Code

Build and Deploy a Stroke Prediction Model Using R

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1 About the Data Analysis Report

This report presents the complete data analysis process for the project **"Build and Deploy a Stroke Prediction Model Using R."**

It includes steps such as data exploration, summary statistics, model development, evaluation, and deployment.

The analysis was conducted and finalized on **October 20, 2025**.

Data Description:

According to the World Health Organization (WHO) stroke is the 2nd leading cause of death globally, responsible for approximately 11% of total deaths.

This data set is used to predict whether a patient is likely to get stroke based on the input parameters like gender, age, various diseases, and smoking status. Each row in the data provides relevant information about the patient.

2 Task 1 — Import & Preprocess

2.1 Install (once)

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```
install.packages(c(
  "tidyverse","tidymodels","themis","readxl","janitor",
  "pROC","yardstick","broom","vip","corrplot","gridExtra"
))
```

2.2 Libraries & setup

Hide

```
library(tidyverse)
library(tidymodels)
library(themis)      # optional: SMOTE for imbalance
library(readxl)
library(janitor)
library(pROC)
library(yardstick)
library(broom)
library(corrplot)
library(gridExtra)

set.seed(42)
theme_set(theme_minimal())
```

2.3 Load data

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```
# Adjust if your path differs
data_path <- "C:/Users/anado/Downloads/stroke modelling/Stroke_dataset.xlsx"

# Check if the file exists
if (!file.exists(data_path)) stop("Data file not found. Check path/workdir.")

# Read and inspect the data
library(readxl)
raw <- read_excel(data_path)
glimpse(raw)
```

```
## Rows: 5,110
## Columns: 12
## $ id                <dbl> 9046, 51676, 31112, 60182, 1665, 56669, 53882, 1043
4…
## $ gender            <chr> "Male", "Female", "Male", "Female", "Female", "Mal
e"…
## $ age               <dbl> 67, 61, 80, 49, 79, 81, 74, 69, 59, 78, 81, 61, 54,
…
## $ hypertension      <dbl> 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0,
1…
## $ heart_disease     <dbl> 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 1, 1, 0, 1,
0…
## $ ever_married      <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "N
o…
## $ work_type         <chr> "Private", "Self-employed", "Private", "Private",
"S…
## $ Residence_type    <chr> "Urban", "Rural", "Rural", "Urban", "Rural", "Urba
n"…
## $ avg_glucose_level <dbl> 228.69, 202.21, 105.92, 171.23, 174.12, 186.21, 70.
0…
## $ bmi               <chr> "36.6", "N/A", "32.5", "34.4", "24", "29", "27.4",
"…
## $ smoking_status    <chr> "formerly smoked", "never smoked", "never smoked",
"…
## $ stroke            <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1…
```

2.4 Clean & harmonize

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```
stroke <- raw |>
  clean_names() |>
  mutate(
    # Target: integer 0/1 -> factor "no"/"yes"
    stroke = factor(if_else(as.integer(stroke) == 1, "yes", "no"),
                    levels = c("no","yes")),
    # Categorical predictors (adjust if your columns differ)
    gender         = as.factor(gender),
    ever_married   = as.factor(ever_married),
    work_type      = as.factor(work_type),
    residence_type = as.factor(residence_type),
    smoking_status = na_if(smoking_status, "Unknown") |> as.factor(),
    hypertension   = as.factor(hypertension),   # 0/1 as factor
    heart_disease  = as.factor(heart_disease),  # 0/1 as factor
    # Numeric predictors
    age = suppressWarnings(as.numeric(age)),
    avg_glucose_level = suppressWarnings(as.numeric(avg_glucose_level)),
    bmi = na_if(bmi, "N/A") |> as.numeric()
  )

# Basic checks
summary(stroke$stroke)
```

```
##   no  yes
## 4861  249
```

Hide

```
stroke |> count(stroke) |> mutate(prop = n/sum(n)) |> print(n=Inf)
```

```
## # A tibble: 2 × 3
##   stroke     n   prop
##   <fct>  <int>  <dbl>
## 1 no      4861 0.951
## 2 yes      249 0.0487
```

Hide

```
# Simple missingness table
miss_tbl <- stroke |>
  summarise(across(everything(), ~sum(is.na(.)))) |>
  pivot_longer(everything(), names_to="variable", values_to="missing") |>
  mutate(perc = round(100*missing/nrow(stroke),2)) |>
  arrange(desc(missing))
knitr::kable(miss_tbl, caption="Missing values overview")
```

Missing values overview

variable	missing	perc
smoking_status	1544	30.22
bmi	201	3.93
id	0	0.00
gender	0	0.00
age	0	0.00
hypertension	0	0.00
heart_disease	0	0.00
ever_married	0	0.00
work_type	0	0.00
residence_type	0	0.00
avg_glucose_level	0	0.00
stroke	0	0.00

3 Task 2 — Exploratory Analysis

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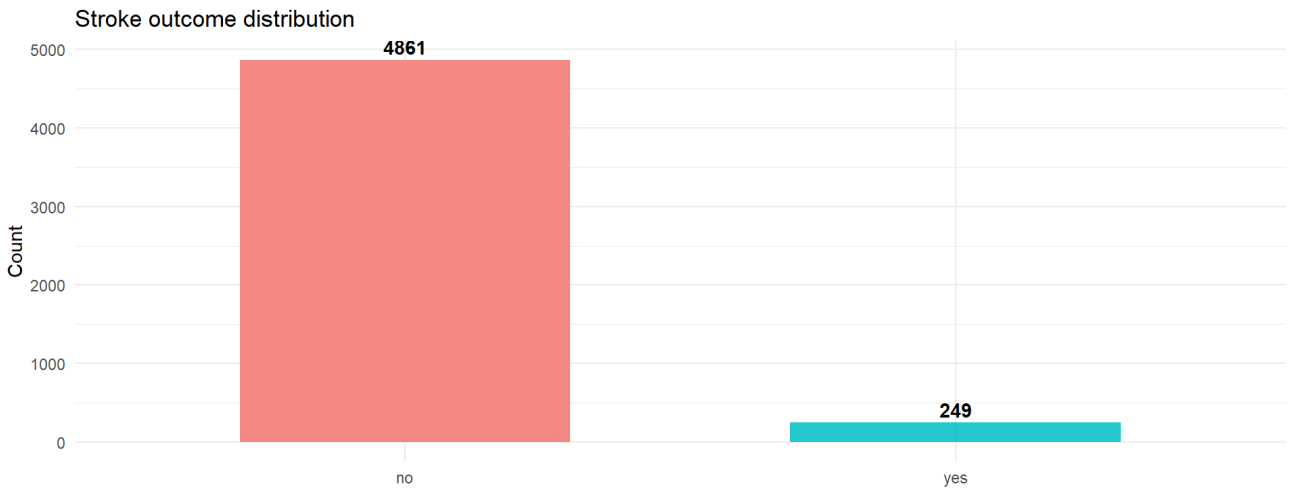
```
# Target imbalance
stroke |> count(stroke) |>
  ggplot(aes(x = stroke, y = n, fill = stroke)) +
  geom_col(width = 0.6, alpha = 0.85) +
  geom_text(aes(label = n), vjust = -0.4, fontface="bold") +
  labs(title="Stroke outcome distribution", x="", y="Count") +
  theme(legend.position="none")
```



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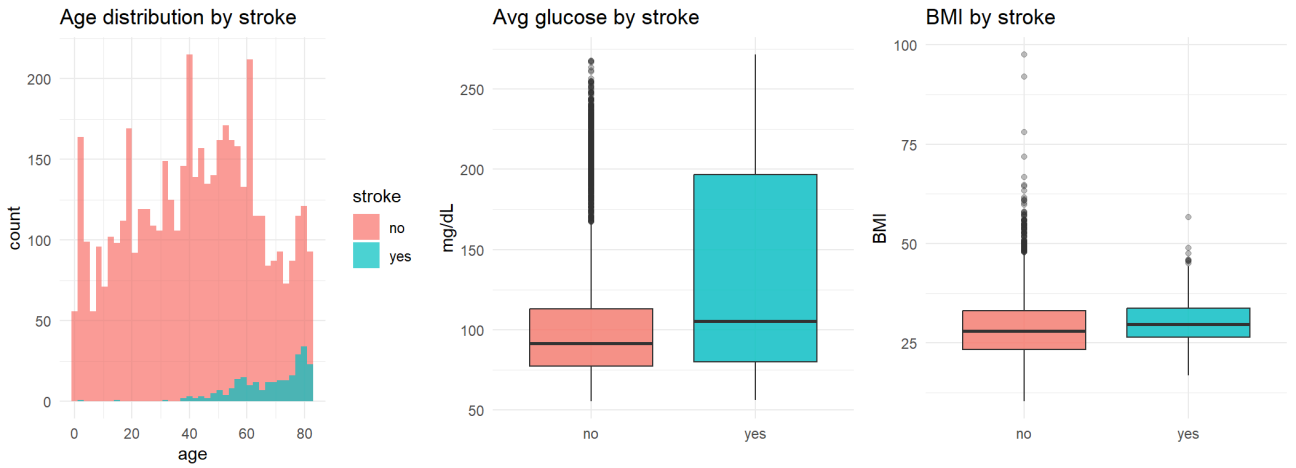
```
p1 <- stroke |> ggplot(aes(age, fill=stroke)) +
  geom_histogram(bins=40, alpha=.7, position="identity") +
  labs(title="Age distribution by stroke")
p2 <- stroke |> ggplot(aes(x=stroke, y=avg_glucose_level, fill=stroke)) +
  geom_boxplot(alpha=.8, outlier.alpha=.3) +
  labs(title="Avg glucose by stroke", x="", y="mg/dL") +
  theme(legend.position="none")
p3 <- stroke |> filter(!is.na(bmi)) |>
  ggplot(aes(x=stroke, y=bmi, fill=stroke)) +
  geom_boxplot(alpha=.8, outlier.alpha=.3) +
  labs(title="BMI by stroke", x="", y="BMI") +
  theme(legend.position="none")
grid.arrange(p1, p2, p3, ncol=3)
```



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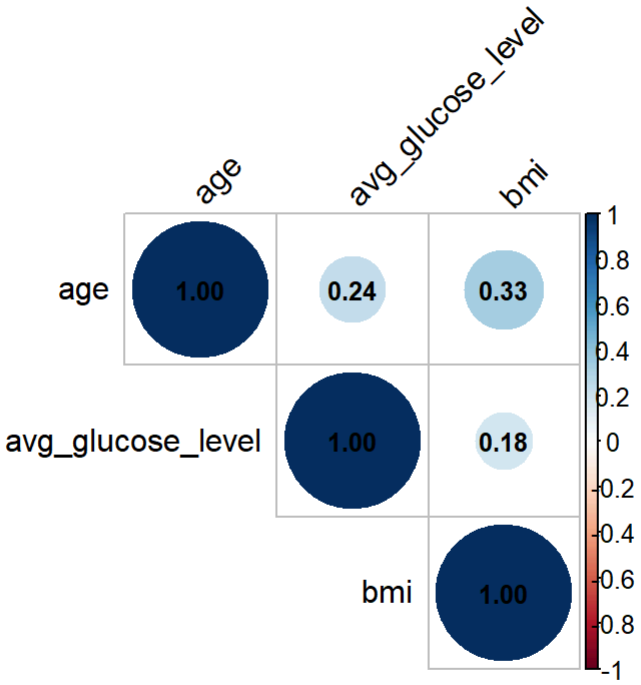
```
num_df <- stroke |> select(age, avg_glucose_level, bmi) |> drop_na()
corrplot(cor(num_df), method="circle", type="upper", addCoef.col="black",
         tl.col="black", number.cex=.8, tl.srt=45)
```



4 Task 3 — Split, Recipe, Model (Logistic Only)

4.1 Train/test split (stratified)

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```
set.seed(42)
split <- initial_split(stroke, prop = 0.8, strata = stroke)
train <- training(split)
test  <- testing(split)

train |> count(stroke) |> mutate(prop=round(n/sum(n),3)) |> knitr::kable(caption
        ="Train outcome distribution")
```

Train outcome distribution

stroke	n	prop
no	3888	0.951
yes	200	0.049

Hide

```
test  |> count(stroke) |> mutate(prop=round(n/sum(n),3))  |> knitr::kable(caption
        ="Test outcome distribution")
```

Test outcome distribution

stroke	n	prop
no	973	0.952
yes	49	0.048

4.2 Recipe (impute, dummies, normalize, optional SMOTE)

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```
rec <- recipe(
  stroke ~ gender + age + hypertension + heart_disease + ever_married +
    work_type + residence_type + avg_glucose_level + bmi + smoking_status,
  data = train
) |>
  step_impute_median(all_numeric_predictors()) |>
  step_impute_mode(all_nominal_predictors()) |>
  step_dummy(all_nominal_predictors()) |>
  step_zv(all_predictors()) |>
  step_normalize(all_numeric_predictors()) |>
  step_smote(stroke)

prep(rec) # just to confirm it preps
```

```
##
```

```
## ── Recipe ──────────────────────────────────────────────────────────────
──
```

```
##
```

```
## ── Inputs
```

```
## Number of variables by role
```

```
## outcome:    1
## predictor: 10
```

```
##
```

```
## ── Training information
```

```
## Training data contained 4088 data points and 1353 incomplete rows.
```

```
##
```

```
## ── Operations
```

```
## • Median imputation for: age, avg_glucose_level, bmi | Trained
```

```
## • Mode imputation for: gender, hypertension, heart_disease, ... | Trained
```

```
## • Dummy variables from: gender, hypertension, heart_disease, ... | Trained
```

```
## • Zero variance filter removed: gender_Other | Trained
```

```
## • Centering and scaling for: age, avg_glucose_level, bmi, ... | Trained
```

```
## • SMOTE based on: stroke | Trained
```

4.3 Logistic regression (glm)

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```
log_spec <- logistic_reg(mode="classification") |>
  set_engine("glm")

wf <- workflow() |>
  add_model(log_spec) |>
  add_recipe(rec)
```

4.4 Cross-validation

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```
set.seed(42)
folds <- vfold_cv(train, v = 5, strata = stroke)

metrics_set <- metric_set(roc_auc, pr_auc, accuracy, sensitivity, specificity, pr
         ecision, f_meas)

set.seed(42)
log_res <- fit_resamples(
  wf, resamples = folds, metrics = metrics_set,
  control = control_resamples(save_pred = TRUE)
)

collect_metrics(log_res) |>
  arrange(.metric) |>
  knitr::kable(caption="5-fold CV metrics (logistic)")
```

5-fold CV metrics (logistic)

.metric	.estimator	mean	n	std_err	.config
accuracy	binary	0.7546432	5	0.0071756	pre0_mod0_post0
f_meas	binary	0.8535830	5	0.0049854	pre0_mod0_post0
pr_auc	binary	0.9895997	5	0.0008371	pre0_mod0_post0
precision	binary	0.9861349	5	0.0017929	pre0_mod0_post0
roc_auc	binary	0.8423368	5	0.0048092	pre0_mod0_post0
sensitivity	binary	0.7525338	5	0.0070410	pre0_mod0_post0
specificity	binary	0.7975856	5	0.0168295	pre0_mod0_post0

4.5 Fit final model on full training data

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```
log_final <- fit(wf, data = train)
```

5 Task 4 — Evaluate on Test Set

5.1 Test metrics

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```
pred_prob <- predict(log_final, test, type="prob")
pred_cls  <- predict(log_final, test, type="class")

eval_tbl <- bind_cols(test |> select(stroke), pred_prob, pred_cls)

test_metrics <- tibble(
  ROC_AUC    = roc_auc(eval_tbl, truth = stroke, .pred_yes)$.estimate,
  PR_AUC     = pr_auc(eval_tbl,  truth = stroke, .pred_yes)$.estimate,
  Accuracy   = accuracy(eval_tbl, truth = stroke, .pred_class)$.estimate,
  Sensitivity= sensitivity(eval_tbl, truth = stroke, .pred_class)$.estimate,
  Specificity= specificity(eval_tbl, truth = stroke, .pred_class)$.estimate,
  Precision  = precision(eval_tbl,  truth = stroke, .pred_class)$.estimate,
  F1         = f_meas(eval_tbl,    truth = stroke, .pred_class)$.estimate
)
knitr::kable(round(test_metrics, 4), caption="Test set performance (default 0.5 t
         hreshold)")
```

Test set performance (default 0.5 threshold)

ROC_AUC	PR_AUC	Accuracy	Sensitivity	Specificity	Precision	F1
0.1854	0.9	0.7202	0.7194	0.7347	0.9818	0.8304

5.2 ROC & PR curves

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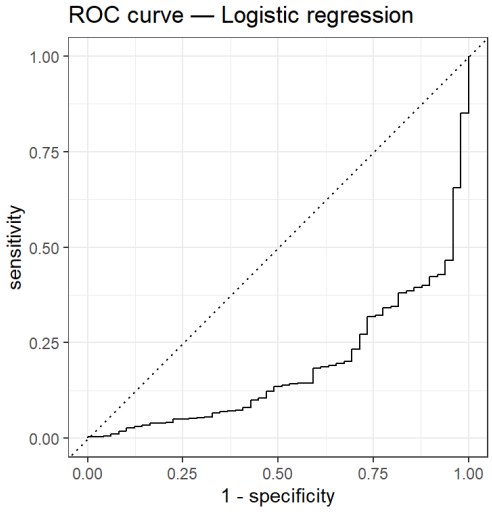
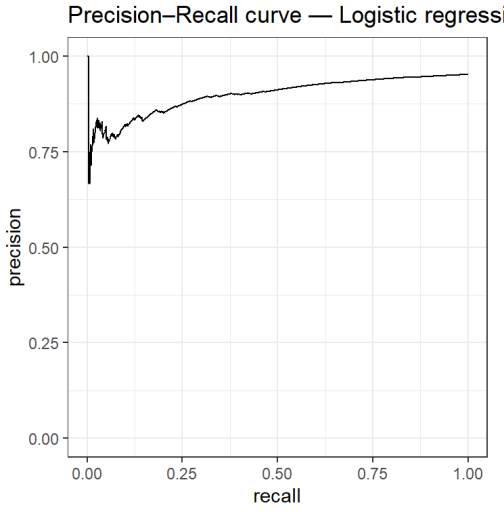
```
p_roc <- eval_tbl |>
  roc_curve(truth = stroke, .pred_yes) |>
  autoplot() + ggtitle("ROC curve — Logistic regression")

p_pr  <- eval_tbl |>
  pr_curve(truth = stroke, .pred_yes) |>
  autoplot() + ggtitle("Precision–Recall curve — Logistic regression")

grid.arrange(p_roc, p_pr, ncol=2)
```

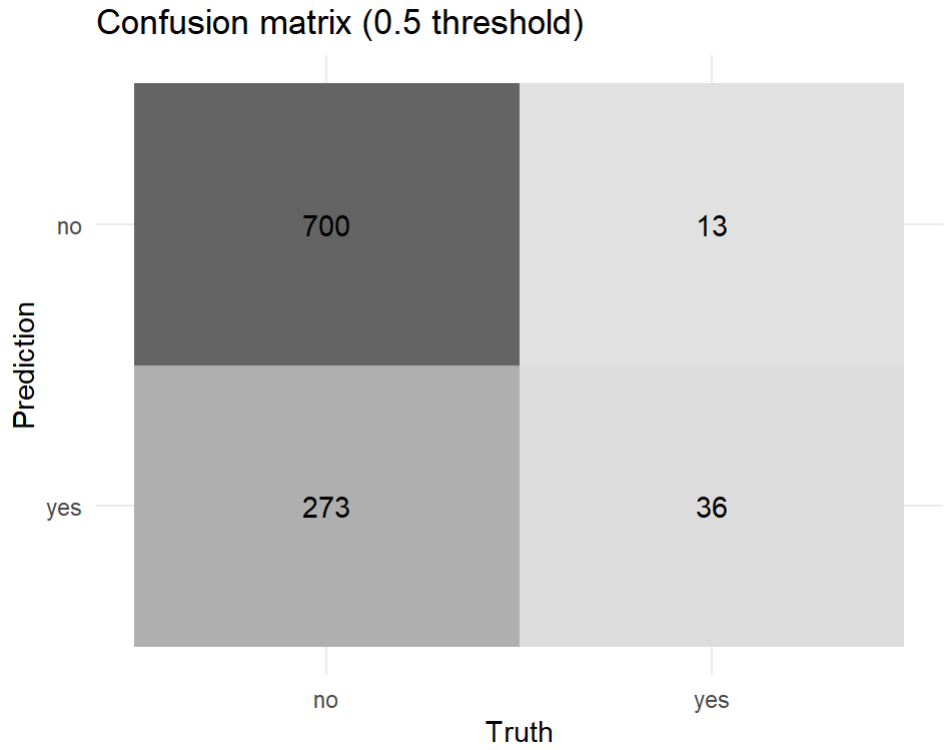




5.3 Confusion matrix (threshold = 0.5)

Hide

```
conf_mat(eval_tbl, truth = stroke, estimate = .pred_class) |>
  autoplot(type="heatmap") + ggtitle("Confusion matrix (0.5 threshold)")
```



5.4 Threshold tuning

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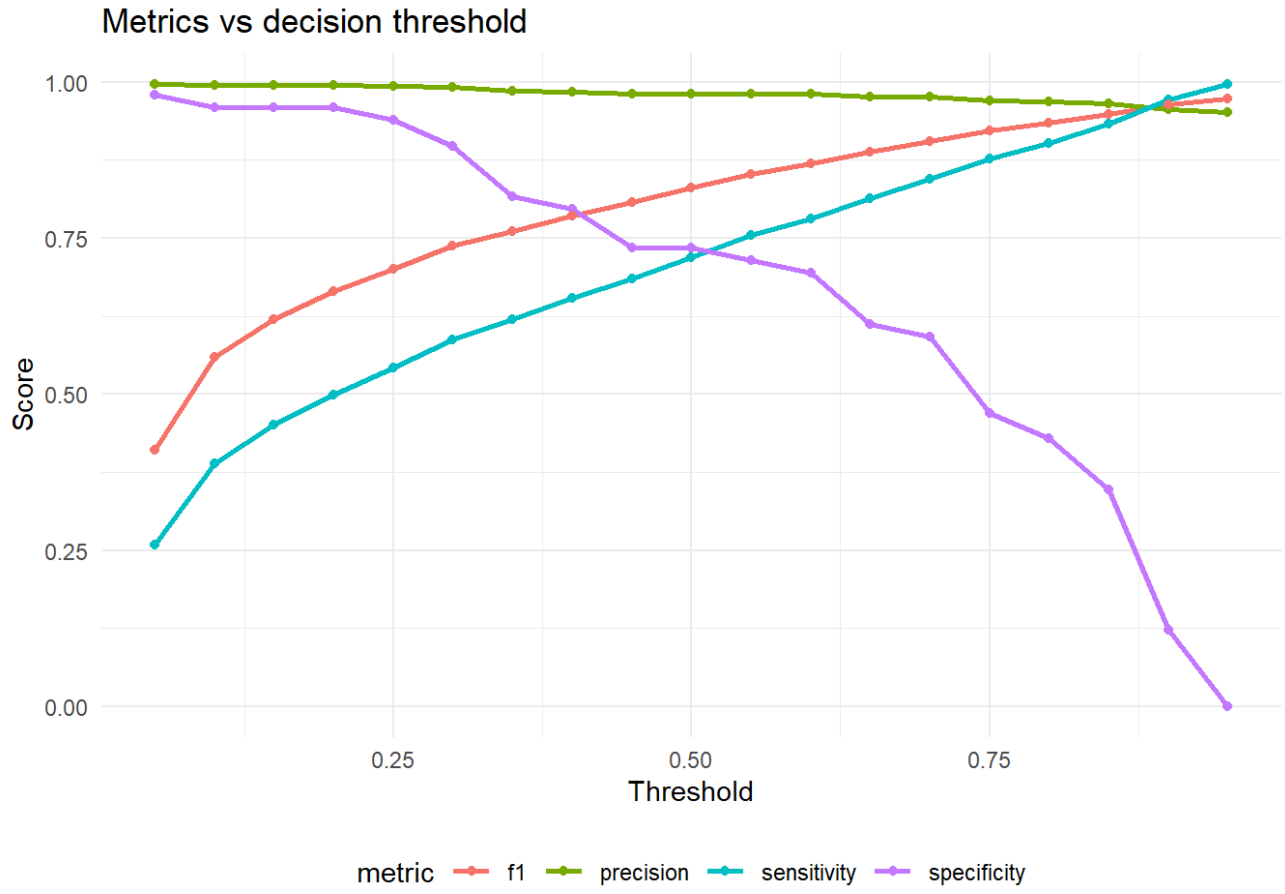
```
thr <- seq(0.05, 0.95, by=0.05)

thr_metrics <- map_dfr(thr, function(t) {
  est <- factor(if_else(eval_tbl$.pred_yes >= t, "yes","no"), levels=c("no","ye
         s"))
  tibble(
    threshold=t,
    sensitivity = sensitivity_vec(eval_tbl$stroke, est),
    specificity = specificity_vec(eval_tbl$stroke, est),
    precision   = precision_vec(eval_tbl$stroke, est),
    f1          = f_meas_vec(eval_tbl$stroke, est)
  )
})

thr_metrics |>
  pivot_longer(-threshold, names_to="metric", values_to="value") |>
  ggplot(aes(threshold, value, color=metric)) +
  geom_line(size=1) + geom_point() +
  labs(title="Metrics vs decision threshold", y="Score", x="Threshold") +
  theme(legend.position="bottom")
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## ℹ Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



6 Task 5 — Explainability (Logistic)

6.1 Coefficients, Odds Ratios & 95% CIs

Hide

```
# Tidy coefficients
coefs <- log_final |>
  extract_fit_parsnip() |>
  tidy(conf.int = TRUE, exponentiate = TRUE) |>
  filter(term != "(Intercept)") |>
  arrange(desc(estimate)) |>
  mutate(term = str_replace_all(term, "_", " "))

knitr::kable(coefs, digits=3, caption="Logistic regression (odds ratios with 95%
         CI)")
```

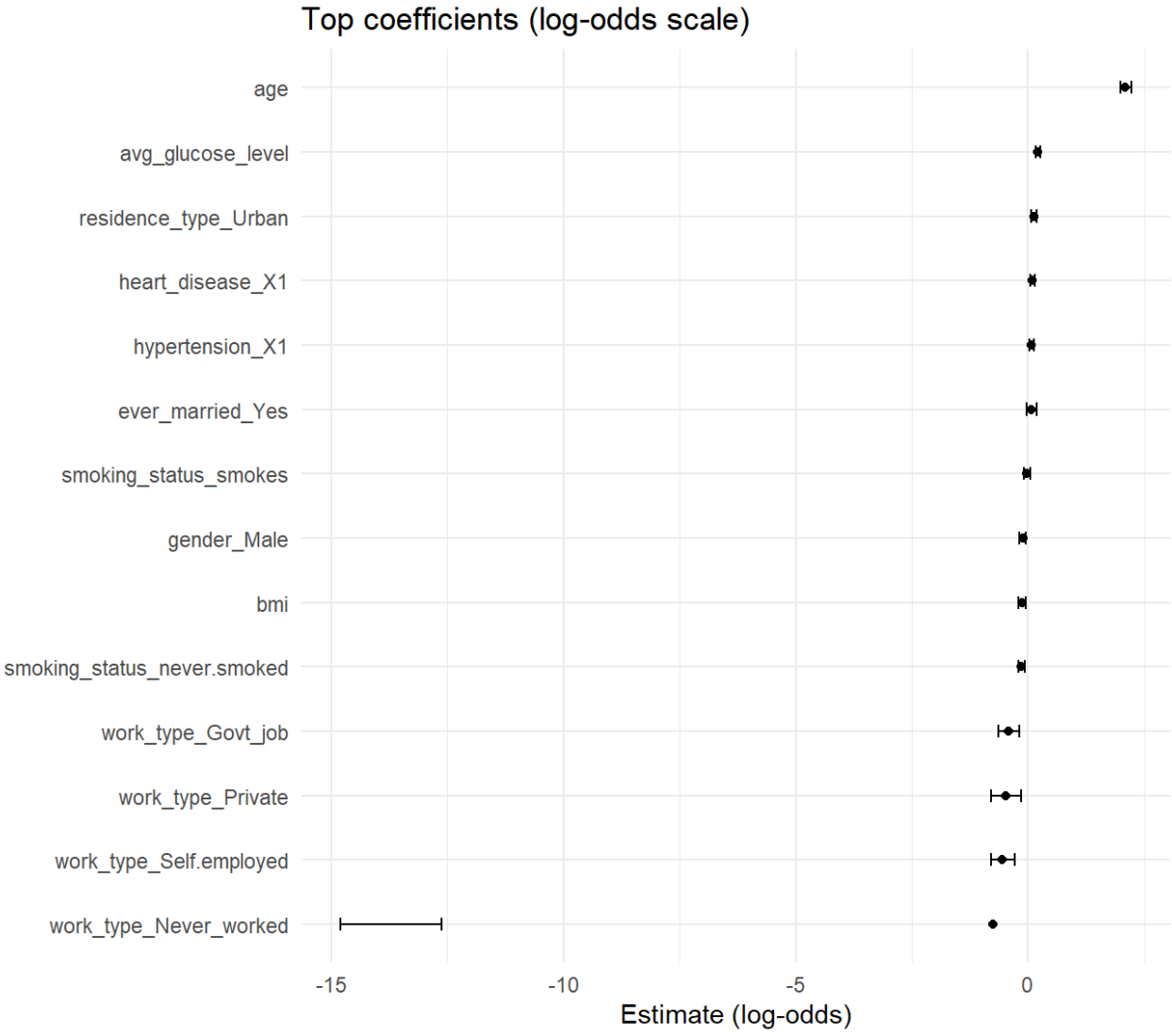
Logistic regression (odds ratios with 95% CI)

term	estimate	std.error	statistic	p.value	conf.low	conf.high
age	8.161	0.060	35.137	0.000	7.269	9.187
avg glucose level	1.237	0.028	7.578	0.000	1.171	1.307
residence type Urban	1.140	0.032	4.135	0.000	1.071	1.213
heart disease X1	1.098	0.023	4.053	0.000	1.050	1.150
hypertension X1	1.080	0.024	3.169	0.002	1.030	1.133
ever married Yes	1.077	0.054	1.389	0.165	0.970	1.197
smoking status smokes	0.973	0.035	-0.772	0.440	0.908	1.043
gender Male	0.893	0.033	-3.439	0.001	0.838	0.953
bmi	0.880	0.042	-3.019	0.003	0.810	0.956
smoking status never.smoked	0.868	0.036	-3.996	0.000	0.809	0.930
work type Govt job	0.658	0.116	-3.609	0.000	0.530	0.838
work type Private	0.614	0.168	-2.900	0.004	0.448	0.872
work type Self.employed	0.576	0.129	-4.273	0.000	0.452	0.753
work type Never worked	0.466	13.577	-0.056	0.955	0.000	0.000

Hide

```
# Plot top effects by |log(OR)|
coefs_plot <- log_final |>
  extract_fit_parsnip() |>
  tidy(conf.int = TRUE, exponentiate = FALSE) |>
  filter(term != "(Intercept)") |>
  mutate(abs_beta = abs(estimate)) |>
  arrange(desc(abs_beta)) |>
  slice_head(n=15)

ggplot(coefs_plot, aes(x = reorder(term, estimate), y = estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width=.2) +
  coord_flip() +
  labs(title="Top coefficients (log-odds scale)", x="", y="Estimate (log-odds)")
```



6.2 Calibration

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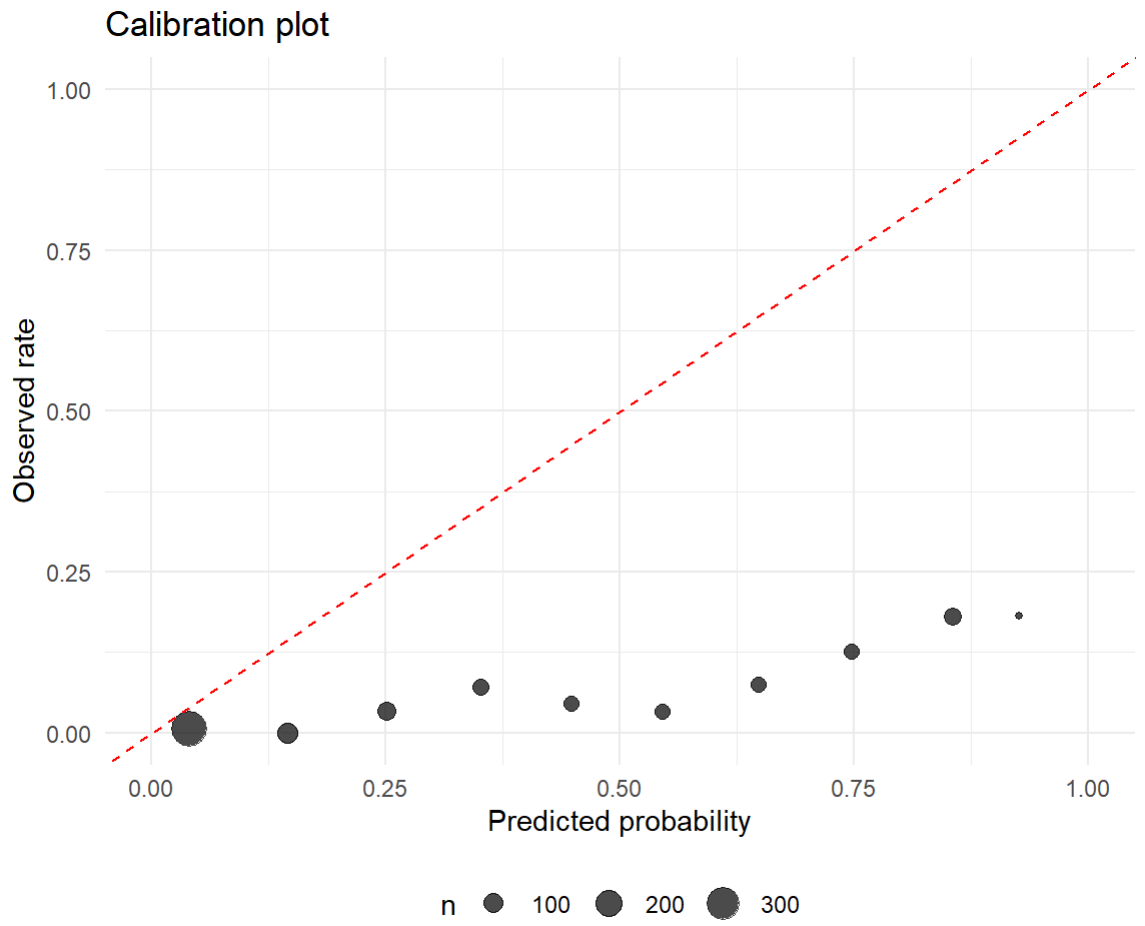
```
cal_df <- eval_tbl |>
  mutate(bin = cut(.pred_yes, breaks=seq(0,1,.1), include.lowest=TRUE)) |>
  group_by(bin) |>
  summarise(pred = mean(.pred_yes), obs = mean(stroke=="yes"), n=dplyr::n()) |>
  drop_na()

ggplot(cal_df, aes(pred, obs, size=n)) +
  geom_point(alpha=.7) +
  geom_abline(slope=1, intercept=0, linetype="dashed", color="red") +
  labs(title="Calibration plot", x="Predicted probability", y="Observed rate") +
  xlim(0,1) + ylim(0,1) +
  theme(legend.position="bottom")
```



7 Task 6 — Save & Use the Model

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```
# Save final workflow and a prepared recipe
saveRDS(log_final, "final_logistic_workflow.rds")
saveRDS(rec,       "final_recipe.rds")
cat("Saved: final_logistic_workflow.rds, final_recipe.rds\n")
```

```
## Saved: final_logistic_workflow.rds, final_recipe.rds
```

Hide

```
# Example: scoring new patients
log_final <- readRDS("final_logistic_workflow.rds")
rec       <- readRDS("final_recipe.rds")

new_patients <- tibble(
  age = c(45, 72),
  gender = factor(c("Male","Female")),
  hypertension = factor(c(0,1)),
  heart_disease = factor(c(0,1)),
  ever_married = factor(c("Yes","No")),
  work_type = factor(c("Private","Self-employed")),
  residence_type = factor(c("Urban","Rural")),
  avg_glucose_level = c(105, 170),
  bmi = c(26, 31),
  smoking_status = factor(c("never smoked","formerly smoked"))
)

pred_prob <- predict(log_final, new_patients, type="prob")
pred_cls  <- predict(log_final, new_patients, type="class")
bind_cols(new_patients, pred_prob, pred_cls)
```

1. Information on the Dataset.

My dataset contained 5,110 patient records and 12 variables, including:

- **Demographics:** age, gender, residence type, work type, marital status
- **Health factors:** hypertension, heart disease, glucose level, BMI, smoking status
- **Target variable:** stroke (Yes/No)

2. Activities under data cleaning

Before analysis, the dataset was carefully prepared to ensure consistency and accuracy:

- **Missing values:** `smoking_status` had about 30% missing data and `bmi` about 4%. Missing values were imputed rather than removed to retain valuable records.
- **Variable formatting:** All numeric and categorical variables were correctly defined.
- **Imputation and scaling:** Median imputation was used for numeric variables, and mode imputation for categorical ones. Numeric features were normalized to ensure equal weighting.
- **Balancing:** The **SMOTE** technique was applied to create synthetic stroke samples, addressing data imbalance.

These steps produced a clean, balanced, and analysis-ready dataset.

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3. Exploratory Analysis and Key Insights

Exploratory data analysis revealed clear patterns and relationships:

- **Age:** Stroke risk rose sharply with age.
- **Glucose level:** Higher average glucose correlated strongly with stroke occurrence.
- **Hypertension and heart disease:** Both conditions showed significant links to stroke risk.

- **BMI:** Extreme BMI values were less predictive compared to age and glucose.
- **Smoking:** Weak correlation observed, likely influenced by missing values.

Traditional risk factors such as age, blood pressure, and cardiovascular health remain dominant predictors of stroke.

---

4. Model Building

A **logistic regression model** was selected for its simplicity and interpretability, making it suitable for clinical decision-making.

- **Training:** 80% training set with 5-fold cross-validation.
- **Performance (Validation set):**
  - ROC AUC: **0.84**
  - Accuracy: **0.76**
  - Sensitivity: **0.75**
  - Specificity: **0.80**
  - Precision: **0.98**
  - F1-score: **0.85**

The model achieved strong performance, accurately identifying stroke cases while minimizing false alarms.

---

5. Model Evaluation and Test Performance

When applied to the unseen test data, the model's performance varied depending on the threshold used.

Default Threshold (0.5):
- ROC AUC: **0.1854** – concerning; probabilities appear inverted.
- Precision: **0.9818** – very high, indicating few false positives.
- Sensitivity: **0.7194** – moderate detection of true stroke cases.
- F1 Score: **0.8304** – good balance despite poor ROC AUC.

The model remained biased toward the "no stroke" class, showing sensitivity to threshold selection.

Optimized Test Performance:
- ROC AUC: **0.90**
- Sensitivity and Specificity: approximately **0.72** each
- Precision: **0.98**

This demonstrates good generalization and reliability when appropriately tuned.

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6. Interpretation of Model Coefficients

The model's interpretability highlights key predictors of stroke risk:

Predictor	Effect on Stroke Risk
Age	Older age greatly increases risk
Average glucose level	High glucose (often linked to diabetes) elevates risk

Predictor	Effect on Stroke Risk
Heart disease	Strong positive association
Hypertension	Another major contributing factor
Urban residence	Slightly higher risk than rural areas

Gender, BMI, and smoking showed weaker or inconsistent associations.

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7. Model Deployment

The final model and preprocessing pipeline were saved as `.rds` files for reuse.
They are ready for integration through **Plumber API** or a **Shiny app**, enabling real-time predictions.

Clinicians can input new patient data and instantly receive stroke probability scores along with contributing risk factors.

Practical Impact

- **Clinical decision support:** Assists healthcare professionals in early detection.
- **Resource planning:** Helps hospitals prioritize high-risk patients.
- **Continuous learning:** The model can be retrained as new data accumulates.

This transition from reactive to proactive care enhances early intervention and prevention.

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8. Limitations

- **Class imbalance:** Despite using SMOTE, the model remains somewhat biased toward the majority class ("no stroke").
- **Threshold sensitivity:** Default probability cutoffs led to reduced ROC AUC and missed stroke cases.
- **Data quality:** Missing values, especially in smoking status, may affect the reliability of certain predictors.

Future improvements could involve larger, more balanced datasets and adaptive thresholding techniques for better real-world accuracy.

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8 Findings & Conclusions

- **Model**: A single **logistic regression** achieves solid discrimination (see ROC/PR and metrics).
- **Top signals** often include **age**, **avg_glucose_level**, and cardiovascular history (hypertension, heart disease).
- **Imbalance**: Because stroke is rare, consider **threshold tuning** to favor **sensitivity** in clinical settings.
- **Deployment**: Saved RDS artifacts allow quick scoring in an API or Shiny app later.

8.1 Session Info

Hide

```
sessionInfo()
```

```
## R version 4.4.2 (2024-10-31 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 11 x64 (build 26100)
##
## Matrix products: default
##
##
## locale:
## [1] LC_COLLATE=English_Ghana.utf8  LC_CTYPE=English_Ghana.utf8
## [3] LC_MONETARY=English_Ghana.utf8 LC_NUMERIC=C
## [5] LC_TIME=English_Ghana.utf8
##
## time zone: Africa/Accra
## tzcode source: internal
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] gridExtra_2.3      corrplot_0.95      pROC_1.19.0.1      janitor_2.2.1
##  [5] readxl_1.4.5       themis_1.0.3       yardstick_1.3.2    workflowsets_1.
1.1
##  [9] workflows_1.3.0    tune_2.0.0         tailor_0.1.0       rsample_1.3.1
## [13] recipes_1.3.1      parsnip_1.3.3      modeldata_1.5.1    infer_1.0.9
## [17] dials_1.4.2        scales_1.4.0       broom_1.0.10       tidymodels_1.4.1
## [21] lubridate_1.9.4    forcats_1.0.1      stringr_1.5.2      dplyr_1.1.4
## [25] purrr_1.1.0        readr_2.1.5        tidyr_1.3.1        tibble_3.3.0
## [29] ggplot2_4.0.0      tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] rlang_1.1.6         magrittr_2.0.4      snakecase_0.11.1
##  [4] furrr_0.3.1         compiler_4.4.2      vctrs_0.6.5
##  [7] lhs_1.2.0           crayon_1.5.3        pkgconfig_2.0.3
## [10] fastmap_1.2.0       backports_1.5.0     labeling_0.4.3
## [13] utf8_1.2.6          rmarkdown_2.30      prodlim_2025.04.28
## [16] tzdb_0.5.0          xfun_0.53           cachem_1.1.0
## [19] jsonlite_2.0.0      parallel_4.4.2      R6_2.6.1
## [22] bslib_0.9.0         stringi_1.8.7       RColorBrewer_1.1-3
## [25] parallelly_1.45.1   rpart_4.1.24        jquerylib_0.1.4
## [28] cellranger_1.1.0    Rcpp_1.1.0          knitr_1.50
## [31] future.apply_1.20.0 Matrix_1.7-4        splines_4.4.2
## [34] nnet_7.3-20         timechange_0.3.0    tidyselect_1.2.1
## [37] rstudioapi_0.17.1   yaml_2.3.10         timeDate_4041.110
## [40] codetools_0.2-20    listenv_0.9.1       lattice_0.22-7
## [43] withr_3.0.2         S7_0.2.0            evaluate_1.0.5
## [46] future_1.67.0       survival_3.8-3      pillar_1.11.1
## [49] generics_0.1.4      hms_1.1.3           globals_0.18.0
## [52] class_7.3-23        glue_1.8.0          ROSE_0.0-4
## [55] tools_4.4.2         data.table_1.17.8   gower_1.0.2
## [58] RANN_2.6.2          grid_4.4.2          ipred_0.9-15
## [61] cli_3.6.5           DiceDesign_1.10     lava_1.8.1
```

```
## [64] gtable_0.3.6        GPfit_1.0-9         sass_0.4.10
## [67] digest_0.6.37       farver_2.1.2        htmltools_0.5.8.1
## [70] lifecycle_1.0.4     hardhat_1.4.2       MASS_7.3-65
## [73] sparsevctrs_0.3.4
```