

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):**

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

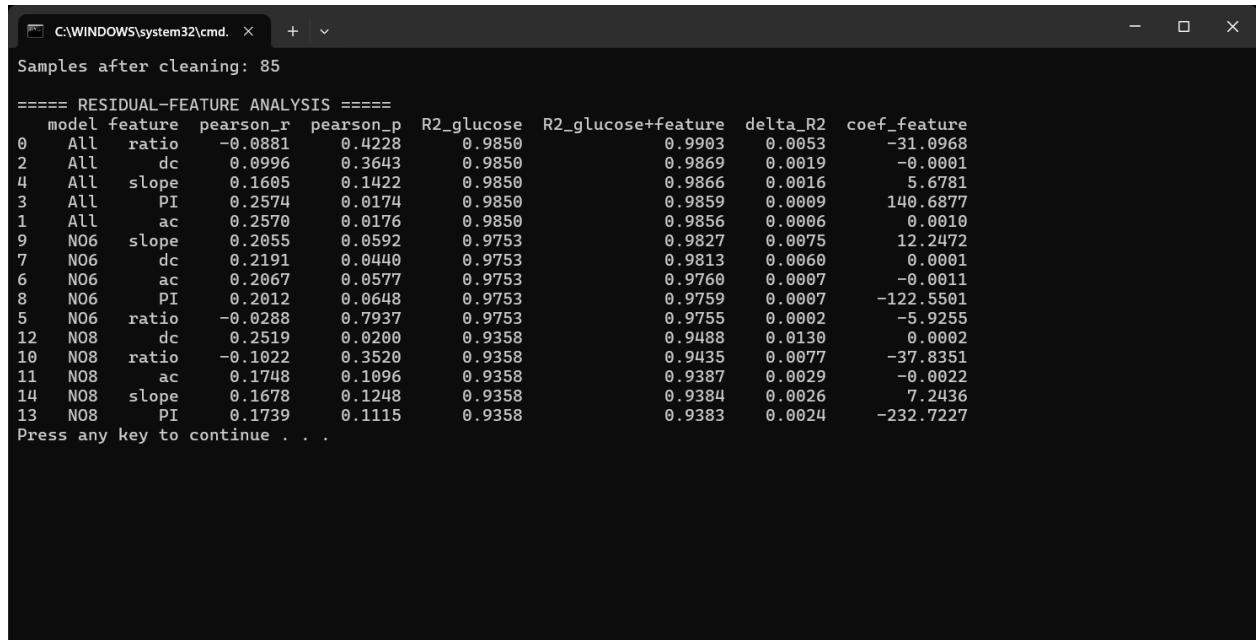
$$\text{Zero Error Glucose} = 115.8 \text{ mg/dL}$$

- **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:



The screenshot shows a Windows command prompt window titled 'C:\WINDOWS\system32\cmd.' with the title bar. The window contains a table of data from a 'RESIDUAL-FEATURE ANALYSIS'. The table has columns for model, feature, pearson_r, pearson_p, R2_glucose, R2_glucose+feature, delta_R2, and coef_feature. The data rows show various models (All, NO6, NO8) and features (ratio, dc, slope, PI, ac) with their corresponding correlation coefficients and R-squared values. The table is preceded by a header 'Samples after cleaning: 85' and followed by a prompt 'Press any key to continue . . .'.

===== 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	N08	dc	0.2519	0.0200	0.9358	0.9488	0.0130	0.0002
10	N08	ratio	-0.1022	0.3520	0.9358	0.9435	0.0077	-37.8351
11	N08	ac	0.1748	0.1096	0.9358	0.9387	0.0029	-0.0022
14	N08	slope	0.1678	0.1248	0.9358	0.9384	0.0026	7.2436
13	N08	PI	0.1739	0.1115	0.9358	0.9383	0.0024	-232.7227

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 + ^

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?

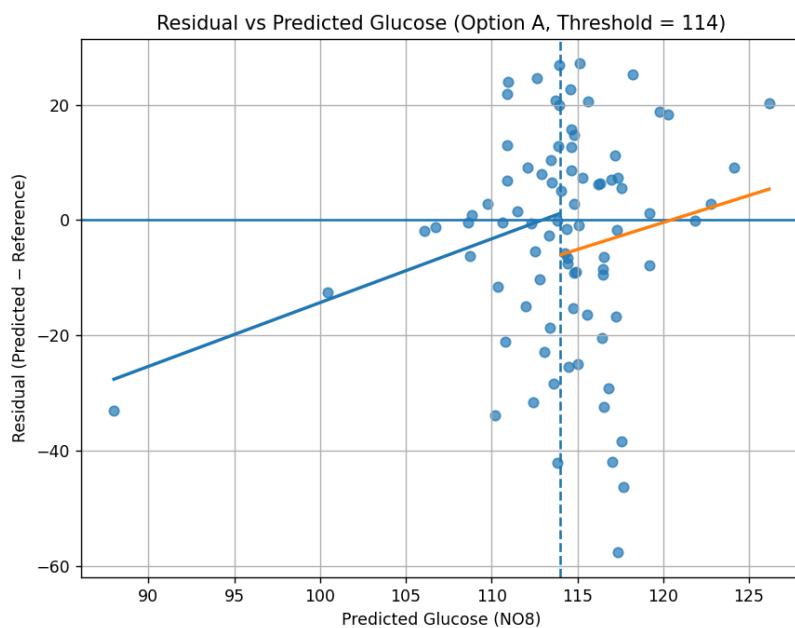
6. Piecewise Correctional Error (with weighted- regimes)

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

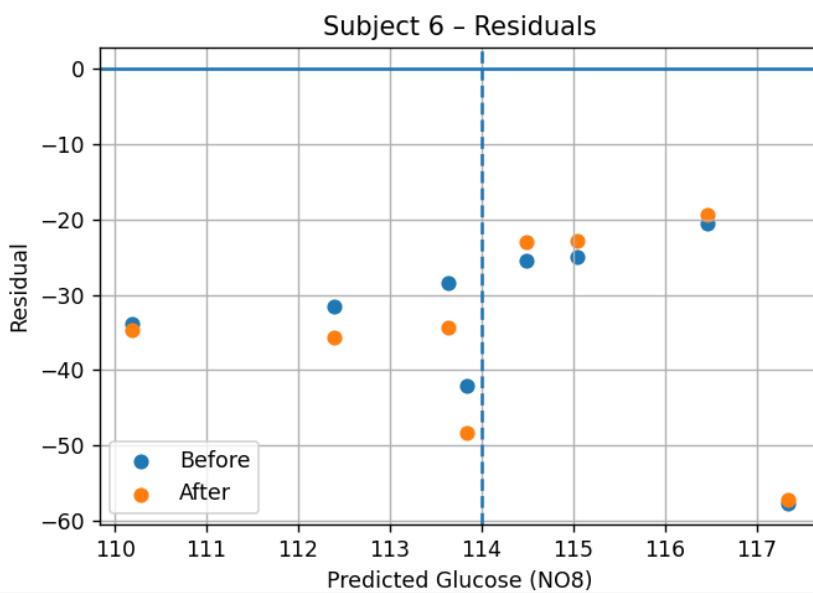
*HIGH: residual $\approx 0.9376 * pred + -112.94$*

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.

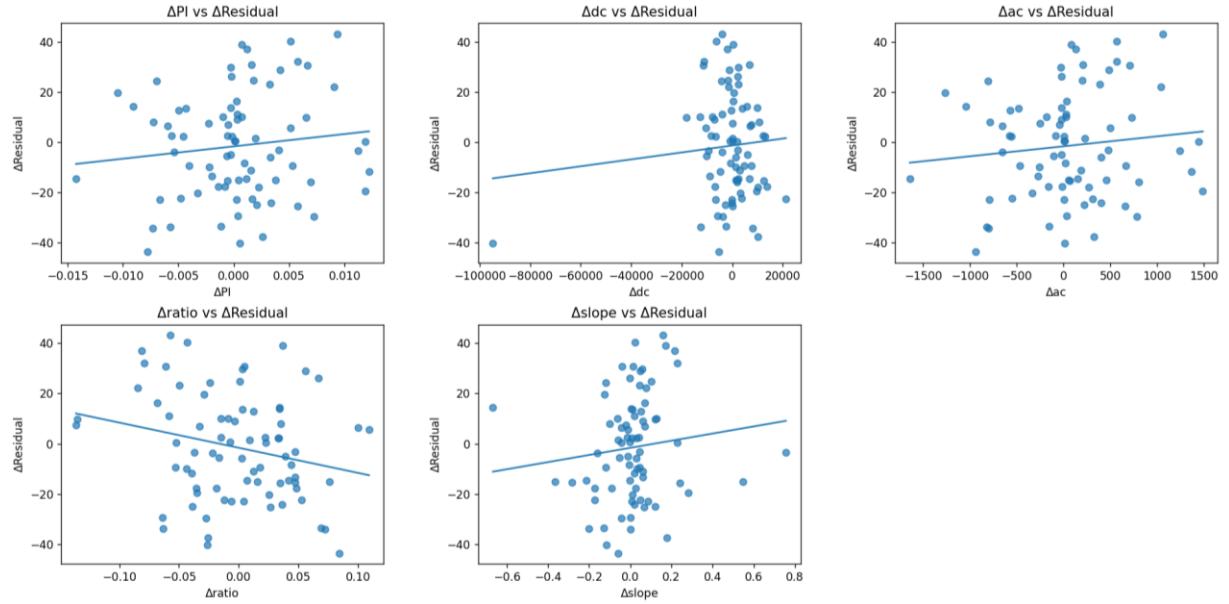


This piecewise correctional equation tested on ID = 6 (Diabetic)



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