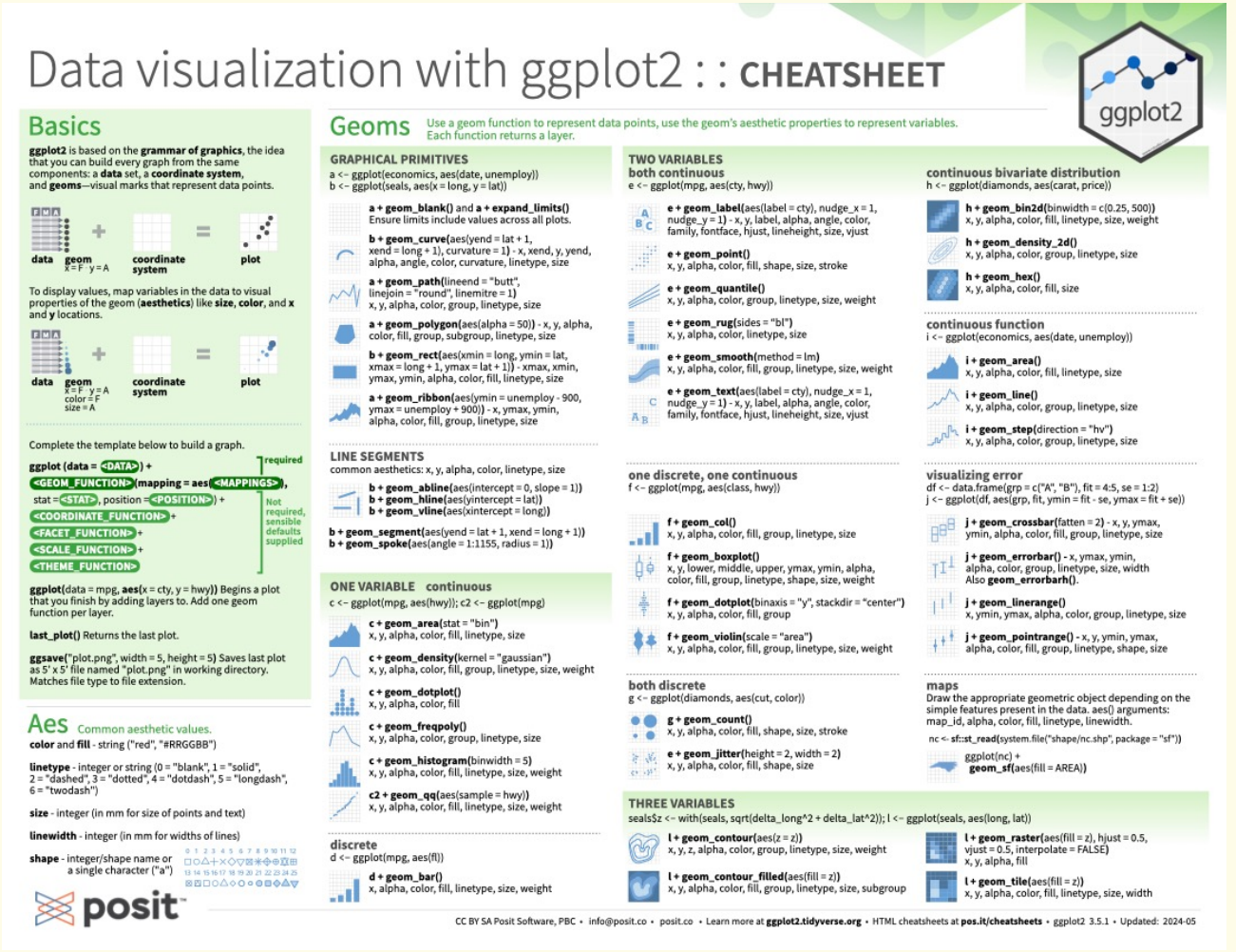
"The outlier screams at you."

Introducing ggplot2

The "Grammar of Graphics"

We build a plot layer by layer, just like Photoshop or a sandwich.

- **Reproducible:** Code-based (not point-and-click).
- **Scalable:** Handles millions of points.
- **Standardized:** Consistent look for every report.



The 3 Pillars of a Plot

1. Data

The raw dataframe

```
df
```

2. Aesthetics

Mapping data to visuals

```
aes(x=Date, y=Result)
```

3. Geometry

The shape of the data

```
geom_point()
```

The Syntax Template

```
ggplot(data = df, aes(x = Col1, y = Col2)) +
   geom_point()
```

The Golden Rule: The + sign connects the layers. It MUST go at the end of the line!

Step 0: Load the Library

ggplot2 is not in "Base R". We must load it from the shelf.

```
# install.packages("ggplot2")  <-- Run once only

library(ggplot2)
```

Geom 1: The Histogram (Distribution)

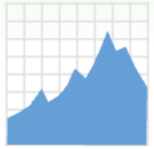
Goal: Check if patient data follows a Normal Distribution.

```
ggplot(df, aes(x = Result)) +
   geom_histogram()
```

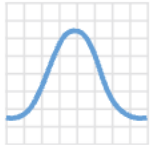
Is it skewed? Are there two peaks (batch effect)?

ONE VARIABLE continuous

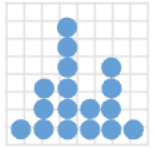
c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)



c + geom_area(stat = "bin"**)**
x, y, alpha, color, fill, linetype, size

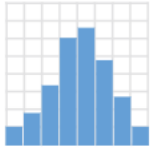


c + geom_density(kernel = "gaussian"**)**
x, y, alpha, color, fill, group, linetype, size, weight

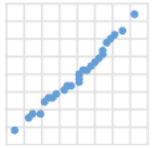


c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly()
x, y, alpha, color, group, linetype, size



c + geom_histogram(binwidth = 5**)**
x, y, alpha, color, fill, linetype, size, weight



c2 + geom_qq(aes(sample = hwy)**)**
x, y, alpha, color, fill, linetype, size, weight

Customizing the Histogram

Make it look scientific by adding color and binwidth.

```
ggplot(df, aes(x = Result)) +
   geom_histogram(binwidth = 0.5,
                  fill = "navy",
                  color = "white")
```

Geom 2: The Boxplot (Comparisons)

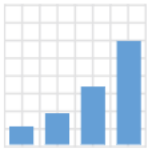
Goal: Compare results between groups (Male vs Female, Machine A vs B).

```
ggplot(df, aes(x = Gender,
               y = Result,
               fill = Gender)) +
   geom_boxplot()
```

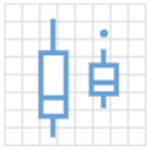
Shows Median, IQR, and Outliers.

one discrete, one continuous

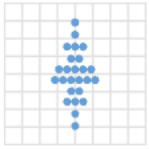
f <- ggplot(mpg, aes(class, hwy))



f + geom_col()
x, y, alpha, color, fill, group, linetype, size



f + geom_boxplot()
x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight



f + geom_dotplot(binaxis = "y", stackdir = “center"**)**
x, y, alpha, color, fill, group

f + geom_violin(scale = “area"**)**
x, y, alpha, color, fill, group, linetype, size, weight

Geom 3: The Scatter Plot (Correlation)

Goal: Comparing two continuous variables.

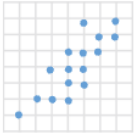
```
ggplot(df, aes(x = Age,
               y = Viral_Load)) +
   geom_point()
```

Are older patients getting sicker?

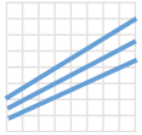
TWO VARIABLES
both continuous

e <- ggplot(mpg, aes(cty, hwy))

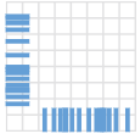
e + geom_label(aes(label = cty)**)** - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust



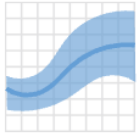
e + geom_point()
x, y, alpha, color, fill, shape, size, stroke



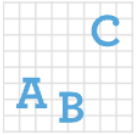
e + geom_quantile()
x, y, alpha, color, group, linetype, size, weight



e + geom_rug(sides = “bl"**)**
x, y, alpha, color, linetype, size



e + geom_smooth(method = lm**)**
x, y, alpha, color, fill, group, linetype, size, weight



e + geom_text(aes(label = cty)**)** - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

Geom 4: The Line Plot (Time Series)

Goal: The QC Levey-Jennings Chart.

```
ggplot(qc_data, aes(x = Date, y = Result)) +
   geom_line() +
   geom_point()
```

Tracking values over time to spot trends or drifts.

Layering: Adding Thresholds

A chart needs context. We draw the "Limit Line".

```
ggplot(df, aes(x = Date, y = Result)) +
   geom_line() +
   geom_hline(yintercept = 6.0,
              color = "red",
              linetype = "dashed")
```

Any point above the red line is instantly recognizable as critical.

Mapping Color to Data

Don't just color it blue. Color it by *meaning*.

```
# Inside aes()
ggplot(df, aes(x = Date,
               y = Result,
               color = Instrument)) +
   geom_line()
```

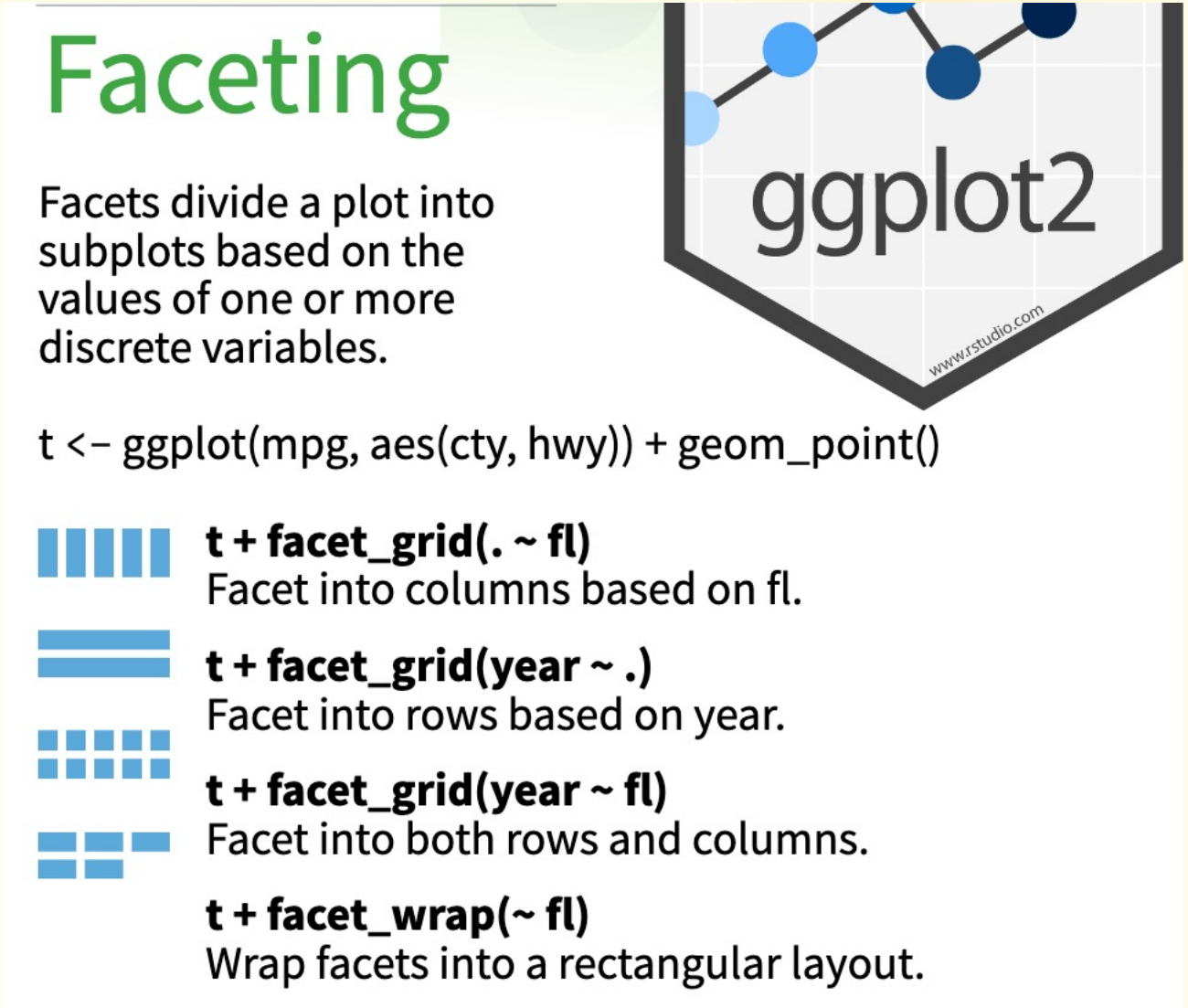
R automatically creates a legend and assigns colors to each Instrument.

Faceting (Small Multiples)

Problem: 10 instruments on one chart is messy.

Solution: Faceting.

```
ggplot(df, aes(x=Date, y=Res)) +
   geom_line() +
   facet_wrap(~ Instrument)
```



Themes (Publication Ready)

Remove the default grey background for a professional look.

```
plot + theme_bw()

# OR

plot + theme_minimal()
```

theme_bw() is best for clinical reports (saves printer ink).

Saving Plots

Don't take screenshots. Export high-res images programmatically.

```
ggsave("Monthly_QC_Report.png",
       width = 8,
       height = 5)
```

Practice: The Levey-Jennings Plan

1. Base

Plot Points & Lines

2. Context

Add Mean Line

3. Limits

Add +/- 2SD Lines

Summary of Geometries

- geom_point(): Scatter Plot
- geom_line(): Time Series
- geom_bar(): Counts
- geom_boxplot(): Stats Comparison
- geom_histogram(): Distribution

Summary of Aesthetics

- x, y: Position coordinates
- color: Line/Point color (outline)
- fill: Bar/Box color (inside)
- size: Size of points
- alpha: Transparency (0=invisible, 1=solid)

Tutorial 4: The QC Trend Analysis

Goal: Build a Monthly Levey-Jennings Chart to compare two instruments.

1. Load Data
2. Visualize Trend
3. Add QC Limits

Step 1: Load Data

library(ggplot2) url <- "https://raw.githubusercontent.com/.../daily_qc_trend.csv" qc_data <- read.csv(url) # Check head(qc_data)

Step 2: Basic Time Series

Ensure Date is recognized, then plot.

```
qc_data$Date <- as.Date(qc_data$Date)

ggplot(qc_data, aes(x = Date,
                    y = Result,
                    color = Instrument)) +
   geom_line() +
   geom_point()
```

Step 3: Interpreting the Mess

The lines overlap. It is hard to see which machine is drifting.

Solution:

Faceting.

Step 4: Faceting

Split into two panels for clarity.

```
ggplot(qc_data, aes(x = Date,
                    y = Result,
                    color = Instrument)) +
   geom_line() +
   geom_point() +
   facet_wrap(~ Instrument)
```

Step 5: Adding QC Limits

Known Values: Mean = 5.0, SD = 0.2

- Mean: 5.0 (Black Line)
- +2SD: 5.4 (Red Dashed)
- -2SD: 4.6 (Red Dashed)

Step 6: Code for Limits

```
... + geom_hline(yintercept = 5.0, color = "black") + geom_hline(yintercept = 5.4, color = "red",
    linetype = "dashed") + geom_hline(yintercept = 4.6, color = "red", linetype = "dashed")
```

Step 7: Final Polish

Add title and clean theme.

```
... +
theme_bw() +
labs(title = "Monthly Levey-Jennings Chart",
     y = "Glucose Level (mmol/L)",
     x = "Date")
```

Analysis: The Diagnosis

Machine B

Flat line.

Very precise.

PASS

Machine A

Bouncing around.

Point on Jan 14 is 5.8 (> 3SD).

FAIL (Outlier)

Step 8: Export

Save your clinical report.

```
ggsave("QC_Dashboard_Jan2026.pdf",
       width = 10,
       height = 6)
```

https://github.com/Koohoko/MSc_Module3_Programming_BioData_HKUSpacce_2026

README

MSc Module 3: Programming for Biological Data (2026)

Instructor: Dr. Gu Haogao
Institution: SPH HKU / HKU SPACE **Date:** January 2026

Course Overview

This repository contains the comprehensive preparation package for **Module 3**, tailored for Postgraduate Certificate in Bioinformatics for Medical Laboratory Technologists (MLTs). This plan integrates the "Code-as-Protocol" pedagogical approach.

Repository Structure

- `lectures/` : Slides and R scripts used during the lecture.
- `tutorials/` : Interactive notebooks for hands-on practice.
- `data/` : Raw datasets used in exercises.
- `setup/` : Scripts to initialize the R environment.

Quick Start

No software installation is required. We will use Google Colab for our "Dry Lab" sessions. Remember to **change runtime to R** while using colab (**Runtime -> Change runtime type -> R**).

- Session 1: Introduction to R (Part 1)
  - Lecture Script
  - Tutorial Notebook: Open in Colab
- Session 2: Introduction to R (Part 2) - Data Frames & I/O
  - Lecture Script
  - Tutorial Notebook: Open in Colab