

Deriving a Glucometer Equation:

1. Obtain Coefficients from Linear + Random Forest Model (*Coeff Model.py*):

Coefficient	Dataset w/ Two Diabetic	Dataset w/ One Diabetic (ID = 6)	Dataset w/ One Diabetic (ID = 8)
B0	117.746339	115.702826	114.106297
B1 (ratio)	-1.468293	-0.566543	-2.911327
B2 (ac)	-18.740200	-12.529524	-43.032404
B3 (dc)	-0.025717	0.873844	2.074895
B4 (PI)	18.321776	10.346518	39.660120
B5 (slope)	0.614418	2.317182	1.600641
RATIO M	-0.000522	-0.000983	0.002816
RATIO S	0.033974	0.032881	0.035950
AC M	15.122963	15.654730	8.656087
AC S	412.982216	415.411025	464.645141
DC M	-423.108476	704.496414	1198.126301
DC S	12556.207636	5755.222950	6235.903169
PI M	0.000133	0.000132	0.000057
PI S	0.003568	0.003593	0.003990
SLOPE M	-0.009106	-0.002956	-0.000139
SLOPE S	0.112513	0.106724	0.111725
Ratio Baseline	1.203559	1.206370	1.200512
AC Baseline	652.865153	648.902829	709.658039
DC Baseline	114251.523529	113954.698197	115009.016961
PI Baseline	0.005637	0.005608	0.006129
Slope Baseline	0.102440	0.107275	0.112296

In *Dataset.csv*:

- Glucose: Reference Invasive Glucose
- Max: Output Max Non-Invasive Glucose (Pre- Anything and w/ All Subjects)
- Offset: Max Non-Invasive Glucose post (-11 mg/dL) offset
- All: Max Non-Invasive Glucose w/Baseline
- NO6: Max Non-Invasive Glucose w/Baseline (ID=8 is Ignored)
- NO8: Max Non-Invasive Glucose w/Baseline (ID=6 is Ignored)

2. Residual – Glucose Equation: (*Residual – Glucose Corr WP*):

- **Max_offset:**

$$\text{Residual} \approx -0.812 * \text{glucose} + 84.426$$

$$\text{Zero Error Glucose} = 104 \text{ mg/dL}$$

- **All (Baseline):**

$$\text{Residual} \approx -0.982 * \text{glucose} + 115.654$$

$$\text{Zero Error Glucose} = 117.8 \text{ mg/dL}$$

- **NO6 (Baseline):**

$$\text{Residual} \approx -0.987 * \text{glucose} + 114.245$$

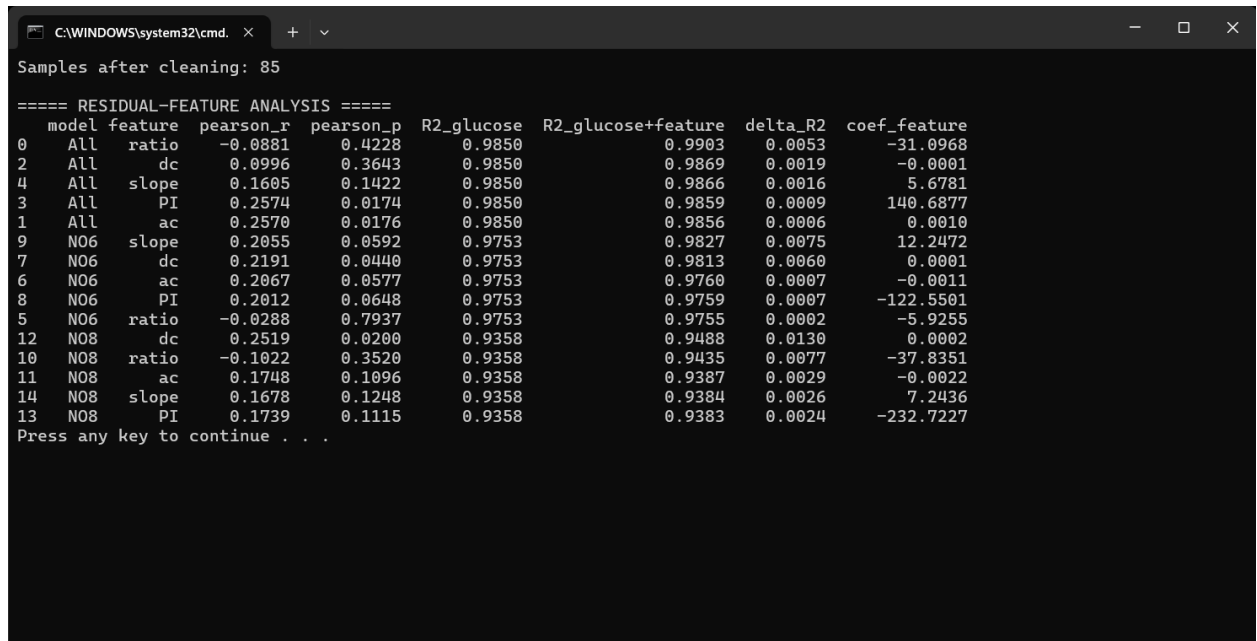
$$\text{Zero Error Glucose} = 115.8 \text{ mg/dL}$$

- **NO8 (Baseline):**

$$\text{Residual} \approx -0.971 * \text{glucose} + 110.828$$

$$\text{Zero Error Glucose} = 114.1 \text{ mg/dL}$$

3. Correlation between Features and Residual:



```
C:\WINDOWS\system32\cmd.  X  +  v
Samples after cleaning: 85

===== RESIDUAL-FEATURE ANALYSIS =====
model feature  pearson_r  pearson_p  R2_glucose  R2_glucose+feature  delta_R2  coef_feature
0 All ratio -0.0881 0.4228 0.9850 0.9903 0.0053 -31.0968
2 All dc 0.0996 0.3643 0.9850 0.9869 0.0019 -0.0001
4 All slope 0.1605 0.1422 0.9850 0.9866 0.0016 5.6781
3 All PI 0.2574 0.0174 0.9850 0.9859 0.0009 140.6877
1 All ac 0.2570 0.0176 0.9850 0.9856 0.0006 0.0010
9 NO6 slope 0.2055 0.0592 0.9753 0.9827 0.0075 12.2472
7 NO6 dc 0.2191 0.0440 0.9753 0.9813 0.0060 0.0001
6 NO6 ac 0.2067 0.0577 0.9753 0.9760 0.0007 -0.0011
8 NO6 PI 0.2012 0.0648 0.9753 0.9759 0.0007 -122.5501
5 NO6 ratio -0.0288 0.7937 0.9753 0.9755 0.0002 -5.9255
12 NO8 dc 0.2519 0.0200 0.9358 0.9488 0.0130 0.0002
10 NO8 ratio -0.1022 0.3520 0.9358 0.9435 0.0077 -37.8351
11 NO8 ac 0.1748 0.1096 0.9358 0.9387 0.0029 -0.0022
14 NO8 slope 0.1678 0.1248 0.9358 0.9384 0.0026 7.2436
13 NO8 PI 0.1739 0.1115 0.9358 0.9383 0.0024 -232.7227
Press any key to continue . . .
```

Feature-based Correction (or in association w/ Glucose) proved to explain only very little of the residual error and therefore is negligible.

4. Optimal Correctional Gain (*Assuming Glucose- Gating*)

- For Model NO8:

```
C:\WINDOWS\system32\cmd. x + v
Low-glucose samples (<114): 42

===== LOW-GLUCOSE OPTIMIZATION =====
Baseline MAE (<114): 11.67 mg/dL
Optimal alpha: 0.000
Corrected MAE (<114): 11.67 mg/dL
MAE improvement: 0.00 mg/dL
High-glucose samples (>114): 42

===== HIGH-GLUCOSE OPTIMIZATION =====
Baseline MAE (>114): 17.53 mg/dL
Optimal alpha: 1.000
Corrected MAE (>114): 17.21 mg/dL
MAE improvement: 0.32 mg/dL
Press any key to continue . . . |
```

No fractional correctional gain CAN fix the error whether gating was done for values < or > than 114

5. The implementation of Adaptive Baselining and Adding Temporal Features (dPI/dt):

Make sure temporal stability is achieved over 6 non-consecutive windows is achieved before calculation

+ Slow Baseline sliding?

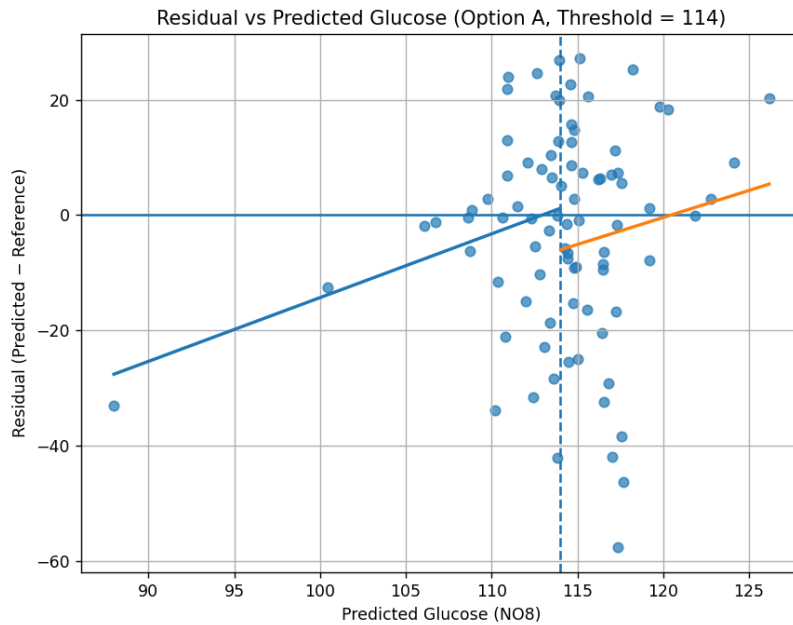
6. Piecewise Correctional Error (with weighted- regimes)

*LOW: residual $\approx 1.1063 * pred + -124.97$*

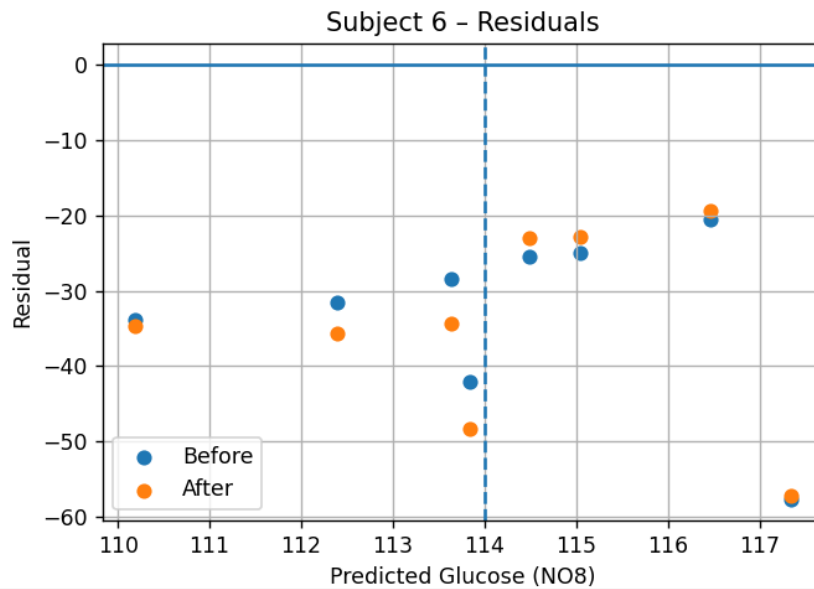
*HIGH: residual $\approx 0.9376 * pred + -112.94$*

Threshold = 124

In ESP-Code, the threshold gating is smoother, to accommodate values that are 113.9 or 114.1, so it uses both high and low residual equations but with weights (W and (1-W)), and the larger weight is on what part of the spectrum the predicted is in relation to threshold. Model uses only ONE of the equations (i.e. W = 1) when predicted < 104 or >124.

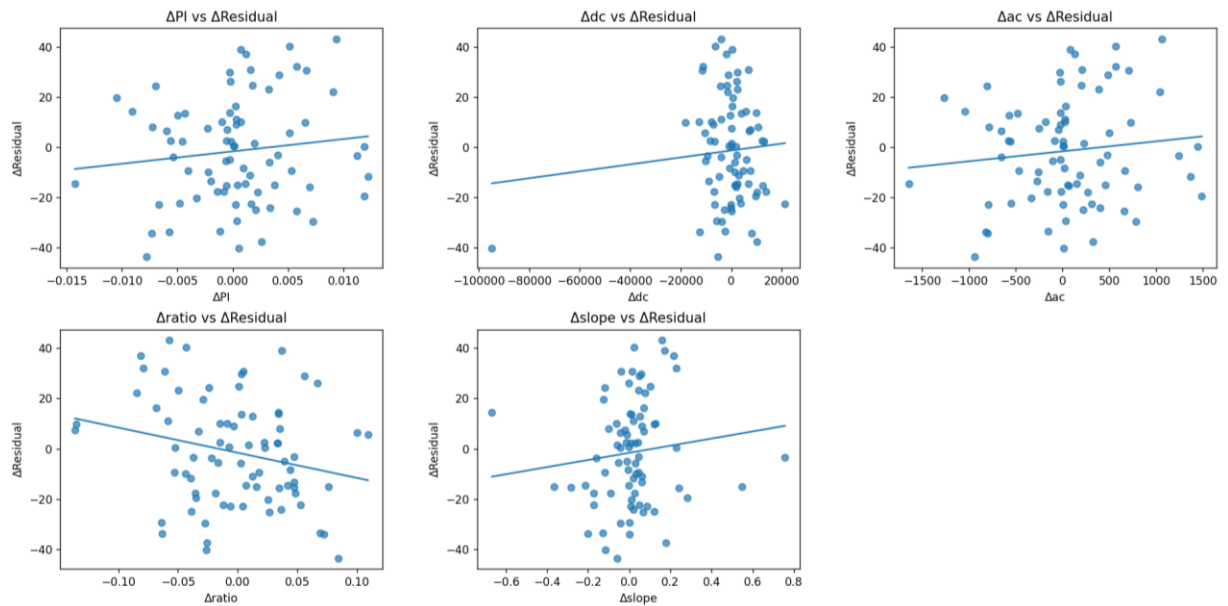


This piecewise correctional equation tested on ID = 6 (Diabetic)



Shows it doesn't help high glucose numbers

7. Correlation Between Temporal Feature Derivatives and Residual (*Offline Tested Per Event*)



$d(\text{Ratio})/dt$ shows the best correlation with residual and therefore can be added as a secondary term in the equation

$$r = -0.235$$

===== ΔRATIO CORRECTION RESULTS =====

Baseline MAE: 14.19 mg/dL

Corrected MAE: 14.89 mg/dL

Improvement: -0.70 mg/dL

Therefore, the highest correlation feature derivative hindered performance

***Baseline Variation and Distance from Training Data also failed to correlate to residual**

***Cross- Feature Inconsistencies could NOT justify residual gating**

8. Comparison:

Reference Glucose	PI-Stability Gate + Offset	PI-Stability Gate + Residual Correctional Error
114	112.8	116.5
112	106	119