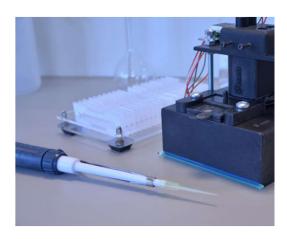


F-POINT ALGORITHM

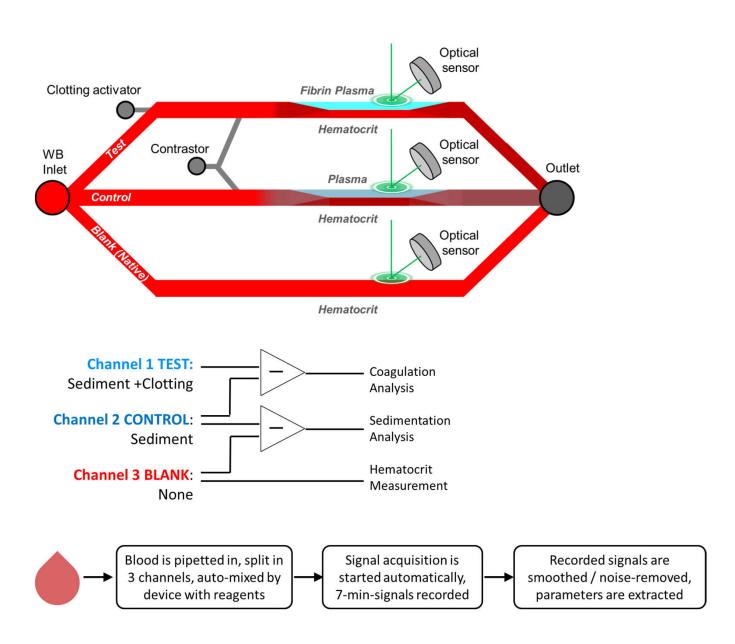
SUMMARY & KEY NOTES ON SIGNAL PROCESSING AND MACHINE LEARNING ASPECTS



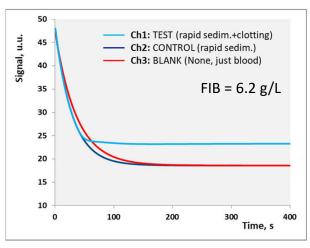
F-POINT ASSAY PROTOTYPE DEVICE



- Aimed to measure FIBRINOGEN
- Especially low FIBRINOGEN
- Works in whole blood (doesn't require sample pretreatment)
- Rapid: 7 minutes turnaround time
- Pocket-size



DATA ACQUISITION & EXTRACTION OF RAW PREDICTORS



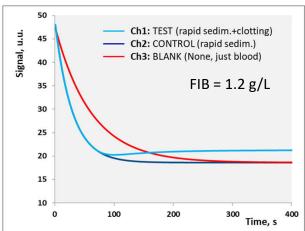
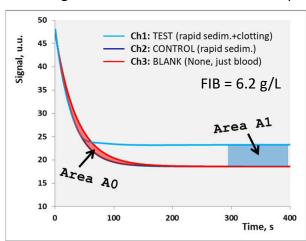


FIG.1. Signals from 3 channels recorded in parallel



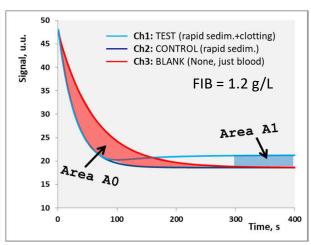
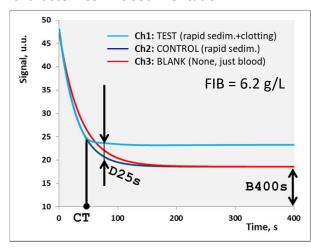


FIG.2. Two Area-Between-Curve values. A1 characterizes fibrin network density; A2 characterizes RBC sedimentation.



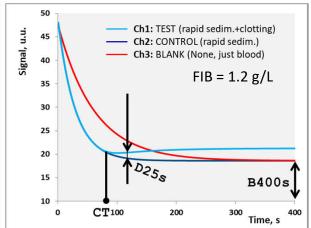


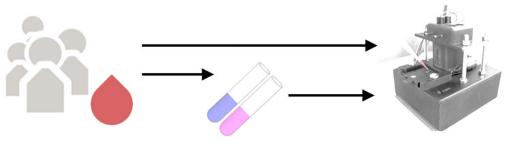
FIG.3. Three timeline values. CT is Clotting Time; B400s is the end value of control channel signal; D25s characterizes fibrin clot growth rate .

FIB = 1.2 g/L: A0 high / A1 low / CT high / D25s low / B400s is FIB-independent FIB = 6.2 g/L: A0 low / A1 high / CT low / D25s high / B400s is FIB-independent



DATA COLLECTION FOR ALGORITHM DEVELOPMENT

DATA COLLECTION SCHEME



107 normal healthy volunteers donated blood samples, then citrated

Samples randomly divided in 2 equal groups: fibrinogen spiked or partially de-fibrinated 214 samples assayed:107 normal,54 spiked,53 de-fibrinated

DATA

FIB	Α0	CT	D25s	A1	B400s
0.4	28	166	0	2	23.9
0.4	30	114	1.2693	1	16.5
0.4	23	88	1.394	11	12.4
0.5	26	100	0	5	16
0.5	23	00	0 6500		

In addition, each sample was HCT assayed by conventional CBC device to have a hematocrit data in hand

DATA SUMMARY

> summary(ffD)				
FIB	A0	B400s	D25s	
Min. :0.400	Min. : 0.00	Min. :12.40	Min. : 0.000	
1st Qu.:1.825	1st Qu.:10.25	1st Qu.:16.50	1st Qu.: 4.093	
Median :3.200	Median :17.00	Median :18.10	Median : 7.393	
Mean :3.256	Mean :16.59	Mean :18.55	Mean : 6.785	
3rd Qu.:4.600	3rd Qu.:23.00	3rd Qu.:20.30	3rd Qu.: 9.542	
Max. :6.900	Max. :33.00	Max. :27.90	Max. :13.310	
A1	CT	HCT		
Min. : 1.00	Min. : 32.00	Min. :21.00		
1st Qu.:13.00	1st Qu.: 42.62	1st Qu.:30.00		
Median :15.00	Median : 50.00	Median :33.00		
Mean :16.23	Mean : 53.11	Mean :33.74		
3rd Qu.:20.00	3rd Qu.: 59.00	3rd Qu.:36.00		
Max. :29.00	Max. :166.00	Max. :53.00	N = 214	
< I				/1
			FIB range: 0.4 – 6.9 g/	/L

RAW FIBRINOGEN PREDICTORS & HCT MODEL

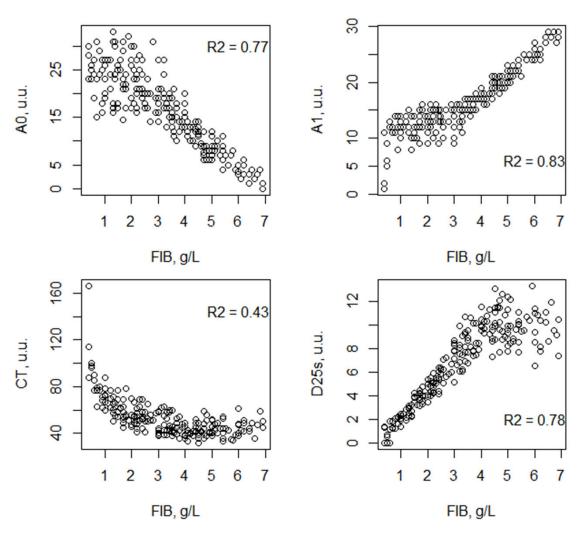


FIG.4. Four extracted parameters as FIB predictors. Looks promising but too weak to be used individually

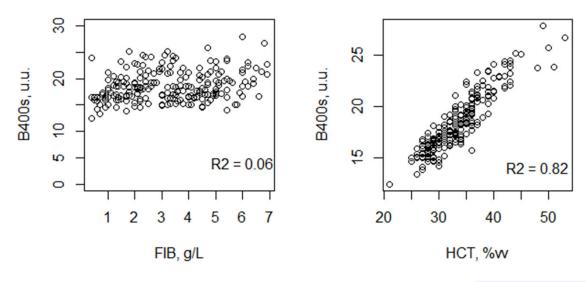


FIG.5. Fifth parameter can be considered as HCT estimator

 $HCT^{EST} = B400s*1.82 + 0.03$



STANDARDIZED INTERPRETABLE PREDICTORS

ASSUMPTIONS FOR LOG SCALES, MINMAXS & CUTS

- Log-Log scale significantly improves R2 for kinetic predictors (CT and D25s)
- HCT must be considered as an interaction variable (HCT takes a significant random part of volume) in a form of $\{*(HCT)^{N1,,2...}\}$ where N1, N2 are unknown

STANDARTIZED INTERPRETABLE PREDICTORS

By-Sedimentation FIB Predictor: ESR.F = cut(AO, >15)/15

By-Fibrin FIB Predictor: $CLOT_DENSITY.F = cut(A1, <15)/15$

By-Clotting Time FIB Predictor: $CLOT_TIME.F = 2*log(CT)-3$

By-Coagulation Rate FIB Predictor: CLOT_RATE.F = cut(log(D25s), >1)

Interaction with HCT: ILogHCT.F = 2*log10(B400s)-2

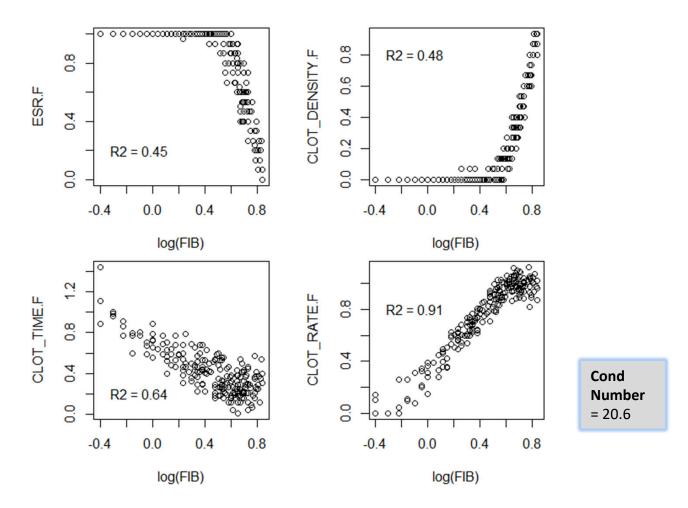


FIG.6. Set of standardized interpretable variables as the log(FIB) predictors



THE MODEL

$$Log10(FIB) = -1.1 + 0.7*PC^{kinetic} + 0.2*PC^{static} + 1.1*ILogHCT.F$$

$$PC^{kinetic} = -0.6*CLOT_TIME.F + 0.8*CLOT_RATE.F$$

 $PC^{static} = 0.7*CLOT_DENSITY.F - 0.7*ESR.F$

Num. of model vars = 3

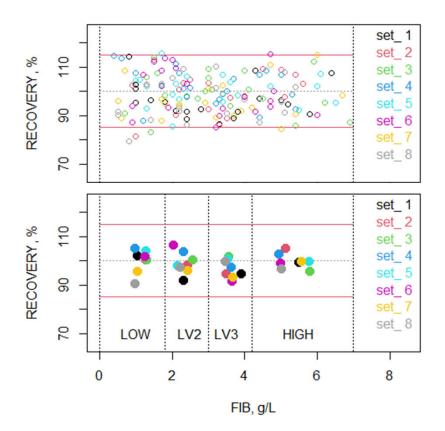
MODEL METRICS BY TRAINING SETS (CROSS-VALIDATION W. EIGHT 91% - RUNS)

Max abs correlation in 3 vars = 0.53

Min R-square = 0.93

Max Cond Number = 4.17

MODEL METRICS BY TESTING SETS (CROSS-VALIDATION W. EIGHT 9%-RUNS)



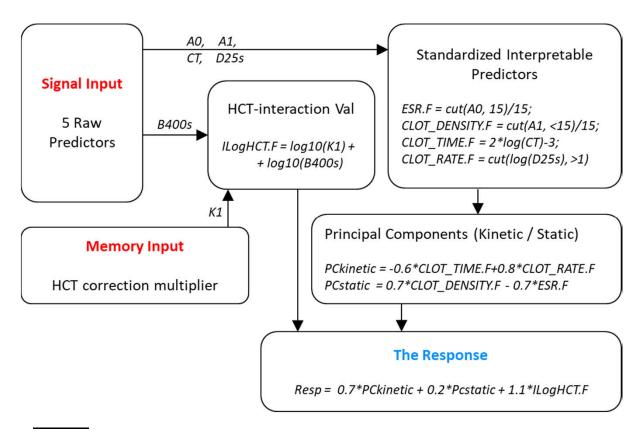
Bio-analytical accuracy criteria is usually defined by recovery threshold values (+/- 15%).

Some separate data can be out of < +/-15% range but Recovery for each analytical range in average is in

FIG.7. Recovery plot for all data in 8 testing sets (top) and the mean recovery values for 4 separate analytical FIB ranges.(bottom).

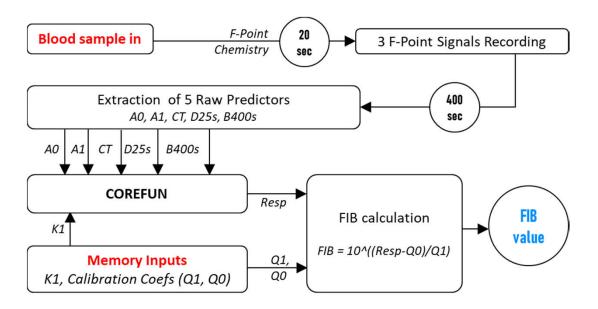
CORE FUNCTION

Resp = COREFUN(A0, A1, CT, D25s, B400s, K1 = 1)

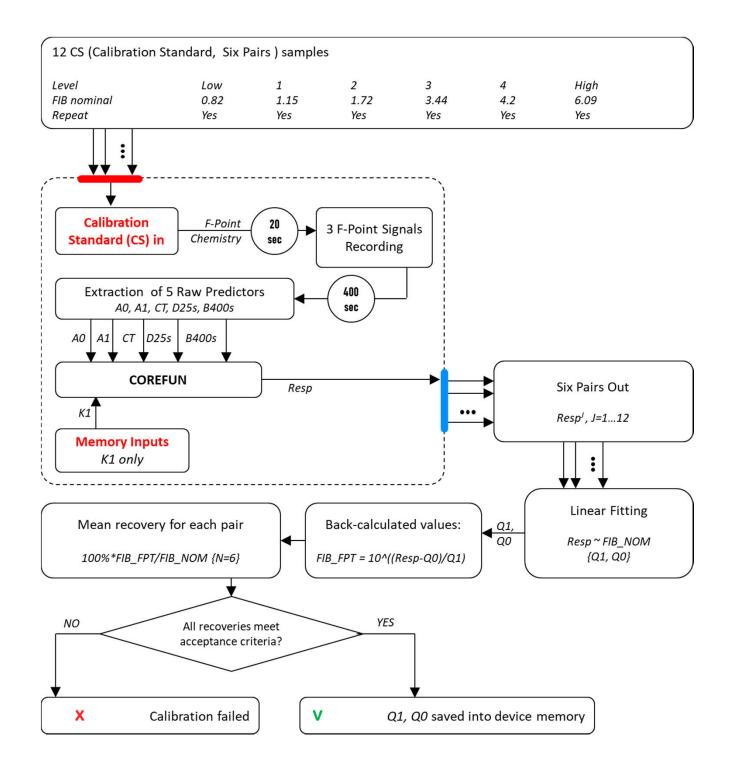


^{*} coefficient K1 is to be defined at periodical HCT-related system adjustment. Default is 1.

MEASUREMENT SCHEME



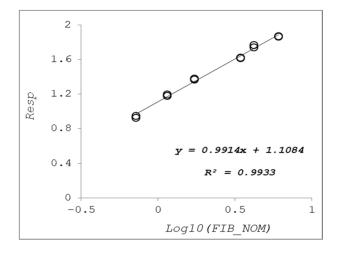
CALIBRATION SCHEME





CALIBRATION STANDARDS, RAW PREDICTORS, RESPONSE & FITTING

CS K	1 FIB_NOM(no	minal) A0	A1	CT	D	25s B40	0s :	Resp(response)
LOW	1	0.72	24	11	86	1.5	16.9	0.94952886
LOW	1	0.72	31	9	80	1.2	17	0.9244608
LEV1	1	1.15	28	12	75	3.3	17	1.19403124
LEV1	1	1.15	25	11	76	3.1	17.1	1.17679593
LEV2	1	1.72	16	14	55	4.4	17.1	1.37994564
LEV2	1	1.72	18	14	54	4	17.2	1.36624521
LEV3	1	3.44	8	18	42	5.5	16.9	1.62030349
LEV3	1	3.44	9	21	43	5.1	17	1.61484069
LEV4	1	4.2	7	23	42	7	17	1.73777372
LEV4	1	4.2	7	24	41	7.2	17.1	1.76555122
HIGH	1	6.09	5	26	37	8	17	1.86315584
HICH	1	6.09	5	26	38	8.3	17.2	1.86796788



Calibration Coefficients

Q1 = 0.99Q0 = 1.11

Back calculated values:

 $FIB_FPT = 10^{((Resp-Q0)/Q1)}$

Fig.8. Calibration plot and a simple linear regression fit

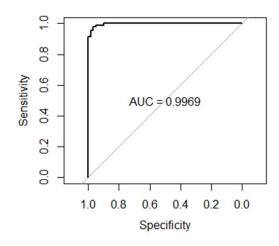
ASSESSMENT OF CALIBRATION QUALITY

			Acceptance				
CS	FIB_NOM Mean	Resp FIB	_FPT	%Recovery	criterion, %	Accepted?	
LOW	0.72	0.94	0.67	93.53	80-120	Yes	
LEV1	1.15	1.18	1.18	102.33	85-115	Yes	
LEV2	1.72	1.37	1.83	106.44	85-115	Yes	
LEV3	3.44	1.62	3.27	95.19	85-115	Yes	
LEV4	4.2	1.75	4.43	105.49	85-115	Yes	
HICH	6.09	1.86	5.72	93.96	85-115	Yes	

All criteria of acceptance are met -> Calibration Coefficients are placed into the device memory for further FIB measurements for the real blood samples

F-POINT AS A CLASSIFIER; REAL MEASUREMENT EXAMPLE

HYPOFIBRINOGENAEMIA (FIB < 1.8 g/L)



F-Point as a descent classifier

REAL MEASUREMENT: A WHOLE BLOOD SAMPLE OF UKNOWN FIB AND HCT

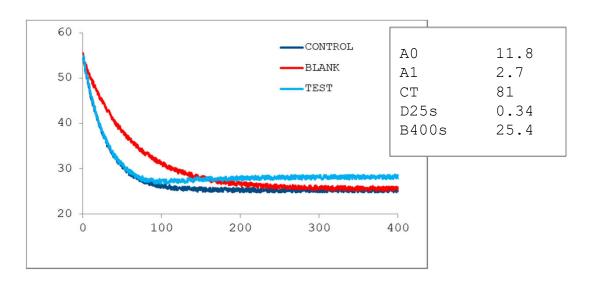


Fig.9. Real 3 channel signals recorded by F-Point and extracted set of raw predictors

$$Resp = 1.03$$
; $Q1 = 0.99$, $Q0 = 1.11$ (taken from the last calibration)

$$FIB = 10^{(Resp-Q0)/Q1} = 0.83 g/L$$

ESTIMATION OF HCT AS A BONUS

$$HCT^{EST} = 1.82*K1*B400s = 46.2 \%v.v.$$

^{*} coefficient K1 is to be defined at periodical HCT-related system adjustment. Default is 1.