Using NIRS to determine sample differences: range, homogeneity,...

Paolo Berzaghi NIRS Consortium/Univ. of Padua, Italy















ADF vs. ADF v SED: 1.180 Number of Samples: 20 Means: 27.595 26.577 Standard Deviations: 1.596 1.830 Bias: 1.018 Bias Limit: 0.000 SED[C]: 0.6612 SED[C] Limit: 0.000 Slope: 0.825 RSQ: 0.893 Ave. Global H: 1.457 1.272 Ave. Neighbor. H: 0.712 0.577 Pos. Sample No. ANL ANL Residual Bias GH1 NH1 GH2 NH2 1 1 27.30 25.12 2.18 1.16 1.41 0.65 1.42 0.68 3 3 25.34 2.391 1.44 0.42 1.09 0.60 0.98 0.47 4 4 26.81 25.95 0.85 -0.16 1.08 0.62 0.92 0.48 5 27.44 26.15 1.29 0.27 1.56 0.61 1.36 0.51 6
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SED[C]: 0.612 SED[C] Limit: 0.00 Slope: 0.825 RSQ: 0.893 Ave. Global H: 1.457 1.272 Ave. Neighbor. H: 0.712 0.577 Pos. Sample No. ANL ANL Residual Bias GH1 NH1 GH2 NH2 1 1 27.30 25.12 2.18 1.16 1.41 0.65 1.17 0.53 2 2 25.12 23.43 1.69 0.67 1.65 0.82 1.42 0.66 3 3 25.34 23.91 1.44 0.42 1.09 0.60 0.98 0.47 4 4 26.81 25.95 0.85 -0.16 1.08 0.62 0.92 0.48 5 5 27.44 26.15 1.29 0.27 1.56 0.61 1.36 0.51 6 6 26.11 25.24 0.87 -0.15 1.64 0.60 0.83
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Pos. Sample No. ANL ANL Residual Bias GH1 NH1 GH2 NH2 1 1 27.30 25.12 2.18 1.16 1.41 0.65 1.17 0.53 2 2 25.12 23.43 1.69 0.67 1.65 0.82 1.42 0.68 3 3 25.34 23.91 1.44 0.42 1.09 0.60 0.98 0.47 4 4 26.81 25.95 0.85 -0.16 1.08 0.62 0.92 0.48 5 5 27.44 26.15 1.29 0.27 1.56 0.61 1.51 0.60 7 7 28.45 27.34 1.11 0.09 1.17 0.68 0.83 0.32 8 28.02 27.28 0.74 -0.28 1.73 0.67 1.64 0.52 9 9 26.11 24.52 1.59 0.58 1.08 0.
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5 27.44 20.13 1.23 0.27 1.30 0.31 6 6 26.11 25.24 0.87 -0.15 1.64 0.61 1.50 0.31 7 7 28.45 27.34 1.11 0.09 1.17 0.68 0.83 0.32 8 8 28.02 27.28 0.74 -0.28 1.73 0.67 1.64 0.52 9 9 26.11 24.52 1.59 0.58 1.08 0.60 0.86 0.34 10 10 26.06 24.38 1.09 0.07 1.16 0.51 0.97 0.42
7 28.45 27.24 1.11 0.09 1.17 0.68 0.83 0.32 8 8 28.02 27.28 0.74 -0.28 1.73 0.67 1.64 0.52 9 9 26.11 24.52 1.59 0.58 1.08 0.60 0.86 0.34 10 10 26.06 24.98 1.09 0.07 1.16 0.51 0.97 0.42
8 8 28.02 27.28 0.74 -0.28 1.73 0.67 1.64 0.52 9 9 26.11 24.52 1.59 0.58 1.08 0.60 0.86 0.34 10 10 26.06 24.98 1.09 0.07 1.16 0.51 0.97 0.42
9 26.11 24.52 1.59 0.58 1.08 0.60 0.86 0.34 10 10 26.06 24.98 1.09 0.07 1.16 0.51 0.97 0.42
10 10 26.06 24.98 1.09 0.07 1.16 0.51 0.97 0.42
11 11 30.48 29.58 0.90 -0.11 1.82 0.94 1.69 0.77
12 12 27.73 25.81 1.92 0.91 1.33 0.54 1.21 0.51

Factors that affect spectra

Real Problem:

"Using NIRSC equation I get good results for NFTA, but predictions don't match composition for my samples"

- 1. Your chemistry is not good!
 - Nope, we get straight A's with NFTA samples
- 2. Is something wrong with your sample prep?
 - Nope, we dry at 60° C and grind at 1mm.







- Chemical composition;
 - Calibration are regression that needs to be built with a range of chemical composition.
 - Odd chemical composition/sample won't contribute to improve calibration;

Look for high NH and GH values. That doesn't mean high NH and GH have odd composition







Analy		tituonte St	atistics								
Anaty	Ze cons	utuents st	ausucs								-
ADF vs.	. ADF				-						
SED:		1.1	80	Nur	nber of Sai	nples:	2	0			
Means:		27.595	26.577	Star	ndard Devi	ations:	1.596	1.83	0		
Bias:		1.0	18	Bia	s Limit:		0.	000			
SEDICI:		0.6	12	SEE	D(C) Limit:		0.	000			
Slope:		0.8	25	RSC	1 :		0.	893			
Ave. Glo	bal H:	1.457	1.272	Ave	. Neiahbor	. H:	0.712	0.57	7		
Pos.	Sampl	le No.	ANL	ANL	Residual	Bias	GH1	NH1	GH2	NH2	
1	1		27.30	25.12	2.18	1.16	1.41	0.65	1.17	0.53	
2	2		25.12	23.43	1.69	0.67	1.65	0.82	1.42	0.68	
3	3		25.34	23.91	1.44	0.42	1.09	0.60	0.98	0.47	
4	4		26.81	25.95	0.85	-0.16	1.08	0.62	0.92	0.48	
5	5		27.44	26.15	1.29	0.27	1.56	0.61	1.36	0.51	
6	6		26.11	25.24	0.87	-0.15	1.64	0.61	1.51	0.60	
7	7		28.45	27.34	1.11	0.09	1.17	0.68	0.83	0.32	
8	8		28.02	27.28	0.74	-0.28	1.73	0.67	1.64	0.52	
9	9		26.11	24.52	1.59	0.58	1.08	0.60	0.86	0.34	
10	10		26.06	24.98	1.09	0.07	1.16	0.51	0.97	0.42	
11	11		30.48	29.58	0.90	-0.11	1.82	0.94	1.69	0.77	
12	12		27.73	25.81	1.92	0.91	1.33	0.54	1.21	0.51	
13	13		29.22	29.29	-0.07	-1.08	1.72	0.85	1.52	0.74	-

ADF vs. ADF		-						
SED:	0.588	Number	of Samples:	2	0			
Means: 26.4	32 26.089	Standar	d Deviations:	1.419	1.58	6		
Bias:	0.342	Bias Lin	nit:	0.	000			
SEDICI:	0.490	SED(C)	imit:	0.	000			
Slone'	0.852	BS0.		0	908			
Ave Clobal H: 1 4	57 1 979	Ave Nei	iabbor H	0.712	0.57	7		
	Ji 1.272			0.712	0.57	0.00		
Pos. Sample No.	. ANL AI	NL Re	sidual Bias	GHT	NHI	GHZ	NH2	
1 1	26.33 24	4.99 1.3	33 0.99	1.41	0.65	1.17	0.53	
2 2	24.06 23	3.21 0.8	35 0.51	1.65	0.82	1.42	0.68	
3 3	24.39 23	3.87 0.9	51 0.17	1.09	0.60	0.98	0.47	
4 4	25.65 25	5.47 0.1	8 -0.16	1.08	0.62	0.92	0.48	
5 5	26.33 25	5.91 0.4	12 0.08	1.56	0.61	1.36	0.51	
6 6	25.15 25	5.10 0.0	-0.29	1.64	0.61	1.51	0.60	
7 7	27.28 27	7.05 0.2	23 -0.11	1.17	0.68	0.83	0.32	
8 8	26.89 26	6.64 0.2	25 -0.09	1.73	0.67	1.64	0.52	
9 9	24.96 24	4.35 0.6	61 0.27	1.08	0.60	0.86	0.34	
10 10	25.38 24	4.76 0.6	62 0.28	1.16	0.51	0.97	0.42	
11 11	28.86 28	8.69 0.1	7 -0.17	1.82	0.94	1.69	0.77	
12 12	26.70 25	5.43 1.2	27 0.93	1.33	0.54	1.21	0.51	



To increase accuracy	SAMPLE	MEAN
run duplicates;	1	Only one sample in group, no RMS possible
Check dups with	2	3100
RMS:	3	2591
nivio,	4	1972
Rescan dups with	5	2028
high PMS:	6	5601
nigh nivið,	7	3997
Average either	8	2181
apostra or prodiction:	9	4217
spectra or prediction,	10	1276
	17	4392
	Overall mean:	2252

