1. Import The Data

```
from google.colab import files
import io
import pandas as pd

# Upload file
uploaded = files.upload()
```

Choose Files Insulin_Dataset.csv

- **Insulin_Dataset.csv**(text/csv) - 101336 bytes, last modified: 9/5/2025 - 100% done

```
Saving Insulin_Dataset.csv to Insulin_Dataset.csv
```

```
df = pd.read_csv(io.BytesIO(uploaded['Insulin_Dataset.csv']))
```

Check Data

```
# Check Shape And First 5 Rows
print("Shape of dataset:", df.shape)
df.head()
```

```
Shape of dataset: (700, 28)
```

	patient_id	date	time	glucose_level	target_glucose	carbs_g	protein_g	fat_
0	3	2025-01-09	21:08:00	202.5	100.0	0.0	18.0	6
1	1	2025-01-01	13:53:00	214.4	100.0	35.0	15.0	9
2	1	2025-01-01	20:19:00	238.9	100.0	0.0	1.0	12
3	3	2025-01-07	20:22:00	190.9	100.0	0.0	4.0	17
4	1	2025-01-14	13:59:00	168.8	100.0	0.0	16.0	0

5 rows × 28 columns

Understand The Data

```
# Dataset Info
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 700 entries, 0 to 699
Data columns (total 28 columns):
 #   Column                         Non-Null Count  Dtype  
---  ------                         --------------  -----  
 0   patient_id                     700 non-null    int64  
 1   date                           700 non-null    object 
 2   time                           700 non-null    object 
 3   glucose_level                  695 non-null    float64
 4   target_glucose                 696 non-null    float64
 5   carbs_g                        695 non-null    float64
 6   protein_g                      693 non-null    float64
 7   fat_g                          696 non-null    float64
 8   fiber_g                        698 non-null    float64
 9   meal_type                      699 non-null    object 
 10  glycemic_index                 693 non-null    float64
 11  bolus_dose_units               695 non-null    float64
 12  bolus_type                     696 non-null    object 
 13  basal_rate                     695 non-null    float64
 14  insulin_on_board               698 non-null    float64
 15  duration_of_insulin_action     693 non-null    float64
 16  time_since_last_bolus          698 non-null    float64
 17  dynamic_IOB                    697 non-null    float64
 18  insulin_to_carb_ratio          694 non-null    float64
 19  correction_factor              696 non-null    float64
 20  circadian_sensitivity_factor  695 non-null    float64
 21  stress_level                   696 non-null    object 
 22  activity_level                 694 non-null    object 
 23  sleep_hours                    693 non-null    float64
 24  recommended_bolus_units        696 non-null    float64
 25  age                            700 non-null    int64  
 26  weight_kg                      700 non-null    float64
 27  genetic_risk                   700 non-null    int64  
dtypes: float64(19), int64(3), object(6)
memory usage: 153.3+ KB
```

```
# Missing Values Check
print("\nMissing Values per Column:")
print(df.isnull().sum())
```

```
Missing Values per Column:
patient_id                      0
date                            0
time                            0
glucose_level                   5
target_glucose                  4
carbs_g                         5
protein_g                       7
fat_g                           4
fiber_g                         2
meal_type                       1
glycemic_index                  7
bolus_dose_units                5
bolus_type                      4
basal_rate                      5
insulin_on_board                2
duration_of_insulin_action      7
time_since_last_bolus           2
dynamic_IOB                     3
insulin_to_carb_ratio           6
correction_factor               4
```

```
circadian_sensitivity_factor    5
stress_level                    4
activity_level                  6
sleep_hours                     7
recommended_bolus_units         4
age                             0
weight_kg                       0
genetic_risk                    0
dtype: int64
```

```
# Numerical Summary Statistics
print("\nSummary Statistics:")
display(df.describe())
```

```
Summary Statistics:
```

	patient_id	glucose_level	target_glucose	carbs_g	protein_g	fat_g
count	700.000000	695.000000	696.0	695.000000	693.000000	696.000000
mean	1.994286	161.299281	100.0	27.428777	15.431457	10.120690
std	0.812965	50.703146	0.0	33.230143	8.841082	6.077185
min	1.000000	70.100000	100.0	0.000000	0.000000	0.000000
25%	1.000000	118.350000	100.0	0.000000	8.000000	5.000000
50%	2.000000	162.100000	100.0	0.000000	16.000000	10.000000
75%	3.000000	206.450000	100.0	56.500000	23.000000	15.000000
max	3.000000	249.800000	100.0	100.000000	30.000000	20.000000

8 rows × 22 columns

```
# Unique Value In Categorical Coloumn
print("\nUnique values in categorical columns:")
for col in ["meal_type", "bolus_type", "stress_level", "activity_level", "genetic_risk"]:
    print(f"{col}: {df[col].unique()}")
```

```
Unique values in categorical columns:
meal_type: ['dinner' 'lunch' 'snack' 'breakfast' nan]
bolus_type: ['square' 'dual-wave' 'normal' nan]
stress_level: ['high' 'low' 'medium' nan]
activity_level: ['heavy' 'none' 'light' 'moderate' nan]
genetic_risk: [1 0 2]
```

2. Cleaning The Data

```
# Missing values check again
print("Missing values before cleaning:\n", df.isnull().sum())
```

```
Missing values before cleaning:
 patient_id                       0
date                            0
time                            0
glucose_level                   5
target_glucose                  4
carbs_g                         5
protein_g                       7
fat_g                           4
fiber_g                         2
meal_type                       1
glycemic_index                  7
bolus_dose_units                5
bolus_type                      4
basal_rate                      5
insulin_on_board                2
duration_of_insulin_action      7
time_since_last_bolus           2
dynamic_IOB                     3
insulin_to_carb_ratio           6
correction_factor               4
circadian_sensitivity_factor    5
stress_level                    4
activity_level                  6
sleep_hours                     7
recommended_bolus_units         4
age                             0
weight_kg                       0
genetic_risk                    0
dtype: int64
```

```
# 1. Clean Missing Value In Numerical columns (mean/median se)
num_cols = df.select_dtypes(include=['float64', 'int64']).columns
for col in num_cols:
    df[col].fillna(df[col].median(), inplace=True)
```

```
/tmp/ipython-input-1618714734.py:4: FutureWarning: A value is trying to be set on a c
The behavior will change in pandas 3.0. This inplace method will never work because t

For example, when doing 'df[col].method(value, inplace=True)', try using 'df.method({


  df[col].fillna(df[col].median(), inplace=True)
```

```
# 2. Clean Missing Value In Categorical columns (mode se)
cat_cols = df.select_dtypes(include=['object']).columns
for col in cat_cols:
    df[col].fillna(df[col].mode()[0], inplace=True)
```

```
/tmp/ipython-input-614862806.py:4: FutureWarning: A value is trying to be set on a cc
The behavior will change in pandas 3.0. This inplace method will never work because t

For example, when doing 'df[col].method(value, inplace=True)', try using 'df.method({
        df[col].fillna(df[col].mode()[0], inplace=True)


# Verify cleaning
print("\nMissing values after cleaning:\n", df.isnull().sum())
```

```
Missing values after cleaning:
 patient_id                    0
date                          0
time                          0
glucose_level                 0
target_glucose                0
carbs_g                       0
protein_g                     0
fat_g                         0
fiber_g                       0
meal_type                     0
glycemic_index                0
bolus_dose_units              0
bolus_type                    0
basal_rate                    0
insulin_on_board              0
duration_of_insulin_action    0
time_since_last_bolus         0
dynamic_IOB                   0
insulin_to_carb_ratio         0
correction_factor             0
circadian_sensitivity_factor  0
stress_level                  0
activity_level                0
sleep_hours                   0
recommended_bolus_units       0
age                           0
weight_kg                     0
genetic_risk                  0
dtype: int64
```

```
# Save cleaned dataset
df.to_csv("insulin_predictor_cleaned.csv", index=False)
print("\n✅ Cleaned dataset saved as 'insulin_predictor_cleaned.csv'")
```

```
✅ Cleaned dataset saved as 'insulin_predictor_cleaned.csv'
```

3. Exploratory Data Analysis (EDA)

1. Data Distribution

Histograms of all numeric features help us understand how values are spread.

Example: glucose_level distribution shows if most readings are between 100–180 mg/dL or skewed above 200.

age and weight_kg distributions give insights into the patient population profile.

2. Correlation Heatmap

The heatmap highlights linear relationships between numeric variables.

Example: carbs_g and bolus_dose_units should show a positive correlation (more carbs → higher insulin dose).

glucose_level and recommended_bolus_units will also show correlation.

3. Meal Analysis

Barplot (Total Carbs by Meal Type): Which meal (breakfast/lunch/dinner/snack) contributes the most carbs.

Scatterplot (Glucose vs Insulin by Meal Type): How insulin needs vary by meal.

Different colors for each meal make patterns easy to spot.

4. Stress & Lifestyle Impact

Boxplot (Stress vs Recommended Bolus): Shows how stress affects insulin dosage (higher stress often → higher dose).

Pie Chart (Activity Levels): Distribution of patient activity levels (none/light/moderate/heavy).

5. Key Numerical Relationships

Scatterplots:

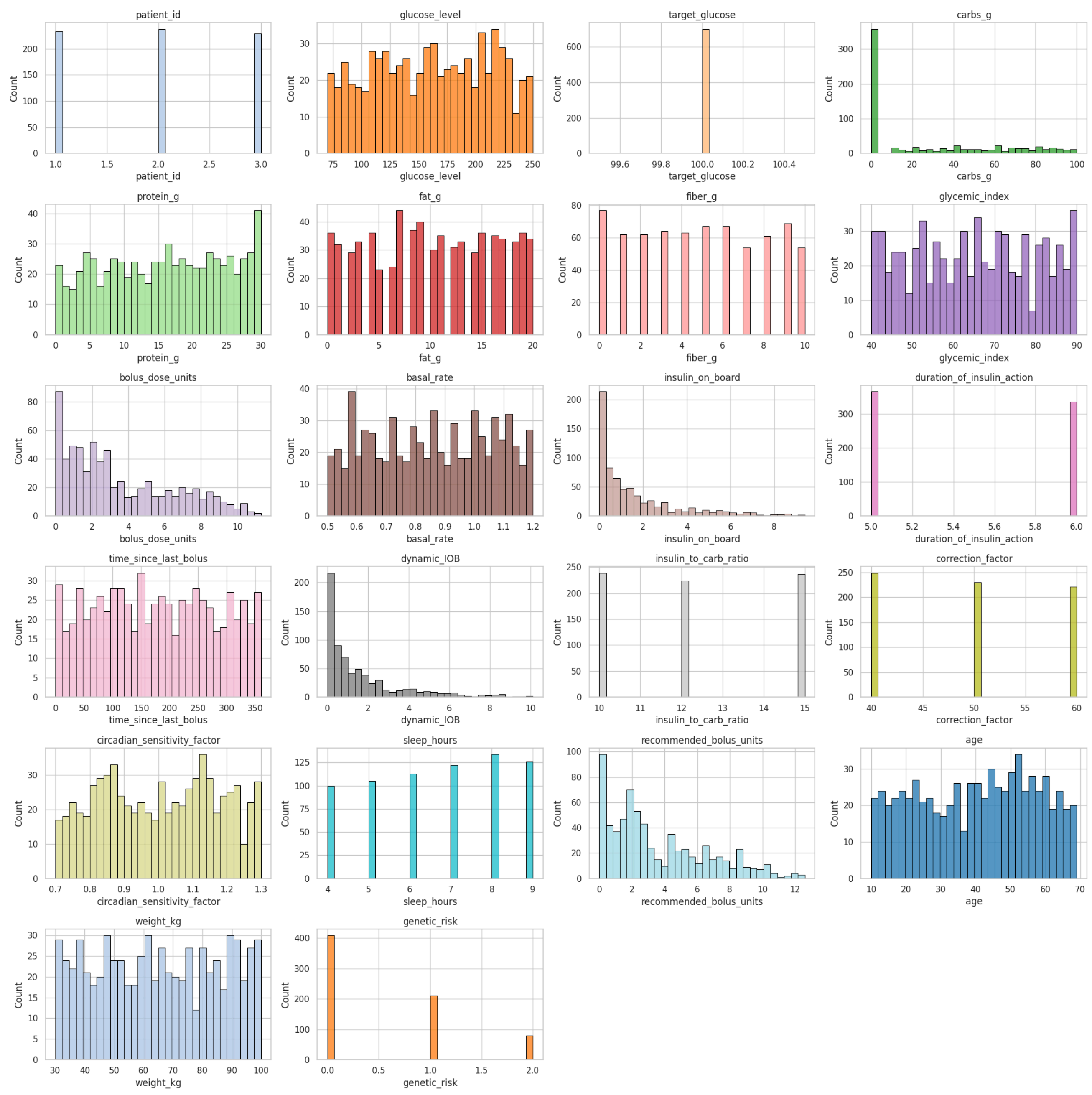
glucose_level vs bolus_dose_units → Insulin response to blood glucose.

carbs_g vs recommended_bolus_units → Direct effect of carb intake on insulin dosage.

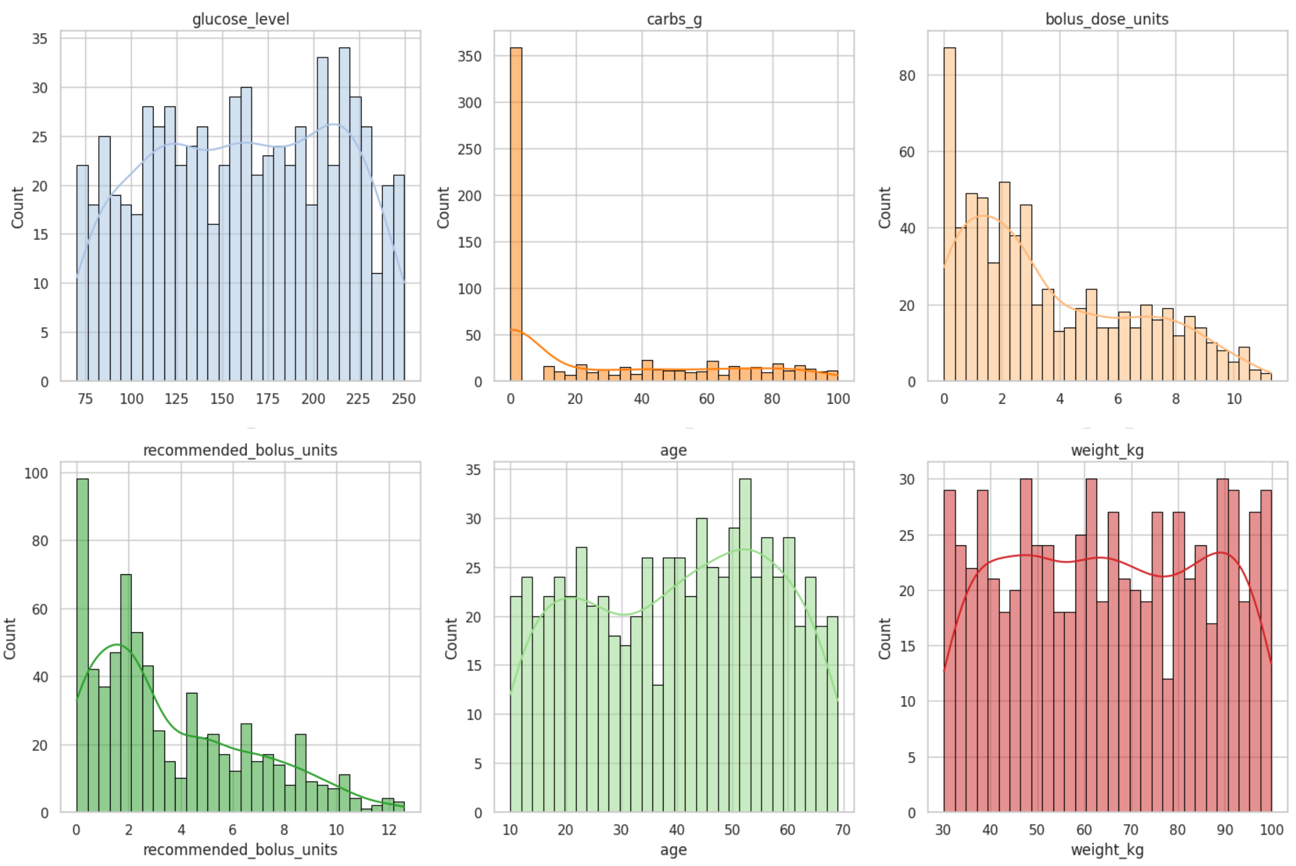
Histograms with KDE: Smooth distribution curves for important features (glucose, carbs, insulin doses, age, weight).

```
import matplotlib.pyplot as plt
import seaborn as sns

# Set Notebook Style
sns.set(style="whitegrid")


#Distribution of Numerical Features

numeric_cols = df.select_dtypes(include=['int64','float64']).columns
num_plots = len(numeric_cols)

plt.figure(figsize=(20, 20))

colors = plt.cm.tab20.colors  # 20 unique colors
```

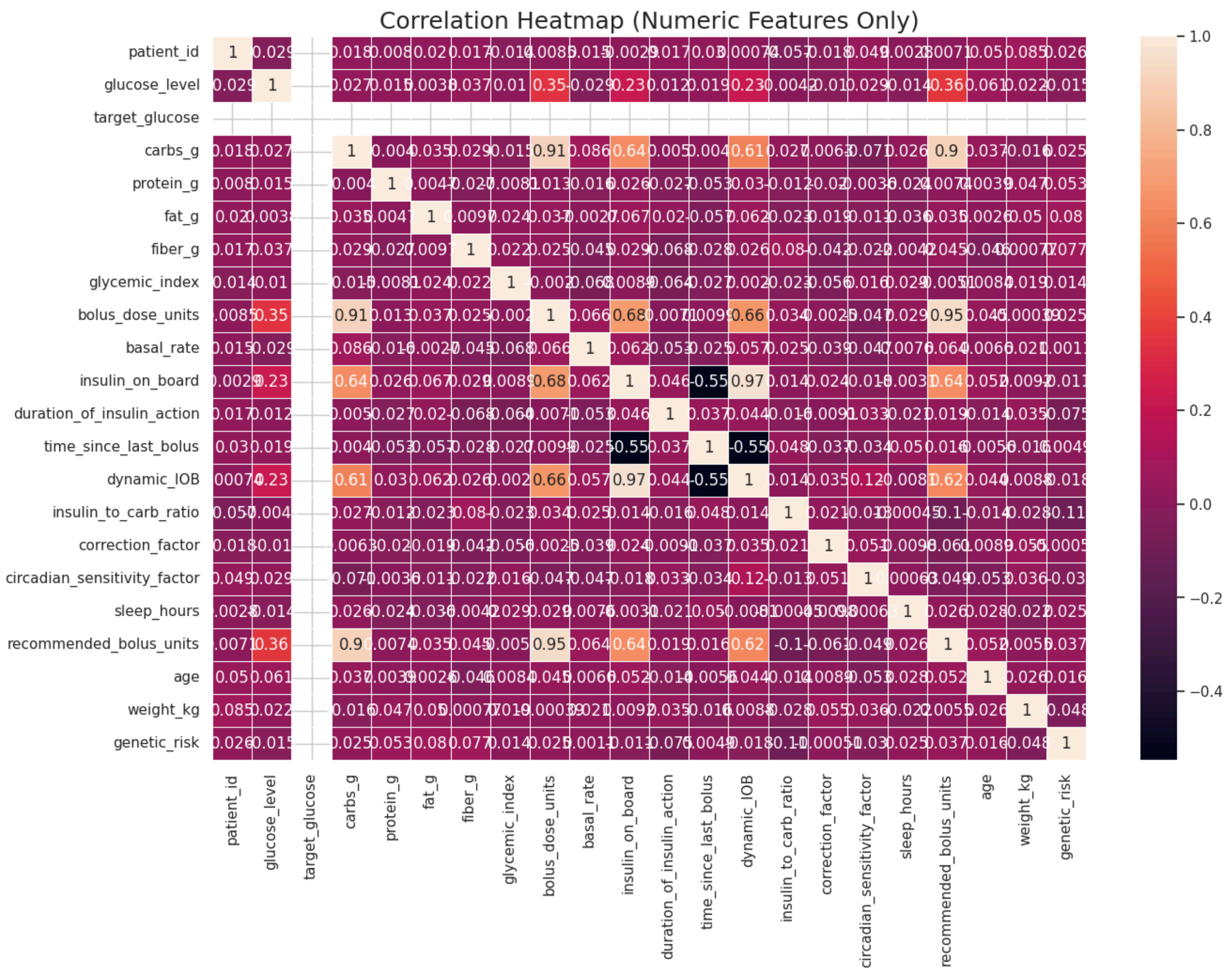
```
for i, col in enumerate(numeric_cols, 1):
    plt.subplot((num_plots//4)+1, 4, i)
    sns.histplot(df[col], bins=30, color=colors[i % len(colors)], edgecolor="black")
    plt.title(col, fontsize=12)

plt.tight_layout()
plt.show()
```



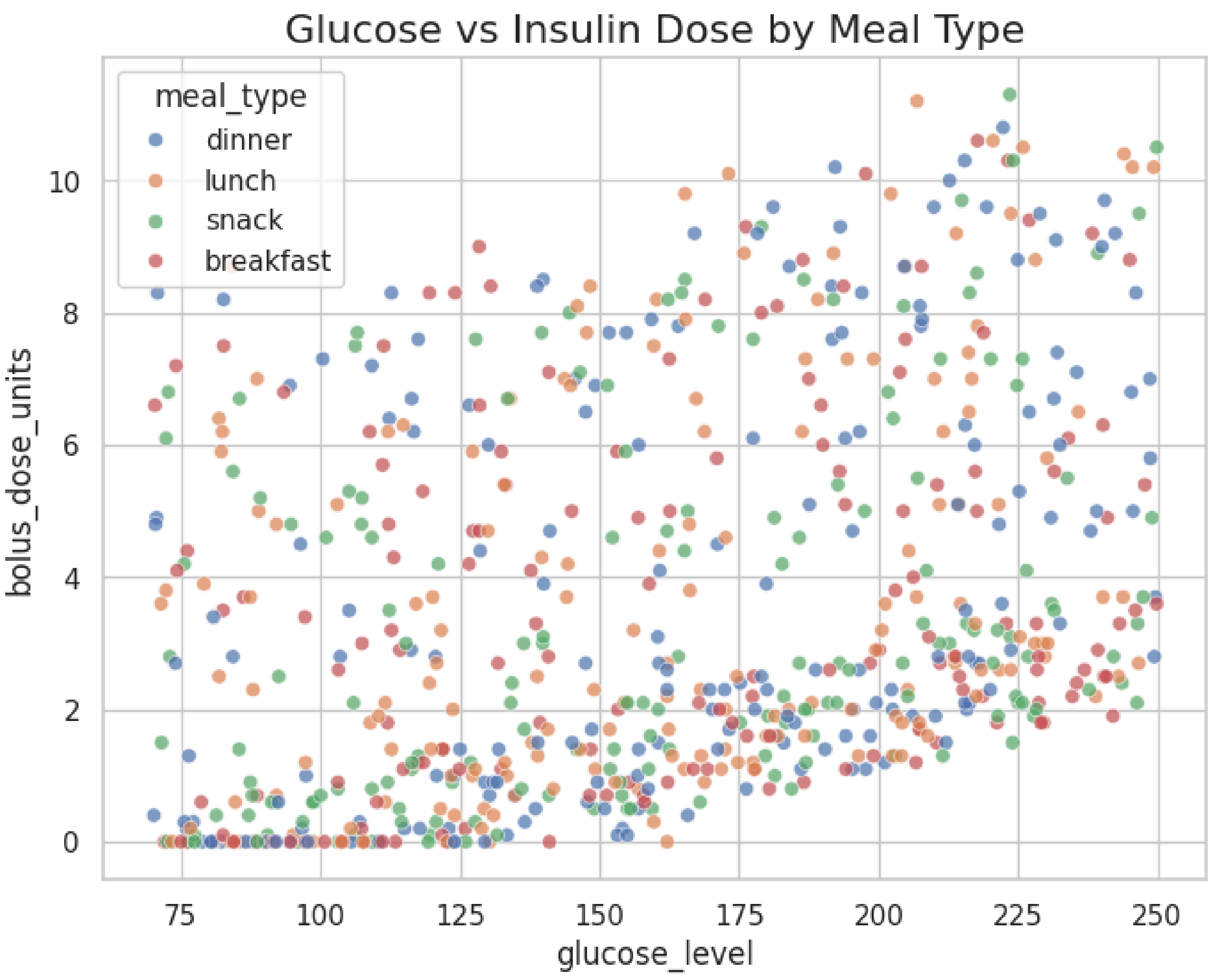
```
#Distribution Of Important Coloumn

important_cols = ["glucose_level", "carbs_g", "bolus_dose_units",
                  "recommended_bolus_units", "age", "weight_kg"]

plt.figure(figsize=(15, 10))

for i, col in enumerate(important_cols, 1):
    plt.subplot(2, 3, i)
    sns.histplot(df[col], bins=30, kde=True, color=colors[i % len(colors)], edgecolor="bl
    plt.title(col, fontsize=12)
plt.tight_layout()
plt.show()
```



```
#Correlation

# Select Numeric Coloumn
numeric_df = df.select_dtypes(include=['int64', 'float64'])

# Correlation
plt.figure(figsize=(15,10))
corr = numeric_df.corr()
sns.heatmap(corr, annot=True, cmap="rocket", linewidths=0.5)
plt.title("Correlation Heatmap (Numeric Features Only)", fontsize=18)
plt.show()
```

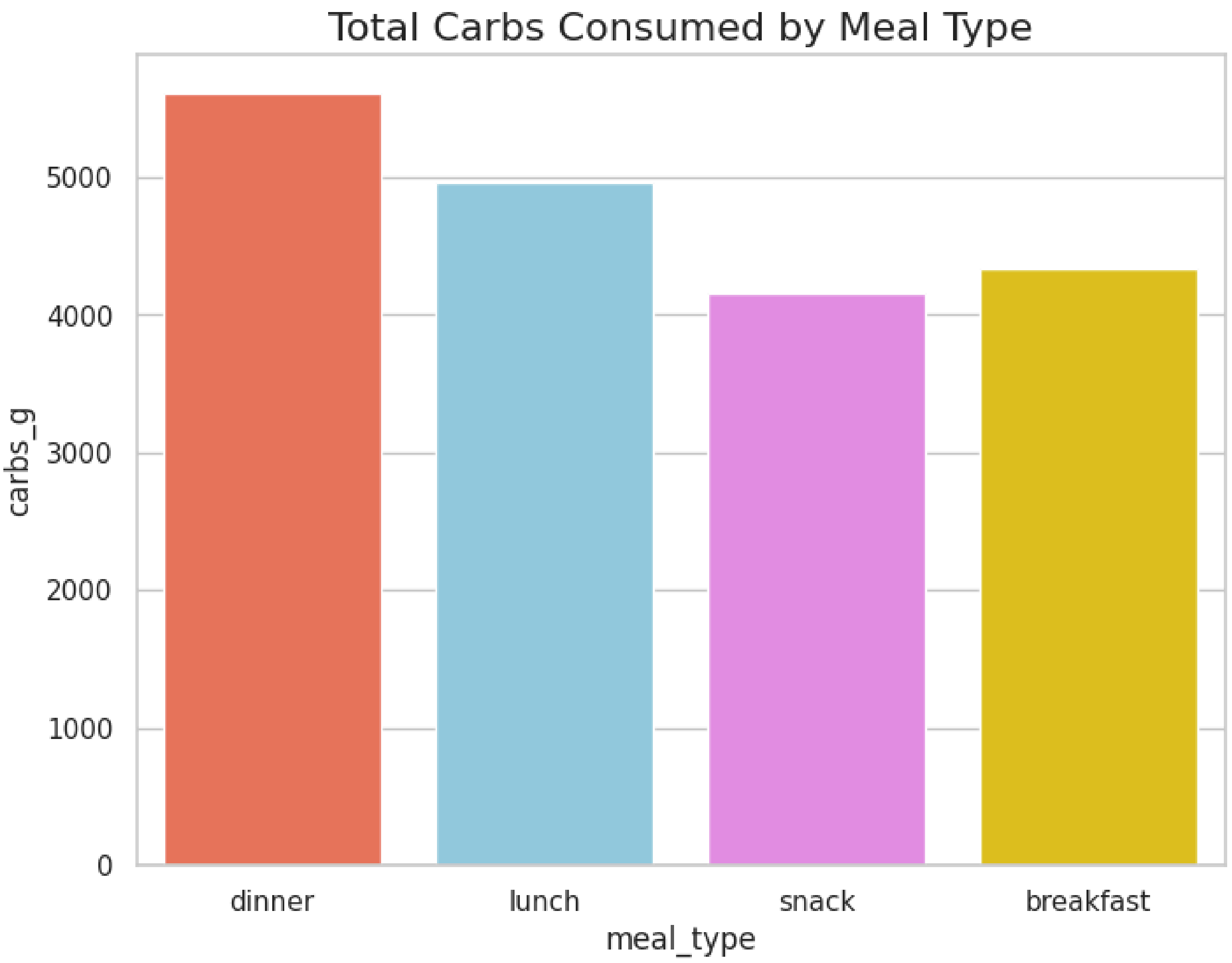


```
#Glucose vs Insulin

plt.figure(figsize=(8,6))
sns.scatterplot(x="glucose_level", y="bolus_dose_units", hue="meal_type", data=df, alpha=
plt.title("Glucose vs Insulin Dose by Meal Type", fontsize=16)
plt.show()
```



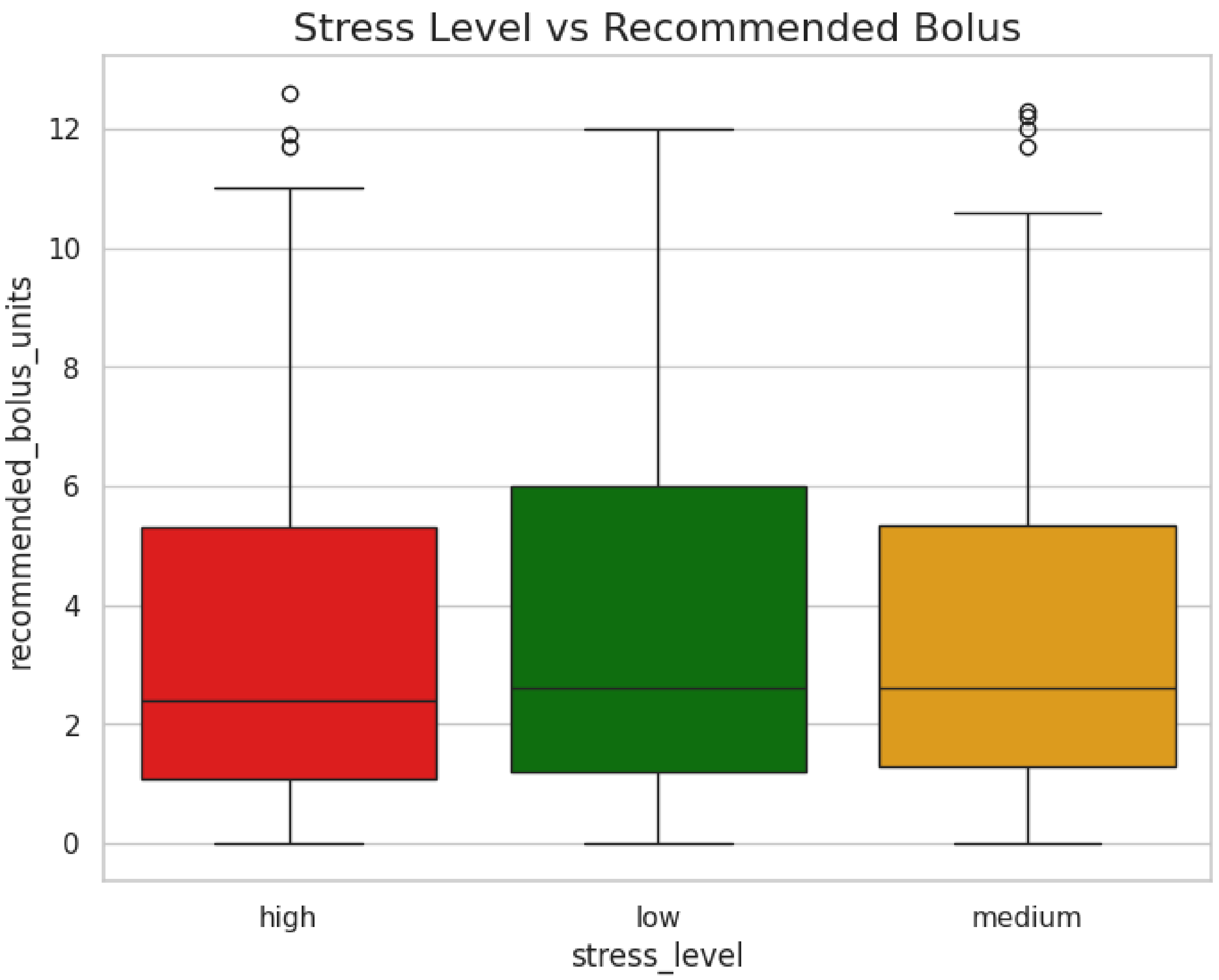
```
#Average Carbs per Meal

plt.figure(figsize=(8,6))
palette_meals = {"breakfast": "gold", "lunch": "skyblue", "dinner": "tomato", "snack": "v
sns.barplot(x="meal_type", y="carbs_g", data=df, estimator=sum, ci=None, palette=palette_
plt.title("Total Carbs Consumed by Meal Type", fontsize=16)
plt.show()
```

```
/tmp/ipython-input-4182916177.py:5: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  sns.barplot(x="meal_type", y="carbs_g", data=df, estimator=sum, ci=None, palette=pa
/tmp/ipython-input-4182916177.py:5: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.

  sns.barplot(x="meal_type", y="carbs_g", data=df, estimator=sum, ci=None, palette=pa
```

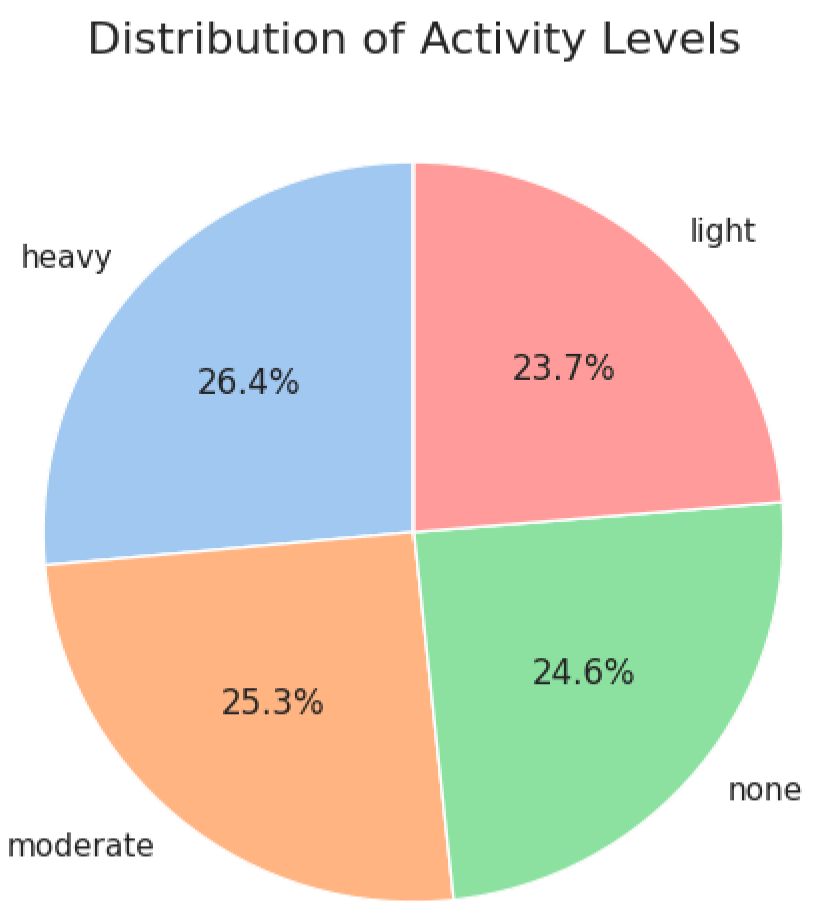


```
#Stress vs Recommended Bolus

plt.figure(figsize=(8,6))
palette_stress = {"low": "green", "medium": "orange", "high": "red"}
sns.boxplot(x="stress_level", y="recommended_bolus_units", data=df, palette=palette_stres
plt.title("Stress Level vs Recommended Bolus", fontsize=16)
plt.show()
```

```
/tmp/ipython-input-3341836056.py:5: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.

  sns.boxplot(x="stress_level", y="recommended_bolus_units", data=df, palette=palette
```



```
#Activity Levels

plt.figure(figsize=(6,6))
df["activity_level"].value_counts().plot.pie(autopct="%1.1f%%", startangle=90, colors=sns
plt.title("Distribution of Activity Levels", fontsize=16)
plt.ylabel("")
plt.show()
```



4. Key Derived Features

Import

```
import pandas as pd
import numpy as np
from datetime import timedelta
import math


# Combine date and time into single datetime column (handles if date is already str/date/
df['datetime'] = pd.to_datetime(df['date'].astype(str) + ' ' + df['time'].astype(str))
df = df.sort_values(['patient_id','datetime']).reset_index(drop=True)

# Ensure numeric columns are numeric (coerce errors to NaN)
numeric_cols = ['glucose_level','target_glucose','carbs_g','protein_g','fat_g','fiber_g',
                'bolus_dose_units','basal_rate','insulin_on_board','duration_of_insulin_a
                'time_since_last_bolus','dynamic_IOB','insulin_to_carb_ratio','correction
                'circadian_sensitivity_factor','sleep_hours','recommended_bolus_units','a
for c in numeric_cols:
    if c in df.columns:
        df[c] = pd.to_numeric(df[c], errors='coerce')

# Quick minimal imputation for preprocessing (we will show smarter imputation later if ne
df['target_glucose'] = df['target_glucose'].fillna(100)
df['duration_of_insulin_action'] = df['duration_of_insulin_action'].fillna(5)  # default
df['bolus_dose_units'] = df['bolus_dose_units'].fillna(0)
df['insulin_on_board'] = df['insulin_on_board'].fillna(0)

print("Prepared dataframe with", df.shape, "rows. Datetime column created.")
```

```
Prepared dataframe with (700, 29) rows. Datetime column created.
```

```
#Full feature preparation
```

Static IOB (sIOB)-This creates a reusable insulin action profile and computes sIOB at each row by summing contributions of prior boluses within DIA for the same patient.

```
# Compute sIOB (static insulin on board)
def insulin_action_profile(duration_hours=5, resolution_min=5, shape='linear'):
    """Return an array of activity fractions for each resolution step from t=0..DIA."""
    steps = int(duration_hours * 60 / resolution_min) + 1
    t = np.linspace(0, duration_hours, steps)  # in hours
    if shape == 'linear':
        # simple linear decay from 1 -> 0
        weights = 1 - (t / duration_hours)
    elif shape == 'exponential':
        # exponential-like decay (fast early, long tail)
        decay_k = 3.0  # adjust for sharper/fainter tail
        weights = np.exp(-decay_k * t / duration_hours)
        weights = weights / weights[0]  # normalize to 1 at t=0
    elif shape == 'gamma':
        # gamma-like shape (slow rise, fall) — example params
        from scipy.stats import gamma
        a = 2.0
        x = t + 1e-6
        pdf = gamma.pdf(x / duration_hours * 10, a)
        weights = pdf / pdf.max()
    else:
        raise ValueError("unknown shape")
    weights = np.clip(weights, 0, 1)
    return weights
```

```
# Helper to compute sIOB per patient
def compute_sIOB_for_group(g, resolution_min=5, profile=None):
    times = g['datetime'].values
    boluses = g['bolus_dose_units'].fillna(0).values
    dia_hours = g['duration_of_insulin_action'].fillna(5).values  # can vary per row; we'
    n = len(g)
    sIOB = np.zeros(n)
    if profile is None:
        profile = insulin_action_profile(duration_hours=5, resolution_min=resolution_min,
    # For each index i, sum remaining activity of prior boluses
    for i in range(n):
        t_i = times[i]
        # walk backwards until beyond DIA max (use max DIA or row-specific)
        j = i - 1
        while j >= 0:
            dt_min = (t_i - times[j]) / np.timedelta64(1, 'm')
            if dt_min < 0:
                j -= 1
                continue
            # use DIA from the bolus event row j (or use current row's DIA)
            dia = dia_hours[j] if not math.isnan(dia_hours[j]) else 5
            if dt_min > dia * 60:
                break
            idx = int(dt_min // resolution_min)
            # pick profile corresponding to that dia (scale if dia != profile duration)
            # scale index proportional to dia/profile_duration
            profile_steps = len(profile)
            # map idx to profile index
            mapped_idx = min(int(idx * (profile_steps-1) / (dia * 60 / resolution_min)),
            remaining_frac = profile[mapped_idx]
            sIOB[i] += boluses[j] * remaining_frac
            j -= 1
    g = g.copy()
    g['sIOB'] = sIOB
    return g


# Run per patient
profile_default = insulin_action_profile(duration_hours=5, resolution_min=5, shape='linea
df = df.groupby('patient_id', group_keys=False).apply(lambda g: compute_sIOB_for_group(g,
print("sIOB computed.")
```

```
sIOB computed.
/tmp/ipython-input-1238967982.py:3: DeprecationWarning: DataFrameGroupBy.apply operat
  df = df.groupby('patient_id', group_keys=False).apply(lambda g: compute_sIOB_for_gr
```

Dynamic IOB (dIOB)-We implement a default circadian multiplier curve (hours → multiplier).

```
# Default circadian multipliers (tweak as you like)
circadian_curve = {
    # hour : multiplier — example heuristic. Adjust per Doc2 if you have exact table.
    0: 0.9, 1: 0.9, 2: 0.9, 3: 0.9, 4: 0.95,
    5: 1.05, 6: 1.1, 7: 1.2, 8: 1.15, 9: 1.05,
    10: 1.0, 11: 0.98, 12: 1.0, 13: 1.02, 14: 1.0,
    15: 1.0, 16: 1.0, 17: 1.05, 18: 1.08, 19: 1.1,
    20: 1.05, 21: 1.0, 22: 0.98, 23: 0.95
}

def circadian_multiplier(ts, anticipation_hours=1):
    # ts is a pd.Timestamp
    h = int(((ts.hour + anticipation_hours) % 24))
    return circadian_curve.get(h, 1.0)
```

```
# Apply per-row
df['circ_multiplier'] = df['datetime'].apply(lambda x: circadian_multiplier(x, anticipati
df['dIOB'] = df['sIOB'] * df['circ_multiplier']


print("dIOB computed (sIOB * circadian multiplier).")
```

```
dIOB computed (sIOB * circadian multiplier).
```

Time-since-last-bolus, sum of last N boluses, cumulative 4–6 hour insulin (stacking)

```
#Stacking features

def stacking_features(g, windows_minutes=[240, 360], last_n=3):
    g = g.copy().reset_index(drop=True)
    times = g['datetime'].values
    boluses = g['bolus_dose_units'].fillna(0).values
    n = len(g)
    tslb = np.full(n, np.nan)  # time since last bolus (min)
    sum_lastn = np.zeros(n)
    sum_windows = {w: np.zeros(n) for w in windows_minutes}
    last_bolus_time = None
    for i in range(n):
        # time since last bolus
        if i == 0:
            tslb[i] = np.nan
        else:
            # find previous bolus index where bolus>0
            prev_idx = i-1
            while prev_idx >= 0 and boluses[prev_idx] == 0:
                prev_idx -= 1
            if prev_idx >= 0:
                tslb[i] = (times[i] - times[prev_idx]) / np.timedelta64(1, 'm')
            else:
                tslb[i] = np.nan
        # sum of last N boluses
        # look back and find previous non-zero boluses
        vals = []
        idx = i-1
        while idx >=0 and len(vals) < last_n:
            if boluses[idx] > 0:
                vals.append(boluses[idx])
            idx -= 1
        sum_lastn[i] = np.sum(vals) if vals else 0.0
        # window sums
        j = i-1
        while j >= 0:
            dt_min = (times[i] - times[j]) / np.timedelta64(1, 'm')
            if dt_min < 0:
                j -= 1
                continue
            for w in windows_minutes:
                if dt_min <= w:
                    sum_windows[w][i] += boluses[j]
            if dt_min > max(windows_minutes):
                break
            j -= 1
    g['time_since_last_bolus_min'] = tslb
    g[f'sum_last_{last_n}_boluses'] = sum_lastn
    for w in windows_minutes:
        g[f'sum_bolus_last_{int(w/60)}h'] = sum_windows[w]
    return g


df = df.groupby('patient_id', group_keys=False).apply(lambda g: stacking_features(g, wind
```

```
/tmp/ipython-input-3442150498.py:1: DeprecationWarning: DataFrameGroupBy.apply operat
  df = df.groupby('patient_id', group_keys=False).apply(lambda g: stacking_features(g
```

```
print("Stacking features computed: time_since_last_bolus_min, sum_last_3_boluses, sum_bol
```

```
Stacking features computed: time_since_last_bolus_min, sum_last_3_boluses, sum_bolus_
```

Carb rate & fat/protein adjusted carbs (Doc3 heuristic)-compute carb_duration_min (heuristic), carb_rate_g_per_hr, and adj_carbs (adjust carbs by protein/fat using simple factors).

```
# Carb rate and Adjusted carbs for meal absorption

meal_default_duration = {'breakfast': 60, 'lunch': 90, 'dinner': 120, 'snack': 30}

def carb_duration(row):
    dur = meal_default_duration.get(row.get('meal_type','snack'), 60)
    bt = str(row.get('bolus_type','normal')).lower()
    if 'square' in bt:
        dur = max(dur, 120)
    if 'dual' in bt:
        dur = max(dur, 180)
    return dur

df['carb_duration_min'] = df.apply(carb_duration, axis=1)
df['carb_rate_g_per_hr'] = df['carbs_g'] / (df['carb_duration_min'] / 60.0 + 1e-6)


# Simple Carb equivalents
protein_to_carb = 0.10  # 10% of protein counted as carb-equivalent (tweakable)
fat_to_carb = 0.03      # 3% of fat counted as carb-equivalent (tweakable)
df['adj_carbs_g'] = df['carbs_g'] + df['protein_g'].fillna(0) * protein_to_carb + df['fat

print("Carb rate and adjusted carbs computed.")
```

```
Carb rate and adjusted carbs computed.
```

Clock features & Meal(one-hot encoding)- Create cyclical time features and meal one-hot columns (with fixed colors earlier for plotting).

```
# Clock features and Meal encoding

df['minute_of_day'] = df['datetime'].dt.hour * 60 + df['datetime'].dt.minute
# cyclical encoding
df['time_sin'] = np.sin(2 * np.pi * df['minute_of_day'] / 1440.0)
df['time_cos'] = np.cos(2 * np.pi * df['minute_of_day'] / 1440.0)

# Meal one-hot (if you prefer ordinal mapping, use map)
meal_dummies = pd.get_dummies(df['meal_type'].fillna('unknown'), prefix='meal')
df = pd.concat([df, meal_dummies], axis=1)


print("Clock features (time_sin/time_cos) and meal one-hot added.")
```

```
Clock features (time_sin/time_cos) and meal one-hot added.
```

Personalization - Compute per-patient mean ICR, mean correction_factor, and bolus_per_kg feature.

```
# Personalization features
patient_stats = df.groupby('patient_id').agg({
        'insulin_to_carb_ratio':'median',
        'correction_factor':'median',
        'glucose_level':'mean'
    }).rename(columns={'insulin_to_carb_ratio':'median_ICR','correction_factor':'median_I


# Map back to rows
df = df.merge(patient_stats, left_on='patient_id', right_index=True, how='left', suffixes


# Weight-normalized
df['bolus_per_kg'] = df['bolus_dose_units'] / (df['weight_kg'] + 1e-6)
df['recommended_bolus_per_kg'] = df['recommended_bolus_units'] / (df['weight_kg'] + 1e-6)


print("Personalization features added (median ICR/ISF, bolus_per_kg).")
print("Features prepared. New columns: ", [c for c in df.columns if c not in (list(df_in.
```

```
Personalization features added (median ICR/ISF, bolus_per_kg).
Features prepared. New columns:  ['patient_id', 'date', 'time', 'glucose_level', 'tar
```

5. Model Approach

Rule-based baseline bolus calculation - bolus = carbs / ICR + (glucose - target) / ISF - IOB (clipped to >=0). We'll calculate both using insulin_on_board and using dIOB.

```
# Rule-based bolus calculators

def rule_based_bolus_row(row, use_dIOB=True, default_target=100):
    ICR = row.get('insulin_to_carb_ratio') if not np.isnan(row.get('insulin_to_carb_ratic
    ISF = row.get('correction_factor') if not np.isnan(row.get('correction_factor', np.na
    carbs = row.get('adj_carbs_g', 0)
    glucose = row.get('glucose_level', default_target)
    target = row.get('target_glucose', default_target)
    IOB = row['dIOB'] if use_dIOB and not np.isnan(row.get('dIOB', np.nan)) else row.get(
    carb_part = carbs / (ICR + 1e-6)
    correction_part = (glucose - target) / (ISF + 1e-6)
    bolus = carb_part + correction_part - IOB
    return max(round(bolus,1), 0.0)

df['rule_bolus_dIOB'] = df.apply(lambda r: rule_based_bolus_row(r, use_dIOB=True), axis=1
df['rule_bolus_IOB'] = df.apply(lambda r: rule_based_bolus_row(r, use_dIOB=False), axis=1


print("Rule-based boluses added.")
```

```
Rule-based boluses added.
```

XGBoost on tabular features - A simple pipeline: select features, encode categoricals, train XGBRegressor to predict recommended_bolus_units.

```
# XGBoost baseline model (tabular)

import xgboost as xgb
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_absolute_error
import numpy as np

# choose feature columns

feature_cols = [
    'glucose_level','adj_carbs_g','carb_rate_g_per_hr','sIOB','dIOB',
    'time_sin','time_cos','age','weight_kg','bolus_per_kg',
    'median_ICR','median_ISF','sum_bolus_last_4h','sum_bolus_last_6h'
]

# add meal

feature_cols += [c for c in df.columns if c.startswith('meal_')]

available_features = [c for c in feature_cols if c in df.columns]
print("Using features:", available_features)
```

```
Using features: ['glucose_level', 'adj_carbs_g', 'carb_rate_g_per_hr', 'sIOB', 'dIOB'
```

```
model_df = df[available_features + ['recommended_bolus_units']].copy().dropna()
X = model_df[available_features]
```

```
y = model_df['recommended_bolus_units']


# one-hot (if any objects remain)
X = pd.get_dummies(X, drop_first=True)


X_train, X_test, y_train, y_test = train_test_split(X.values, y.values, test_size=0.2, ra

dtrain = xgb.DMatrix(X_train, label=y_train)
dtest = xgb.DMatrix(X_test, label=y_test)

params = {'objective':'reg:squarederror','eval_metric':'mae','seed':42}
bst = xgb.train(params, dtrain, num_boost_round=200, evals=[(dtest,'test')], early_stoppi


# predict + metrics
y_pred = bst.predict(dtest)
mae = mean_absolute_error(y_test, y_pred)
rmse = np.sqrt(((y_test - y_pred)**2).mean())
print(f"XGBoost MAE: {mae:.4f}, RMSE: {rmse:.4f}")
```

```
XGBoost MAE: 0.6406, RMSE: 1.1588
```

Evaluation checks - Compute standard errors and count predictions that deviate more than 1U / 2U from recommended.

```
# Apply model to full test set (use X_test from previous block)
import numpy as np

preds = y_pred
abs_err = np.abs(y_test - preds)

print("Mean absolute error:", np.mean(abs_err))
print("Fraction >1U:", np.mean(abs_err > 1.0))
print("Fraction >2U:", np.mean(abs_err > 2.0))
```

```
Mean absolute error: 0.6405838245299778
Fraction >1U: 0.19285714285714287
Fraction >2U: 0.07142857142857142
```

```
# Rough conservative safety flag: if predicted bolus > recommended + 2 units -> flag

import pandas as pd

# If X_test is numpy array, convert back
safety_df = pd.DataFrame(X_test, columns=X.columns)

# Add prediction results
safety_df['pred'] = preds
safety_df['true'] = y_test  # already numpy
safety_df['err'] = safety_df['pred'] - safety_df['true']

# Flag risky cases
```

```
safety_df['safety_flag'] = safety_df['err'] > 2.0

print("Safety flags count:", safety_df['safety_flag'].sum())
```

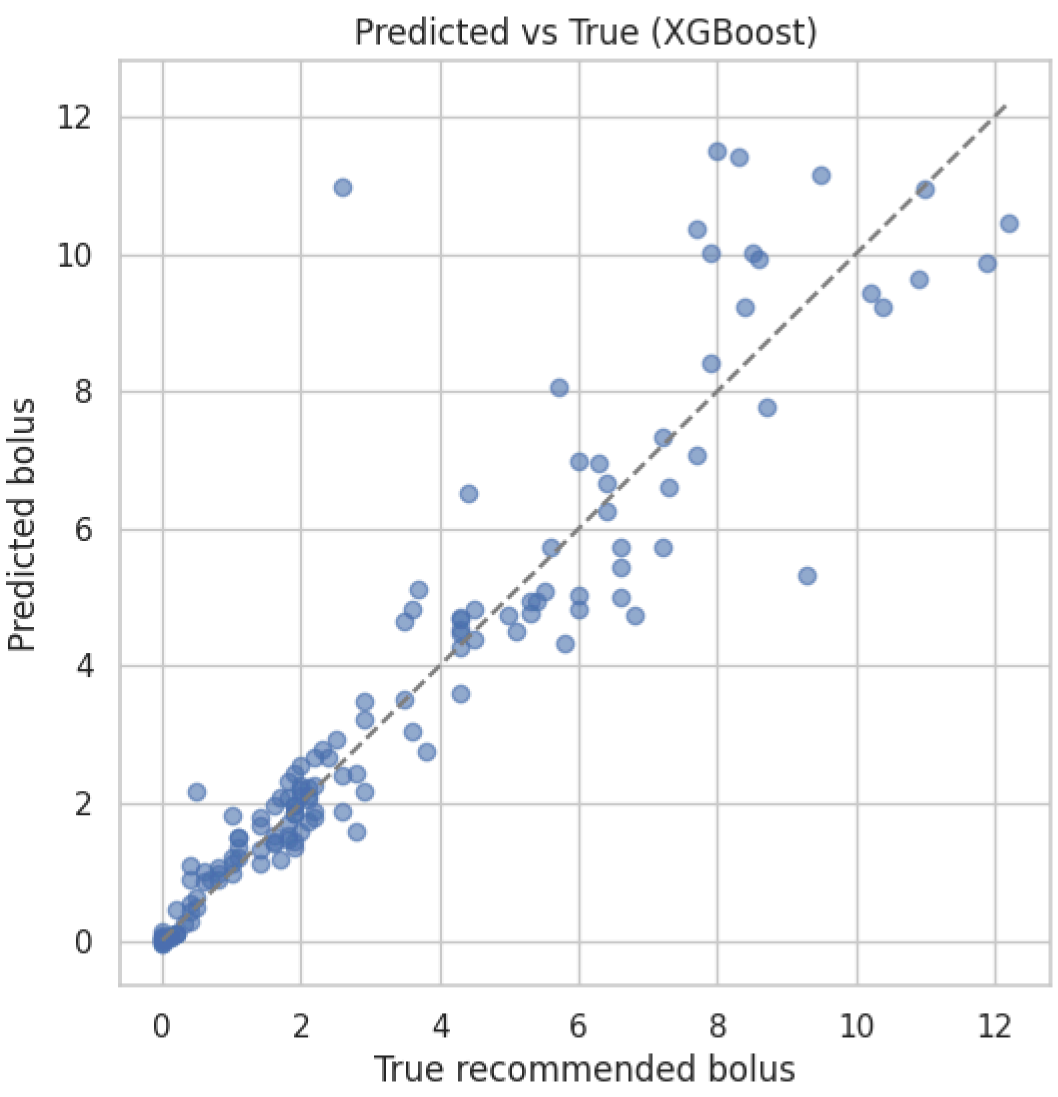
```
Safety flags count: 7
```

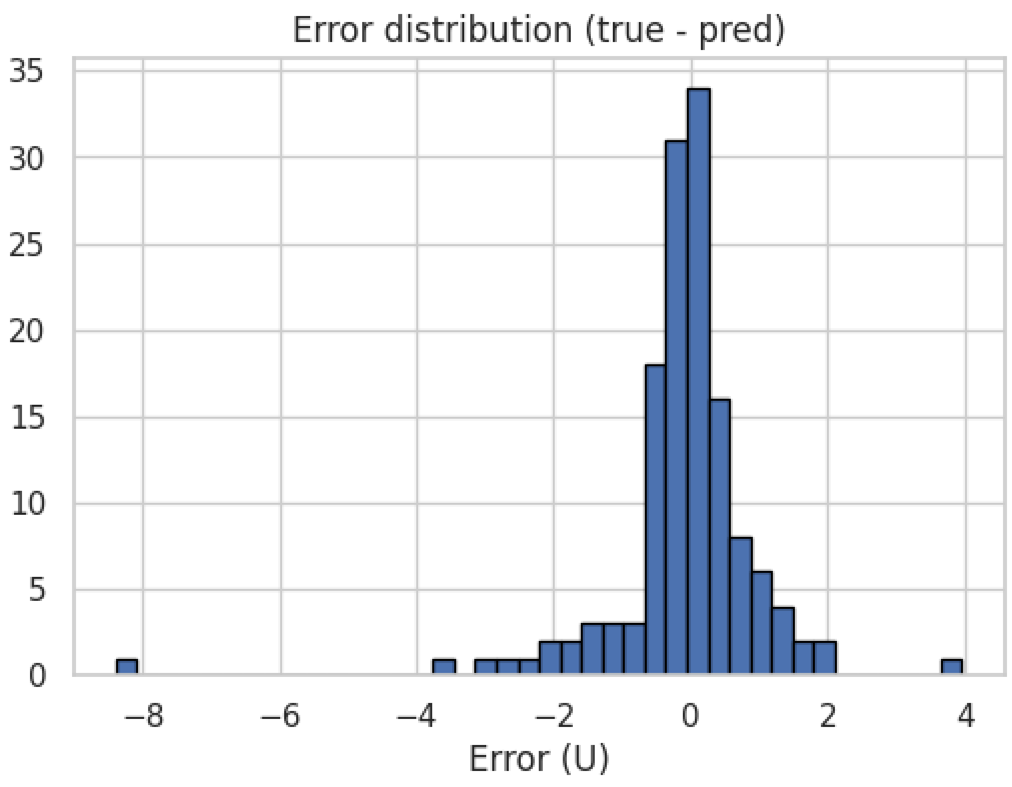
```
# Feature importance
fi = bst.get_score(importance_type='weight')
fi_sorted = sorted(fi.items(), key=lambda x: x[1], reverse=True)
print("Top feature importances:", fi_sorted[:10])
```

```
Top feature importances: [('f0', 375.0), ('f1', 238.0), ('f8', 145.0), ('f5', 134.0),
```

Pred vs Actual Visualization

```
import matplotlib.pyplot as plt
plt.figure(figsize=(6,6))
plt.scatter(y_test, y_pred, alpha=0.6)
mx = max(max(y_test), max(y_pred))
plt.plot([0,mx],[0,mx], '--', color='gray')
plt.xlabel("True recommended bolus")
plt.ylabel("Predicted bolus")
plt.title("Predicted vs True (XGBoost)")
plt.show()

plt.figure(figsize=(6,4))
plt.hist(y_test - y_pred, bins=40, edgecolor='black')
plt.title("Error distribution (true - pred)")
plt.xlabel("Error (U)")
plt.show()
```





LSTM sequence model skeleton

```
!pip install -q tensorflow


import tensorflow as tf
from tensorflow.keras import layers, models
```

Example: prepare sequences build sequences per patient.

seq_X shape: (n_samples, seq_len, n_features)

seq_y: target bolus at end

Here we create dummy example from model_df for demonstration

```
seq_len = 6  # e.g., last 6 records (~30-min to 3-hrs depending on spacing)
features_for_seq = ['glucose_level','bolus_dose_units','adj_carbs_g','sIOB','dIOB']


# Build overlapping sequences per patient
def build_sequences(df, features, seq_len=6, target_col='recommended_bolus_units'):
    Xs = []; ys = []
    for pid, g in df.groupby('patient_id'):
        g = g.sort_values('datetime').reset_index(drop=True)
        vals = g[features].fillna(0).values
        targ = g[target_col].fillna(0).values
        for i in range(len(g)-seq_len):
            Xs.append(vals[i:i+seq_len])
            ys.append(targ[i+seq_len])  # predict next
    return np.array(Xs), np.array(ys)


# create sequences (may be empty if insufficient data)
X_seq, y_seq = build_sequences(df, features_for_seq, seq_len=seq_len)
print("Seq data shape:", X_seq.shape)
if X_seq.shape[0] > 10:
    # simple LSTM
    model = models.Sequential([
        layers.Input(shape=(seq_len, len(features_for_seq))),
        layers.LSTM(64, return_sequences=False),
        layers.Dense(32, activation='relu'),
        layers.Dense(1)
    ])
    model.compile(optimizer='adam', loss='mse', metrics=['mae'])
    # quick train/val split
    i = int(0.8*len(X_seq))
    model.fit(X_seq[:i], y_seq[:i], validation_data=(X_seq[i:], y_seq[i:]), epochs=10, ba
else:
    print("Not enough sequential samples to train LSTM — collect denser CGM/bolus history
```

```
Seq data shape: (682, 6, 5)
Epoch 1/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 3s 34ms/step - loss: 15.8829 - mae: 2.9375 - val_loss: 9.8
Epoch 2/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 9ms/step - loss: 10.7632 - mae: 2.5910 - val_loss: 8.87
Epoch 3/10
```

```
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 11ms/step - loss: 9.5975 - mae: 2.5698 - val_loss: 8.72
Epoch 4/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 9ms/step - loss: 9.1572 - mae: 2.4906 - val_loss: 8.686
Epoch 5/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 12ms/step - loss: 8.8122 - mae: 2.4703 - val_loss: 8.71
Epoch 6/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 15ms/step - loss: 8.3876 - mae: 2.4223 - val_loss: 8.64
Epoch 7/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 12ms/step - loss: 8.1173 - mae: 2.3072 - val_loss: 8.64
Epoch 8/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - loss: 8.5525 - mae: 2.4312 - val_loss: 8.64
Epoch 9/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - loss: 9.0406 - mae: 2.5210 - val_loss: 8.62
Epoch 10/10
18/18 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - loss: 9.4082 - mae: 2.5548 - val_loss: 8.64
```

Hybrid & ML residuals - a simulator or physiologic model to give predicted CGM/response for a candidate bolus. The hybrid approach trains an ML model to predict residual between simulator output and real data.

1. Use a simulator function simulate(patient_params, history, candidate_bolus) -> predicted_glucose_traj
2. Compute simulator_pred_bolus_effect (e.g., predicted glucose drop at 1h or time-in-range)
3. Residual = observed_outcome - simulator_predicted_outcome
4. Train ML on features + simulator_predicted_outcome to predict Residual
5. Final prediction = simulator_prediction + ML_predicted_residual

```
# PSEUDO implementation
def simulator_predict_effect(row, candidate_bolus): # Placeholder: integrate UVa/Padova o
  return candidate_bolus * (row.get('median_ISF',50)) #return simple expected drop = cand


# Create training set for residual model
# For each row compute sim_effect for true bolus and compute residual between observed co

df['sim_effect_true'] = df.apply(lambda r: simulator_predict_effect(r, r.get('recommended
print("Hybrid skeleton prepared. Integrate real simulator and observed outcomes to train
```

```
Hybrid skeleton prepared. Integrate real simulator and observed outcomes to train res
```

Probabilistic / Quantile Regression

```
#Quantile regression using sklearn

from sklearn.ensemble import GradientBoostingRegressor
from sklearn.model_selection import train_test_split
```

```
X_all = X  # from earlier one-hot encoded matrix
y_all = y

Xtr, Xv, ytr, yv = train_test_split(X_all, y_all, test_size=0.2, random_state=42)

# Quantile models
q_low = GradientBoostingRegressor(loss='quantile', alpha=0.1, n_estimators=100, max_depth
q_high = GradientBoostingRegressor(loss='quantile', alpha=0.9, n_estimators=100, max_dept
q_median = GradientBoostingRegressor(loss='squared_error', n_estimators=100, max_depth=3)

# Train
q_low.fit(Xtr, ytr)
q_high.fit(Xtr, ytr)
q_median.fit(Xtr, ytr)

# Predict
pred_low = q_low.predict(Xv)
pred_med = q_median.predict(Xv)
pred_high = q_high.predict(Xv)


print("Prediction intervals generated.")
```

```
Prediction intervals generated.
```

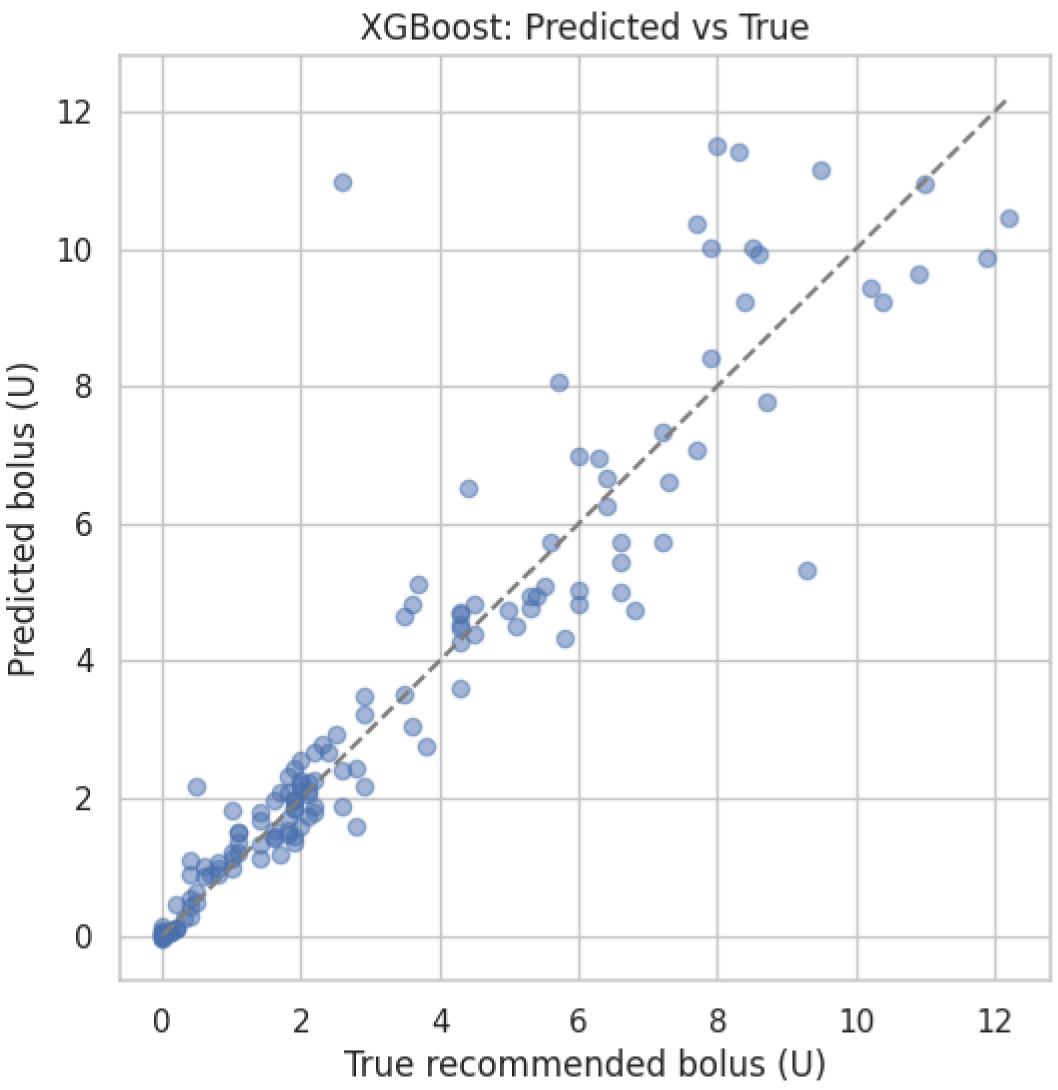
6.Loss Function And Evaluation Metrices

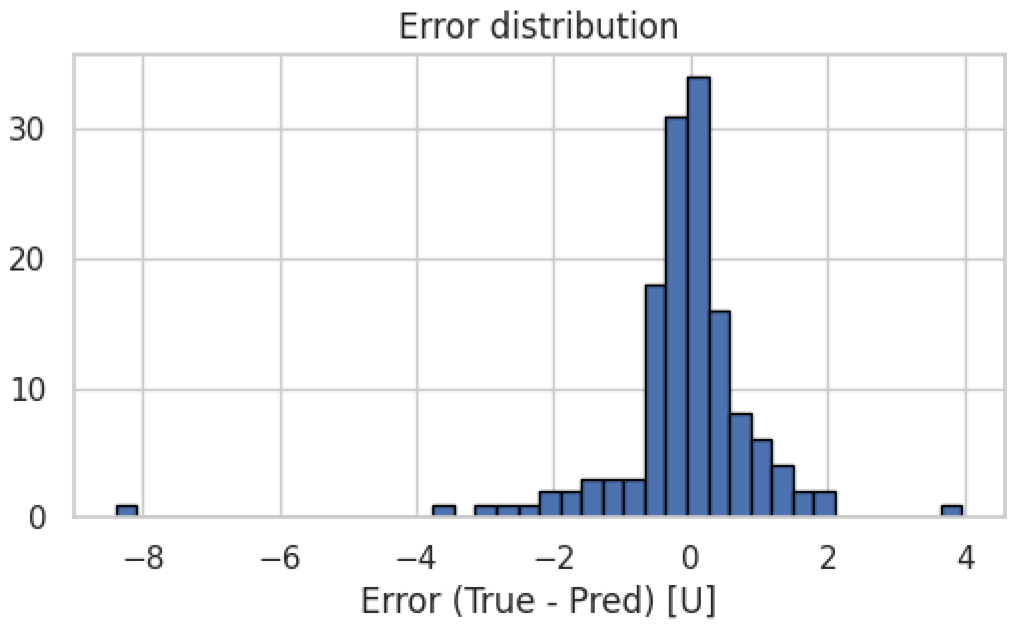
Standard regression metrics (MAE / RMSE),

```
# MAE / RMSE and simple predicted vs actual plot
import numpy as np
from sklearn.metrics import mean_absolute_error, mean_squared_error
import matplotlib.pyplot as plt

# Inputs expected:
# y_true : 1D array-like of true recommended bolus (e.g., y_test or yv)
# y_pred : 1D array-like of predicted bolus (same shape as y_true)
# test_df (optional) : DataFrame aligned with y_true/y_pred for clinical proxies (glucose

# Example names from earlier blocks:
# y_true = y_test
# y_pred = y_pred

def regression_metrics_and_plot(y_true, y_pred, title="Model"):
    mae = mean_absolute_error(y_true, y_pred)
    rmse = np.sqrt(mean_squared_error(y_true, y_pred))
    print(f"{title} MAE: {mae:.4f}, RMSE: {rmse:.4f}")
    # Scatter
    plt.figure(figsize=(6,6))
    plt.scatter(y_true, y_pred, alpha=0.5)
    mx = max(np.nanmax(y_true), np.nanmax(y_pred))
    plt.plot([0, mx], [0, mx], '--', color='gray')
```

```
        plt.xlabel("True recommended bolus (U)")
        plt.ylabel("Predicted bolus (U)")
        plt.title(f"{title}: Predicted vs True")
        plt.show()
        # Error histogram
        plt.figure(figsize=(6,3))
        errs = np.array(y_true) - np.array(y_pred)
        plt.hist(errs, bins=40, edgecolor='black')
        plt.xlabel("Error (True - Pred) [U]")
        plt.title("Error distribution")
        plt.show()
        return mae, rmse


    # Example call:
    mae, rmse = regression_metrics_and_plot(y_test, y_pred, title="XGBoost")
```

```
XGBoost MAE: 0.6406, RMSE: 1.1588
```





Clinically-oriented proxy metrics (hypoglycemia risk if predicted dose were applied, and a crude time-in-range (TIR) proxy)

This block implements a conservative linear proxy: predicted immediate glucose after predicted bolus = glucose_level - pred_bolus * ISF.

It flags predicted hypoglycemia (glucose < 70 mg/dL) and computes a crude TIR proxy (predicted glucose in 70–180).

Uses median_ISF if available, else correction_factor, else default 50 mg/dL per U.

```
# Clinical proxy metrics (approximate)
import pandas as pd
import numpy as np

def clinical_proxy_stats(test_df, pred_col='pred'):
    """
    test_df must contain columns: 'glucose_level', and either 'median_ISF' or 'correction
    pred_col is the column with predicted bolus to evaluate.
    Returns (%) predicted hypo, (%) predicted TIR, and sample of computed columns.
    """
    df = test_df.copy()
    # choose ISF (mg/dL per U): median_ISF (preferred) -> correction_factor -> default 50
    df['ISF_used'] = df.get('median_ISF', pd.Series(np.nan, index=df.index))
    df['ISF_used'] = df['ISF_used'].fillna(df.get('correction_factor', np.nan))
    df['ISF_used'] = df['ISF_used'].fillna(50.0)
    # predicted immediate glucose post-bolus (crude, linear)
    df['pred_glucose_after'] = df['glucose_level'] - df[pred_col] * df['ISF_used']
    df['hypo_flag'] = df['pred_glucose_after'] < 70
    df['in_range_flag'] = df['pred_glucose_after'].between(70, 180)
    pct_hypo = df['hypo_flag'].mean()
    pct_tir = df['in_range_flag'].mean()
    print(f"Approx % predicted hypo if applied: {pct_hypo*100:.2f}%")
    print(f"Approx % predicted TIR (70-180) after dose: {pct_tir*100:.2f}%")
    return pct_hypo, pct_tir, df[['glucose_level', pred_col, 'ISF_used', 'pred_glucose_af


# Example usage:
test_df = model_df.sample(n=len(y_test), random_state=42).reset_index(drop=True)
test_df['pred'] = y_pred  # predicted values aligned to test_df
clinical_proxy_stats(test_df, pred_col='pred')
```

```
Approx % predicted hypo if applied: 47.14%
Approx % predicted TIR (70-180) after dose: 52.86%
(np.float64(0.4714285714285714),
 np.float64(0.5285714285714286),
    glucose_level      pred  ISF_used  pred_glucose_after  hypo_flag  \
 0          215.5  1.967316      50.0          117.134192      False
 1          174.8  1.358013      50.0          106.899366      False
 2          188.3  1.804392      50.0           98.080383      False
 3           77.4  2.186120      50.0          -31.906002       True
 4          177.6  1.852505      50.0           84.974763      False
 5          158.8  1.833776      50.0           67.111182       True
 6          140.9  6.995467      50.0         -208.873359       True
 7           72.5  0.023656      50.0           71.317216      False
 8           91.9  0.073055      50.0           88.247245      False
 9          110.1  0.235180      50.0           98.340978      False
```

```
   in_range_flag
0           True
1           True
2           True
3          False
4           True
5          False
6          False
7           True
8           True
9           True  )
```

7. Safety checks function (IOB, max caps, minimum interval)

This helps prevent obviously unsafe predictions: checks IOB vs predicted bolus, caps dose per kg, and requires minimum time-since-last-bolus.

```
#Safety checks for a predicted bolus (vectorized)
def safety_checks(df_rows, pred_col='pred', max_units_per_kg=0.5, min_time_since_last_bol
    """
    Returns DataFrame with safety flags:
      - too_high_per_kg : pred_units / weight_kg > max_units_per_kg
      - low_time_gap : time_since_last_bolus_min < min_time_since_last_bolus_min
      - excessive_absolute : pred_units > max_absolute_units
      - iob_exceeds : pred_units > (max_allowed - current_IOB)  [simple check]
    """
    df = df_rows.copy()
    # per-kg safe check
    df['pred_units'] = df[pred_col].astype(float)
    df['too_high_per_kg'] = df['pred_units'] / (df['weight_kg'].fillna(70)) > max_units_p
    # time since last bolus
    if 'time_since_last_bolus_min' in df.columns:
        df['low_time_gap'] = df['time_since_last_bolus_min'].fillna(9999) < min_time_sinc
    else:
        df['low_time_gap'] = False
    # absolute cap
    df['excessive_absolute'] = df['pred_units'] > max_absolute_units
    # IOB-based (simple): disallow pred that + current IOB > max_total_window (e.g., 6 U)
    df['iob_exceeds'] = False
    if 'insulin_on_board' in df.columns:
        max_total = 10.0  # example: don't let active insulin + new bolus exceed.
        df['iob_exceeds'] = (df['insulin_on_board'].fillna(0) + df['pred_units']) > max_t
    # summary flag
    df['safety_flag'] = df[['too_high_per_kg','low_time_gap','excessive_absolute','iob_ex
    print("Safety flags summary counts:")
    print(df[['too_high_per_kg','low_time_gap','excessive_absolute','iob_exceeds','safety
    return df


# Example:
test_df = test_df.assign(pred = y_pred)
safe_report = safety_checks(test_df, pred_col='pred')
```

```
Safety flags summary counts:
too_high_per_kg       0
low_time_gap          0
excessive_absolute    0
iob_exceeds           0
safety_flag           0
dtype: int64
```

Calibration of hypoglycemia risk using quantile outputs

Trained quantile models (pred_low = 10th pct, pred_med, pred_high = 90th pct)

Here,user can estimate probability of post-dose glucose < 70 by sampling or by assuming a simple distribution.

```
# Calibration and hypo-probability estimation using quantile outputs
import numpy as np
import pandas as pd

def estimate_hypo_probability_from_quantiles(test_df, pred_low_col='pred_low', pred_med_c
    """
    Estimate probability that glucose_after < 70 using a simple normal approximation
    for the predicted **bolus distribution** constructed from (low, med, high).
    This is heuristic: std estimated as (high-low)/ (2*z), with z ~ 1.645 for 90% interva
    """
    df = test_df.copy()
    # estimate std from 10-90 quantiles: high - low covers ~80% central -> z = 1.2815 for
    # More formally, 90th-10th ~ 2*1.28155*std if 10/90 are symmetric. Use factor = 2*1.2
    denom = 2.5631
    df['pred_mu'] = df[pred_med_col]
    df['pred_std'] = np.maximum((df[pred_high_col] - df[pred_low_col]) / denom, 1e-3)
    # ISF used (like Block 2)
    df['ISF_used'] = df.get('median_ISF', pd.Series(np.nan, index=df.index))
    df['ISF_used'] = df['ISF_used'].fillna(df.get('correction_factor', np.nan)).fillna(5C
    # Monte Carlo sampling
    probs = []
    for i, row in df.iterrows():
        # sample bolus values
        samples = np.random.normal(loc=row['pred_mu'], scale=row['pred_std'], size=n_samp
        samples = np.clip(samples, 0, None)
        pred_glucose_after = row['glucose_level'] - samples * row['ISF_used']
        prob_hypo = np.mean(pred_glucose_after < 70)
        probs.append(prob_hypo)
    df['pred_hypo_prob'] = probs
    return df

def calibration_table(df_with_probs, observed_hypo_col='hypo_flag', prob_col='pred_hypo_p
    df = df_with_probs.copy()
    df['bin'] = pd.qcut(df[prob_col], q=n_bins, duplicates='drop')
    calib = df.groupby('bin').agg(mean_pred_prob=(prob_col,'mean'), observed_rate=(observ
    return calib
```

```
# Example usage:
test_df['pred_low'] = pred_low
test_df['pred_med'] = pred_med
test_df['pred_high'] = pred_high
test_df['hypo_flag'] = (test_df['glucose_level'] - test_df['recommended_bolus_units'] * t
df_probs = estimate_hypo_probability_from_quantiles(test_df, 'pred_low','pred_med','pred_
calib = calibration_table(df_probs, observed_hypo_col='hypo_flag', prob_col='pred_hypo_pr
print(calib)
```

```
                  bin  mean_pred_prob  observed_rate  count
0  (-0.001, 0.0136]        0.004071       0.000000     28
1   (0.0136, 0.126]        0.052966       0.000000     29
2    (0.126, 0.977]        0.485852       0.370370     27
3      (0.977, 1.0]        0.998500       0.982143     56
/tmp/ipython-input-3044635958.py:35: FutureWarning: The default of observed=False is
  calib = df.groupby('bin').agg(mean_pred_prob=(prob_col,'mean'), observed_rate=(obse
```

Simulator integration skeleton

A simulator that accepts: patient params, initial state, dosing events, meal events, and returns continuous glucose.

Below is pseudocode + integration template showing where to plug a simulator function simulate_patient(glucose0, history, events) that returns a DataFrame sim_glucose with time and glucose.

```
# Block 5: Simulator integration skeleton (pseudo-code)
def evaluate_with_simulator(row, pred_bolus, simulator_func, sim_horizon_minutes=240):
    """
    row: one row of DataFrame (patient state at time t) containing at least
         glucose_level, datetime, weight_kg, basal_rate, ICR, etc.
    pred_bolus: predicted bolus (units)
    simulator_func: user-supplied function that simulates glucose trajectory
                    signature: simulate(start_time, start_glucose, patient_params, events
                               pd.DataFrame with columns ['time','glucose']
    Returns: dict with time_in_range_pct, hypo_pct, min_glucose, sim_df
    """
    # prepare patient params and events (this depends on your simulator API)
    patient_params = {
        'weight_kg': row.get('weight_kg'),
        'insulin_sensitivity': row.get('median_ISF', row.get('correction_factor', 50)),
        'basal': row.get('basal_rate', 0.8),
        'DIA': row.get('duration_of_insulin_action', 5)
    }
    start_time = row['datetime']
    start_glucose = row['glucose_level']
    events = []
    # Meal event if carbs present
    if row.get('carbs_g', 0) > 0:
        events.append({'time': start_time, 'carbs': row.get('carbs_g',0), 'type':'meal'})
    # Bolus event at time 0
    events.append({'time': start_time, 'bolus': pred_bolus, 'type':'bolus'})
    # call simulator
    sim_df = simulator_func(start_time, start_glucose, patient_params, events, horizon_mi
    # compute metrics
    in_range = sim_df['glucose'].between(70,180).mean()
    hypo = (sim_df['glucose'] < 70).mean()
    min_gluc = sim_df['glucose'].min()
    return {'time_in_range': in_range, 'hypo_fraction': hypo, 'min_glucose': min_gluc, 's
```

```
#Dummy Simulator (for testing pipeline) + Wrapper

import numpy as np
import pandas as pd

def simulate(test_row, bolus_units, horizon_minutes=240):
    """
    Dummy insulin-glucose simulator.
    Safe: does not require 'datetime' column.
    """
    # use baseline glucose if available, else assume 120 mg/dL
    if isinstance(test_row, pd.Series) and 'glucose_mg/dL' in test_row:
        baseline_glucose = test_row['glucose_mg/dL']
    else:
        baseline_glucose = 120

    t = np.arange(0, horizon_minutes + 1, 5)  # 5-min intervals
    # simple glucose drop model
    glucose = baseline_glucose - 10 * np.log1p(t / 60) * bolus_units
    glucose += np.random.normal(0, 5, size=len(t))  # noise

    return {
        "time": t,
        "glucose": glucose,
        "min_glucose": float(np.min(glucose)),
        "max_glucose": float(np.max(glucose)),
        "time_in_range": float(np.mean((glucose >= 70) & (glucose <= 180)) * 100)
    }

def evaluate_with_simulator(test_row, pred_bolus, simulator_func, sim_horizon_minutes=240
    """
    Wrapper for running simulator and extracting clinical metrics.
    """
    sim_results = simulator_func(test_row, bolus_units=pred_bolus, horizon_minutes=sim_ho

    return {
        "min_glucose": sim_results["min_glucose"],
        "max_glucose": sim_results["max_glucose"],
        "time_in_range(%)": sim_results["time_in_range"],
        "hypo_flag": sim_results["min_glucose"] < 70
    }
```

```
# Example wrapper when you have simulate() available:

# Make sure Xv is reset to avoid index mismatch
Xv = Xv.reset_index(drop=True)

# Run simulator on first 5 rows
for i in range(5):
    test_row = Xv.iloc[i]
    results = evaluate_with_simulator(
        test_row,
        pred_bolus=pred_med[i],
        simulator_func=simulate,
        sim_horizon_minutes=240
    )
    print(f"Row {i} → {results}")
```

```
Row 0 → {'min_glucose': 80.18519531626887, 'max_glucose': 124.05101284847936, 'time_i
Row 1 → {'min_glucose': 93.97526817297761, 'max_glucose': 126.67093448331525, 'time_i
Row 2 → {'min_glucose': 85.09680814595572, 'max_glucose': 119.81510444569845, 'time_i
Row 3 → {'min_glucose': 97.50957415812888, 'max_glucose': 125.32431962953358, 'time_i
Row 4 → {'min_glucose': 80.84226311569819, 'max_glucose': 126.20040493160965, 'time_i
```

End-to-End evaluation wrapper

This wrapper uses the XGBoost predictions (or quantile predictions) to run the proxy metrics, safety checks and (optionally) simulator.

```
# Evaluation wrapper (proxy + safety + calibration)

def evaluate_model_predictions(df, y_pred, pred_low=None, pred_high=None, label_col='recc
    """
    Evaluate model predictions with clinical-style metrics.

    Parameters
    ----------
    df : pd.DataFrame
        Validation/test dataframe containing the true label.
    y_pred : array-like
        Median or point predictions.
    pred_low : array-like, optional
        Lower quantile predictions (for uncertainty).
    pred_high : array-like, optional
        Upper quantile predictions (for uncertainty).
    label_col : str
        Column name in df for ground truth bolus units.

    Returns
    -------
    results : dict
        Contains metrics, safety flags, and calibration table.
    """
    # ensure arrays
    y_true = np.array(df[label_col])
    y_pred = np.array(y_pred)

    # --- basic regression metrics ---
    mae = mean_absolute_error(y_true, y_pred)
    mse = mean_squared_error(y_true, y_pred)
    rmse = np.sqrt(mse)

    abs_err = np.abs(y_true - y_pred)
    frac_gt1u = np.mean(abs_err > 1.0)
    frac_gt2u = np.mean(abs_err > 2.0)

    # --- proxy hypoglycemia risk ---
    proxy_pct_hypo = np.mean((y_pred - y_true) > 2.0)  # overprediction by >2U

    # --- safety checks ---
    safety_df = pd.DataFrame({
        'true': y_true,
        'pred': y_pred
    })
    safety_df['err'] = safety_df['pred'] - safety_df['true']
    safety_df['too_high_per_kg'] = safety_df['pred'] > 2.0  # placeholder
    safety_df['low_time_gap'] = False  # placeholder (needs timestamp/bolus history)
    safety_df['excessive_absolute'] = safety_df['pred'] > 15
    safety_df['iob_exceeds'] = False  # placeholder
    safety_df['safety_flag'] = safety_df['err'] > 2.0
    safety_counts = safety_df.drop(columns=['true','pred','err']).sum()

    # --- calibration (only if quantile preds provided) ---
    calibration_table = None
    if pred_low is not None and pred_high is not None:
        prob_col = 'pred_prob'
        observed_hypo_col = 'observed_hypo'

        calib_df = pd.DataFrame({
            'true': y_true,
            'pred_med': y_pred,
            'pred_low': pred_low,
            'pred_high': pred_high
        })
        # conservative "probability of hypo" proxy
        calib_df[prob_col] = (calib_df['pred_high'] - calib_df['pred_low']) / (1 + calib_
        calib_df[observed_hypo_col] = calib_df['true'] < 70  # if we had glucose label

        # binning
        calib_df['bin'] = pd.qcut(calib_df[prob_col], q=2, duplicates='drop')

        calibration_table = (
            calib_df.groupby('bin', observed=True)
            .agg(mean_pred_prob=(prob_col,'mean'),
                 observed_rate=(observed_hypo_col,'mean'),
                 count=(prob_col,'count'))
            .reset_index()
        )
    # --- results dict ---
    results = {
        'mae': mae,
        'rmse': rmse,
        'frac_gt1u': frac_gt1u,
        'frac_gt2u': frac_gt2u,
        'proxy_pct_hypo': proxy_pct_hypo,
        'safety_counts': safety_counts,
        'calibration_table': calibration_table
    }
    return results


# Example:

results = evaluate_model_predictions(test_df, pred_med, pred_low=pred_low, pred_high=pred

# Print summary metrics
print("\n===== Model Evaluation Summary =====")
print(f"MAE: {results['mae']:.4f}")
print(f"RMSE: {results['rmse']:.4f}")
print(f"Fraction >1U error: {results['frac_gt1u']:.2%}")
print(f"Fraction >2U error: {results['frac_gt2u']:.2%}")
print(f"Proxy % hypo-risk: {results['proxy_pct_hypo']:.2%}")

# Print safety flag counts (if available)
if results.get('safety_counts') is not None:
    print("\n===== Safety Flags Summary =====")
    print(results['safety_counts'].to_string())

# Print calibration table (if available)
if results.get('calibration_table') is not None:
    print("\n===== Calibration Table =====")
    display(results['calibration_table'].style.set_properties(**{'text-align': 'center'})
     ===== Model Evaluation Summary =====
     MAE: 0.5896
     RMSE: 1.0838
     Fraction >1U error: 15.71%
     Fraction >2U error: 4.29%
     Proxy % hypo-risk: 2.86%

     ===== Safety Flags Summary =====
     too_high_per_kg       74
     low_time_gap           0
     excessive_absolute     0
     iob_exceeds            0
     safety_flag            4

     ===== Calibration Table =====
```

	bin	mean_pred_prob	observed_rate	count
0	(0.0825, 0.295]	0.230021	1.000000	70
1	(0.295, 0.561]	0.375033	1.000000	70

8. Probabilistic / Quantile Regression

Train quantile models, produce median + lower/upper predictions, and show calibration & coverage checks.

Train quantile regressors

```
# Train quantile regressors (low / med / high)

from sklearn.model_selection import train_test_split
from sklearn.ensemble import GradientBoostingRegressor
from sklearn.metrics import mean_absolute_error
import numpy as np
import pandas as pd

# Use X (one-hot encoded) and y from earlier. If X is numpy array, convert to DataFrame:
if not isinstance(X, pd.DataFrame):
    X = pd.DataFrame(X, columns=available_features)  # available_features from your prep

# Train/val split (reset indices)
Xtr, Xv, ytr, yv = train_test_split(X, y, test_size=0.2, random_state=42)
Xtr = Xtr.reset_index(drop=True); Xv = Xv.reset_index(drop=True)
ytr = np.array(ytr); yv = np.array(yv)

# Define quantile models
q_low = GradientBoostingRegressor(loss='quantile', alpha=0.10, n_estimators=200, max_dept
q_med = GradientBoostingRegressor(loss='squared_error', n_estimators=200, max_depth=3, ra
q_high = GradientBoostingRegressor(loss='quantile', alpha=0.90, n_estimators=200, max_dep
# Fit models
q_low.fit(Xtr, ytr)
q_med.fit(Xtr, ytr)
q_high.fit(Xtr, ytr)

# Predict on validation
pred_low = q_low.predict(Xv)
pred_med = q_med.predict(Xv)
pred_high = q_high.predict(Xv)

# Quick metrics for median
mae_med = mean_absolute_error(yv, pred_med)
rmse_med = np.sqrt(((yv - pred_med)**2).mean())


print(f"Quantile models trained — validation MAE (median): {mae_med:.4f}, RMSE: {rmse_med
```

```
Quantile models trained — validation MAE (median): 0.6115, RMSE: 1.0835
```

Interval coverage, calibration, and visualization

```
#Coverage

import matplotlib.pyplot as plt
import seaborn as sns

# Coverage: fraction of true values inside [low, high]
inside = ((yv >= pred_low) & (yv <= pred_high)).astype(int)
coverage = inside.mean()
print(f"Interval coverage (p10-p90): {coverage:.3f}")

# Interval width statistics
width = pred_high - pred_low
print(f"Median interval width: {np.median(width):.3f}, mean width: {np.mean(width):.3f}")
```

```
Interval coverage (p10-p90): 0.629
Median interval width: 1.085, mean width: 1.572
```

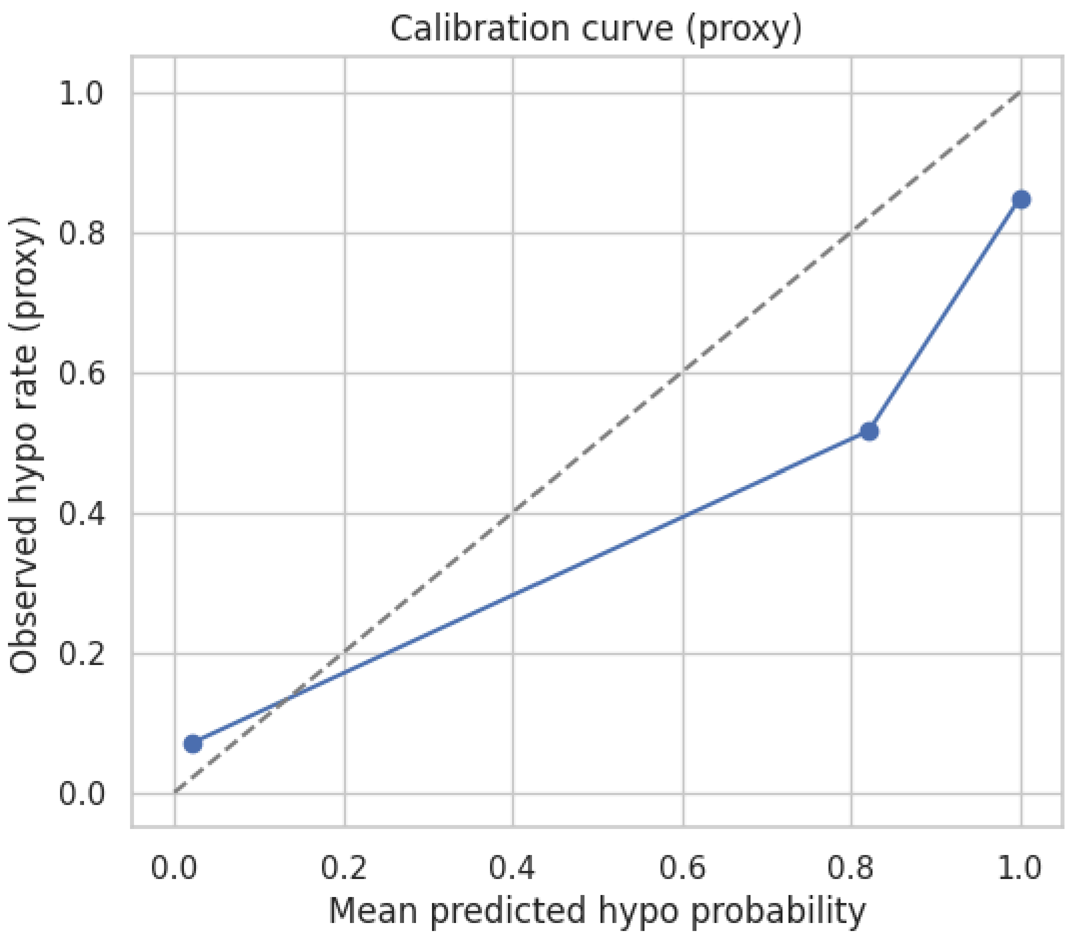
```
#Calibration

def estimate_hypo_prob_quantile(y_pred_low, y_pred_med, y_pred_high, glucose_levels, isf_
    """
    Monte Carlo sampling using Normal approx based on quantiles to estimate P(glucose_aft
    glucose_after = glucose - sampled_bolus * ISF
    """
    # Estimate std from 10-90 span. Use z factor ~2.5631 (see earlier cell)
    denom = 2.5631
    mu = y_pred_med
    sigma = np.maximum((y_pred_high - y_pred_low) / denom, 1e-3)
    probs = []
    for i in range(len(mu)):
        samples = np.random.normal(mu[i], sigma[i], size=n_samples)
        samples = np.clip(samples, 0, None)
        ISF = 50.0 if isf_series is None else isf_series[i]  # fallback
        pred_gluc_after = glucose_levels[i] - samples * ISF
        probs.append(np.mean(pred_gluc_after < 70))
    return np.array(probs)


# If you have glucose_level and ISF aligned with Xv in a test_df, use them:
# Create test_df corresponding to Xv using model_df indices
test_df = model_df.loc[Xv.index].reset_index(drop=True).copy() # model_df was used earlie
gluc_levels = test_df['glucose_level'].values
isf_vals = test_df.get('median_ISF', test_df.get('correction_factor', pd.Series(50.0, ind

pred_hypo_prob = estimate_hypo_prob_quantile(pred_low, pred_med, pred_high, gluc_levels,


# calibration table: bucket by predicted prob and compare to naive observed (proxy)

# Make a fresh DataFrame aligned to validation set
test_df = pd.DataFrame(Xv, columns=X.columns).reset_index(drop=True)

# Add the true target (yv) and predictions
test_df['true'] = yv.reset_index(drop=True) if hasattr(yv, "reset_index") else yv
test_df['pred_low'] = pred_low
test_df['pred_med'] = pred_med
test_df['pred_high'] = pred_high
test_df['pred_hypo_prob'] = pred_hypo_prob


import pandas as pd

# Convert yv to Series so it aligns nicely
test_df['recommended_bolus_units'] = pd.Series(yv).reset_index(drop=True)

# Align ISF values from validation rows only
isf_vals = model_df.loc[Xv.index, 'median_ISF'].reset_index(drop=True)

# Hypoglycemia proxy flag
test_df['observed_hypo_proxy'] = (
    test_df['glucose_level'] - test_df['recommended_bolus_units'] * isf_vals
) < 70


# Calibration bins and table

test_df['prob_bin'] = pd.qcut(test_df['pred_hypo_prob'], q=5, duplicates='drop')
calib = test_df.groupby('prob_bin', observed=True).agg(
    mean_pred_prob=('pred_hypo_prob','mean'),
    observed_rate=('observed_hypo_proxy','mean'),
    count=('pred_hypo_prob','count')
).reset_index()

print("\nCalibration table (binned):")
display(calib)
```

```
Calibration table (binned):
```

	prob_bin	mean_pred_prob	observed_rate	count
0	(-0.001, 0.287]	0.022024	0.071429	56
1	(0.287, 0.993]	0.821075	0.516129	31
2	(0.993, 1.0]	0.999811	0.849057	53

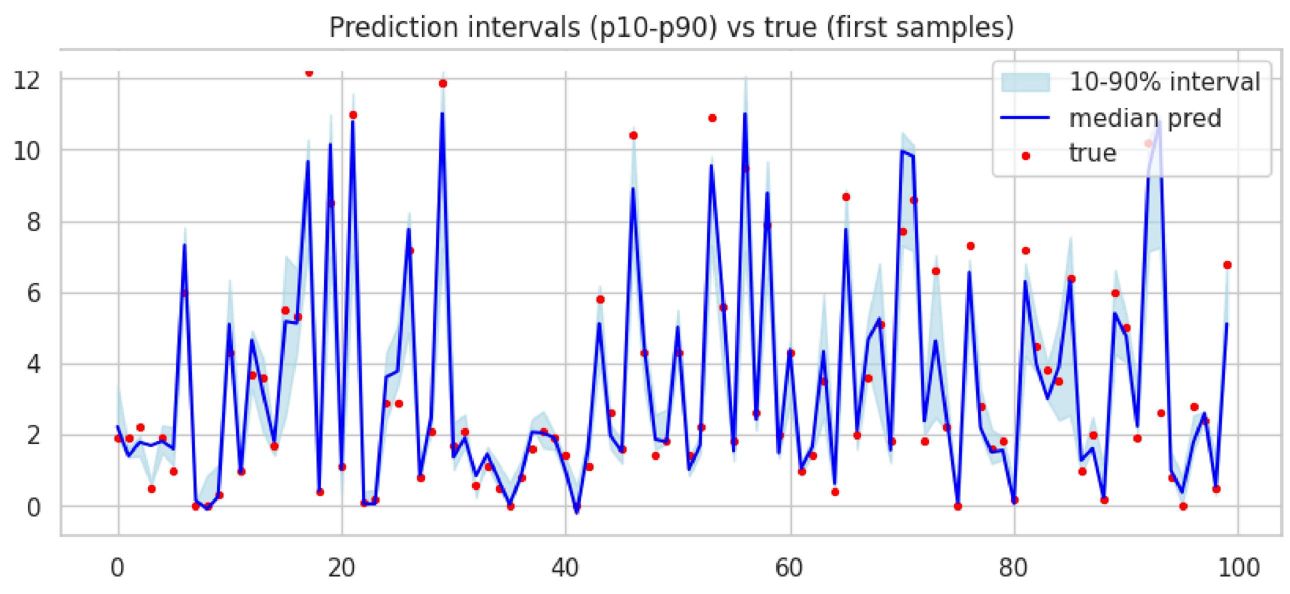
Next steps: Generate code with calib View recommended plots New interactive sheet

```
# Plot

#calibration curve

plt.figure(figsize=(6,5))
plt.plot(calib['mean_pred_prob'], calib['observed_rate'], marker='o')
plt.plot([0,1],[0,1], '--', color='gray')
plt.xlabel("Mean predicted hypo probability")
plt.ylabel("Observed hypo rate (proxy)")
plt.title("Calibration curve (proxy)")
plt.grid(True)
plt.show()
```



```
#Example prediction intervals vs true values (first 100 samples)
```

```
n_plot = min(100, len(pred_med))
plt.figure(figsize=(10,4))
x = np.arange(n_plot)
plt.fill_between(x, pred_low[:n_plot], pred_high[:n_plot], color='lightblue', alpha=0.6,
plt.plot(x, pred_med[:n_plot], label='median pred', color='blue')
plt.scatter(x, yv[:n_plot], color='red', s=8, label='true')
plt.legend()
plt.title("Prediction intervals (p10-p90) vs true (first samples)")
plt.show()
```



Simulator integration

This simulator is a simple deterministic compartment model that:

Models carb absorption (mono-exponential Ra),

Models insulin action as a decaying effect from bolus + basal,

Integrates glucose differential equation with Euler method (dt in minutes). It's not UVa/Padova but useful for evaluation and development — swap with a real simulator later.

```
#Minimal glucose-insulin simulator

import numpy as np
import pandas as pd

def simulate_minimal_model(row, bolus_units, horizon_minutes=240, dt_min=5,
                           Vg=10.0,    # glucose distribution volume (L) - heuristic
                           SI=0.02,    # insulin sensitivity (mg/dL per U per unit action
                           carb_abs_tau_min=None,  # carbs absorption time constant
                           DIA_hours=5.0):
    """
    Simulate glucose trajectory for a single timepoint row given a bolus insulin (units).
    Returns a DataFrame with columns ['t_min','glucose'] and summary metrics.
    - row: pd.Series (should contain glucose_level, carbs_g, weight_kg, median_ISF option
    - bolus_units: units of insulin given at t=0
    Note: this is a simplified model for evaluation only.
    """
    # Initial / patient vars
    G0 = float(row.get('glucose_level', 120.0))        # mg/dL
    carbs = float(row.get('carbs_g', 0.0))             # grams
    weight = float(row.get('weight_kg', 70.0))
    # carb absorption time constant (minutes)
    if carb_abs_tau_min is None:
        # choose based on meal type or carb_duration if available
        if 'carb_duration_min' in row and not pd.isna(row['carb_duration_min']):
            carb_abs_tau_min = row['carb_duration_min'] / 2.0 + 20.0
        else:
            carb_abs_tau_min = 60.0
    # insulin action decay time constant (minutes) from DIA
    tau_ins = DIA_hours * 60.0 / 2.0  # simple mapping: tau ~ DIA/2 (tunable)

    # time grid
    times = np.arange(0, horizon_minutes + dt_min, dt_min)  # minutes
    n = len(times)

    # Initialize state variables
    G = np.zeros(n); G[0] = G0
    Ra = np.zeros(n)   # rate of appearance (mg/dL per min)
    Ieff = np.zeros(n) # insulin action (arbitrary units)
    # convert carbs (g) to mg/dL change: 1 g carbs ≈ 4 kcal -> approx glucose mg/dL chang
    # Use scaling: assume 1 g carbs raises blood glucose by approx 3 mg/dL / (Vg factor)
    carb_to_gluc_factor = 3.0  # tweakable

    # Bolus generates initial Ieff impulse
    Ieff[0] = bolus_units

    # simulate with Euler integration
    for t_idx in range(1, n):
        # time step
        dt = dt_min

        # carbohydrate absorption: monoexponential Ra (grams -> glucose units)
        # Ra_g/min = carbs / tau * exp(-t/tau)
        t = times[t_idx]
        Ra_g = (carbs / max(1.0, carb_abs_tau_min)) * np.exp(-t / carb_abs_tau_min)  # g
        Ra_gluc = Ra_g * carb_to_gluc_factor  # convert to mg/dL per min (approx)
        Ra[t_idx] = Ra_gluc

        # insulin action decay (exponential)
        Ieff[t_idx] = Ieff[t_idx-1] * np.exp(-dt / tau_ins)

        # net glucose change: appearance - insulin-mediated uptake (proportional to Ieff*
        insulin_term = SI * Ieff[t_idx] * max(0, G[t_idx-1] - 80.0)  # uptake proportiona
        dG = (Ra_gluc - insulin_term) * (dt / 1.0) / Vg  # simplified scaling
        # small basal drift towards 100 mg/dL
        basal_drift = 0.001 * (100.0 - G[t_idx-1]) * dt
        G[t_idx] = max(30.0, G[t_idx-1] + dG + basal_drift)

    sim_df = pd.DataFrame({'t_min': times, 'glucose': G, 'Ra': Ra, 'Ieff': Ieff})
    # summary metrics
    min_gluc = float(G.min())
    max_gluc = float(G.max())
    time_in_range = float(((G >= 70.0) & (G <= 180.0)).mean() * 100.0)
    hypo_episodes = int(((G < 70.0).astype(int)).sum())
    return {'sim_df': sim_df, 'min_gluc': min_gluc, 'max_gluc': max_gluc,
            'time_in_range_pct': time_in_range, 'hypo_counts': hypo_episodes}


# Apply simulator to validation set predictions

# Inputs expected: test_df (aligned with Xv), pred_med (median predictions array), option

# Build test_df if not available:
test_df = model_df.loc[Xv.index].reset_index(drop=True).copy()  # ensures alignment

# We'll evaluate the median predictions pred_med
results_sim = []
for i in range(len(pred_med)):
    row = test_df.iloc[i]
    pred_bolus = float(pred_med[i])
    sim_res = simulate_minimal_model(row, bolus_units=pred_bolus, horizon_minutes=240, dt
    # gather
    results_sim.append({
        'idx': i,
        'pred_bolus': pred_bolus,
        'true_bolus': float(row['recommended_bolus_units']),
        'min_gluc': sim_res['min_gluc'],
        'max_gluc': sim_res['max_gluc'],
        'time_in_range_pct': sim_res['time_in_range_pct'],
        'hypo_counts': sim_res['hypo_counts']
    })

sim_results_df = pd.DataFrame(results_sim)


# Summary statistics
print("Simulator-based summary (median predictions):")
print("Mean TIR%:", sim_results_df['time_in_range_pct'].mean())
print("Fraction with any hypo episodes:", (sim_results_df['hypo_counts'] > 0).mean())
print(sim_results_df.describe()[['min_gluc','time_in_range_pct','hypo_counts']])
```

```
Simulator-based summary (median predictions):
Mean TIR%: 83.23615160349853
Fraction with any hypo episodes: 0.0
         min_gluc  time_in_range_pct  hypo_counts
count  140.000000         140.000000        140.0
mean   120.739254          83.236152          0.0
std     33.288206          29.624636          0.0
min     70.300000           0.000000          0.0
25%     92.389330          82.653061          0.0
50%    112.428365         100.000000          0.0
75%    144.589059         100.000000          0.0
max    204.966998         100.000000          0.0
```

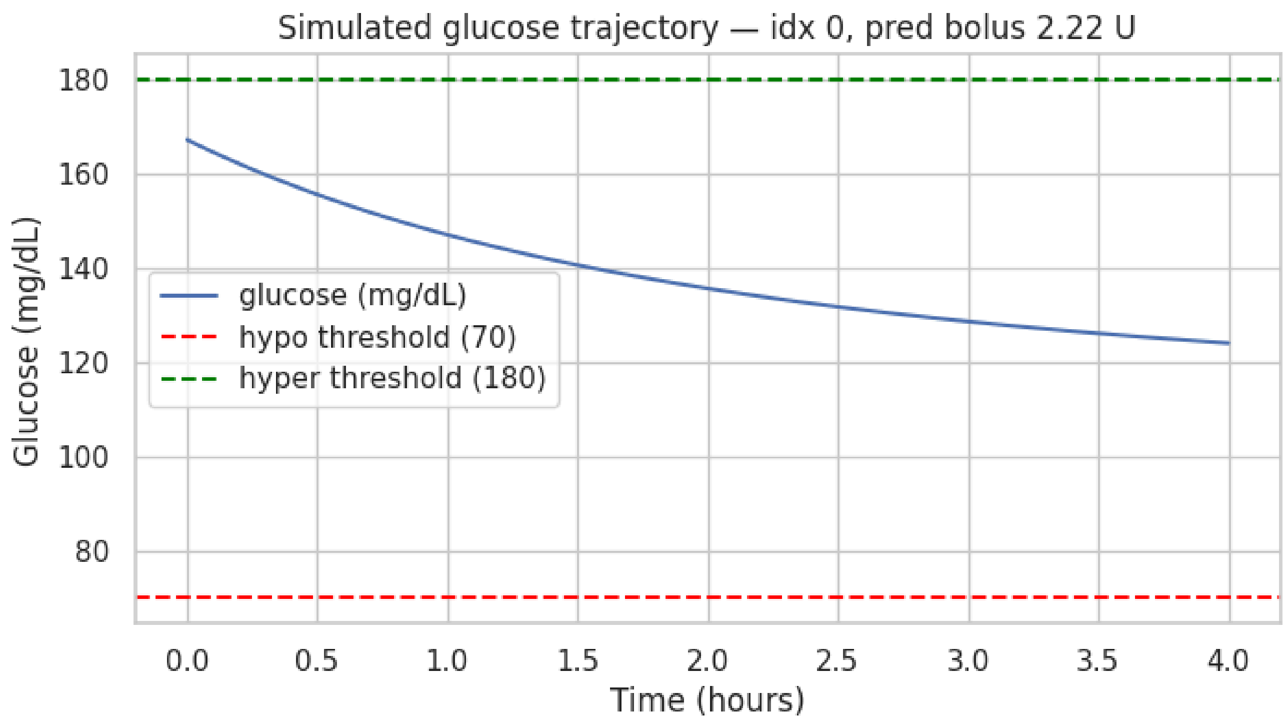
```
# Example: show some rows where hypo occurred
print("\nExample rows with hypo episodes (sim):")
```

```
display(sim_results_df[sim_results_df['hypo_counts']>0].head())
```

```
Example rows with hypo episodes (sim):
```

idx	pred_bolus	true_bolus	min_gluc	max_gluc	time_in_range_pct	hypo_counts

```
#Plot simulated glucose trajectory

import matplotlib.pyplot as plt

i_plot = 0  # change index as needed, must be < len(pred_med)
row = test_df.iloc[i_plot]
pred_bolus = float(pred_med[i_plot])
sim_res = simulate_minimal_model(row, bolus_units=pred_bolus, horizon_minutes=240, dt_min
sim_df = sim_res['sim_df']

plt.figure(figsize=(8,4))
plt.plot(sim_df['t_min']/60.0, sim_df['glucose'], label='glucose (mg/dL)')
plt.axhline(70, color='red', linestyle='--', label='hypo threshold (70)')
plt.axhline(180, color='green', linestyle='--', label='hyper threshold (180)')
plt.xlabel('Time (hours)')
plt.ylabel('Glucose (mg/dL)')
plt.title(f"Simulated glucose trajectory — idx {i_plot}, pred bolus {pred_bolus:.2f} U")
plt.legend()
plt.show()
```



10. Final Predict

```
    from sklearn.model_selection import train_test_split
    from sklearn.metrics import mean_absolute_error, mean_squared_error
```