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Multi-center evaluation of analytical performance of the Beckman Coulter AU5822 chemistry analyzer

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ABSTRACT

Objectives: Our three academic institutions, Indiana University, Northwestern Memorial Hospital, and Wake Forest, were among the first in the United States to implement the Beckman Coulter AU5822 series chemistry analyzers. We undertook this post-hoc multi-center study by merging our data to determine performance characteristics and the impact of methodology changes on analyte measurement.

Design and methods: We independently completed performance validation studies including precision, linearity/analytical measurement range, method comparison, and reference range verification. Complete data sets were available from at least one institution for 66 analytes with the following groups: 51 from all three institutions, and 15 from 1 or 2 institutions for a total sample size of 12,064.

Results: Precision was similar among institutions. Coefficients of variation (CV) were <10% for 97%. Analytes with CVs >10% included direct bilirubin and digoxin. All analytes exhibited linearity over the analytical measurement range. Method comparison data showed slopes between 0.900-1.100 for 87.9% of the analytes. Slopes for amylase, tobramycin and urine amylase were <0.8; the slope for lipase was >1.5, due to known methodology or standardization differences. Consequently, reference ranges of amylase, urine amylase and lipase required only minor or no modification.

Conclusion: The four AU5822 analyzers independently evaluated at three sites showed consistent precision, linearity, and correlation results. Since installations, the test results had been well received by clinicians from all three institutions.

Introduction

Our three academic institutions, Indiana University (IU), Northwestern Memorial Hospital (NMH), and Wake Forest (WF), were among the first in the United States to adopt the Beckman Coulter AU5800 series chemistry analyzers. The previous analyzer systems at all three institutions were the Beckman Coulter Synchron DxC800 series. At each institution these analyzers were, on average, 5–7 years old and having problems typical for such systems at the end of their useful life. In addition, during the timeframe that the DxC800 analyzers were in use, the test volume at each of the institutions had increased substantially. At IU the annual volume of billable chemistry tests increased from 5.7 million in 2005 to 7.9 million in 2012; at NMH the volume increased from 0.9 million (2005) to 1.2 million (2012); while at WF the volume increased from 1.2 million (2007) to 1.5 million (2012). These increases in test volume were predominantly due to expansion of the outreach client base, addition of satellite draw sites and the acquisition or establishment of new affiliated hospitals. Moreover, given the increasing pressures to contain healthcare cost, consolidation of testing also added to the increased central core laboratory volume. At all three institutions, specimens on which testing is not performed at outlying locations are sent by courier to the main core laboratory where the Beckman Coulter AU5822 analyzers and the robotic automation lines are located. At IU four DxC800 analyzers were replaced by two AU5822 and two AU680 analyzers. At NMH four DxC800 analyzers were replaced by one AU5822 and two AU680 analyzers. At WF three

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DxC800 analyzers were replaced by one AU5822 and two AU680 analyzers. At all three institutions the AU5822 analyzers are the primary chemistry system in the highly automated core laboratory. The AU680 analyzers are used primarily as back-up systems and/or for low volume testing. Other studies [1] have shown that results from the AU5822 and AU680 analyzers are essentially equivalent. For our study all data are from the core laboratories' primary analyzer, the AU5822.

Previously in our core laboratories the increase in specimen volume had created a situation in which bottlenecks occurred even when all DxC800 analyzers were running at or near capacity. The speed of the DxC800 system was the rate-limiting factor. The theoretical throughput for the DxC800 analyzer is 1440 tests/h while the AU5822 analyzer has a theoretical throughput of 4000 photometric tests/h plus 1800 ion selective electrode (ISE) tests/h when equipped with the double flow cell modules [1]. Migration to the AU5822 system along with other changes to the automated chemistry instrumentation mix and/or robotic lines at each institution provides the needed throughput while also giving increased capacity for future growth.

Switching to a new analyzer system, even from the same manufacturer, is a major undertaking for any laboratory. In this case, the DxC800 and the AU5822 systems were developed and manufactured by different R&D and Product Development teams, so they might be expected to perform differently. In addition, the AU5822 system uses different methodologies than the DxC800 for a number of analytes, possibly requiring modification of the reference ranges. At each institution we independently undertook a study to determine if the performance characteristics of our new AU5822 systems were comparable to our previous analyzers and to determine the impact of methodology changes on analyte measurement including precision, linearity/analytical measurement range (AMR), method comparison, and reference ranges. Later we compared the data across multiple systems ($n = 4$) and multiple sites ($n = 3$). Single center or multi-center evaluations have previously been published [2–4], but our study is unique in that the validation was performed without up-front collaboration and data was only compared after the three individual studies had been completed. Most multi-center studies are planned and executed collaboratively and often include sites that are related or geographically in proximity. Our study included three independent institutions at diverse, widespread geographic locations and provided a very large set of combined data.

Materials and methods

Four AU5822 systems were installed by independent installation teams at our three institutions. AU5822 systems for IU, NMH, and WF are located within each institution's core lab, with IU having an AU5822 on each of two adjacent but duplicated automation lines. Validation studies including precision, linearity/AMR and method comparison were conducted independently at each site as described below. At each site, reference ranges were also verified for each analyte and compared to those for current methods. The data from all sites were subsequently compared and consolidated for this multicenter evaluation.

The AU5822 analyzers, the DxC800 analyzers, and most reagents and calibrators were from Beckman Coulter (Brea, CA USA). TDM reagents and calibrators were from Siemens (Newark, DE USA). Quality control materials were obtained from BioRad (Irvine, CA USA). Linearity standard materials were from Verichem Laboratories (Providence, RI USA) and Cliniqa LiniCAL TDM (Fisher Scientific, Houston, TX USA).

Validation studies

Validation studies were performed by manufacturer representatives and/or laboratory staff at each institution. These studies included precision, linearity/analytical measurement range (AMR), and method comparison correlating each institution's DxC800 and AU5822 analyzers using EP Evaluator® software (Build 10.0.0.517, Data Innovations, LLC, South Burlington, VT). Precision studies were performed according to the CLSI EP05 protocol [5], using at least two levels of quality control (QC) material. Precision was evaluated by analyzing 20 replicates of each level of the quality control material and compiling the data for analysis. To determine the linearity and AMR for each analyte, we performed studies according to the CLSI EP06 protocol [6]. Depending on the analyte being evaluated, 4 to 7 concentrations of linearity standards material were used to evaluate linearity over the AMR. Triplicate measurements were taken at each concentration spanning the analytical range of the analyte as specified by the manufacturer. Method comparison studies were performed according to the CLSI EP09-A2 protocol [7]. For most analytes, a minimum of 20 to 40 patient specimens were included at each institution for each analyte, as required by the protocol. The range was from 12 (CRP by NMH) to 111 (ALP by IU). Additionally, we consolidated method comparison data points from multiple institutions, and recalculated method comparison statistics based on the consolidated data set. For the 66 analytes studied, the total number of specimens tested ranged from 40 for IgM to 342 for ALP with 58 assays (87.9%) having more than 100 specimens and 27 assays (40.9%) having more than 200 specimens in the merged data set. Specimens were analyzed on each of the two chemistry systems, the DxC800 and AU5822. Deming regression was used to calculate slope, intercept and correlation coefficient (R) for each analyte at each site independently and also for the larger merged data set.

Reference ranges

Reference ranges were established independently at each institution using samples from 20 to 110 normal individuals, or were verified using samples from at least 20 individuals according to the protocols described in CLSI EP28-A3 [8]. There were ten tests sets with less than 20 samples due to infrequent order. All individuals were presumptively normal and the samples were de-identified prior to use. All studies were conducted in compliance with each institution's IRB policies.

Compilation of data from all three institutions

WF and NMH contributed data from one AU5822 analyzer each; IU contributed data from two analyzers (IU1 and IU2). The precision and linearity/AMR data were tabulated. For the method comparison studies, the data from each institution were analyzed separately and then combined for additional analysis with the exception of lactate which was only analyzed separately for 2 institutions. Supplemental Table 4 showed the correlation and bias plots. The Deming regression line for the combined data was calculated and plotted along with the 95% confidence limits.

Results and discussion

Data were available for 84 analytes at IU, 58 analytes at NMH, and 87 analytes at WF. Of these, complete data sets that included precision, linearity/AMR, method comparison and reference ranges were available from one or more institutions for 66 analytes. For these 66 analytes being studied as a group, the specimen types included serum/plasma for 53 analytes, urine for 12 analytes and CSF for 1 analyte, totalling 12,064. Of the 53 analytes using serum/plasma, 40 were chemistries and the remaining 13 were drugs used for therapeutic drug monitoring (TDM). For this paper we focused on those 66 analytes evaluated for all elements of the study, i.e., precision, linearity/AMR, method comparison, and reference range at one or more of the institutions. At each site the individual data were examined to ensure results were within acceptable limits for that institution.

Precision

Data from precision studies conducted at each of the three institutions were collated to evaluate the combined precision at multiple analyte levels for the QC materials tested. Each precision set includes 20 data points. The precision data set for 66 analytes is available online as Supplemental Table 1 measured assay precision.

For the 40 chemistries, CVs ranged from 0.0% to 14.6%, with 97.5% having CVs ≤10% and 92.5% being ≤5%. The single precision outlier, i.e., analyte with precision >10%, was Direct Bilirubin (DBIL) analyzed in one data set on one system, IU#1 (mean 0.33, SD 0.05, CV 14.6%). Overall, a total of 14 data sets were analyzed by all systems for DBIL. The DBIL on IU#1 at Indiana University showed a CV of 14.6% for one low level sample. The analyzer resulted 0.3 mg/dL 65% of the time and 0.4 mg/dL for the remaining 35% of the time. On a different low level sample on the same IU instrument, 100% of the results gave 0.3 mg/dL. These two precision evaluations were performed approximately 3 months apart.

For the 12 urine analytes, CVs ranged from 0.3% to 2.2%. All data sets had CVs <5%. For the 13 therapeutic drugs (TDM), the precision CVs ranged from 0.6% to 17.9%, with 92.3% being <10%. The precision outlier (CV ≥10%) was digoxin with 4 out of 14 data sets having CVs >10%: IU#1 (mean 0.41, SD 0.04, CV 10.9%), IU#2 (mean 0.47, SD 0.09, CV 17.9% and mean 0.61, SD 0.10, CV 16.1%) and WF (mean 0.45, SD 0.05, CV 11.4%). For digoxin, a low level sample performed on IU#1 resulted 0.4 ng/mL 80% of the time. For the remaining 4 points, one point was resulted as 0.3 ng/dL, approximately −2.5 SD from the mean, and three points (0.5 ng/dL) were approximately 2 SD from the mean. For IU#2, the 2 SD range for a low level sample was 0.42 to 0.81 ng/mL. Points 19 and 20 gave results of 0.9 ng/mL and 0.8 ng/mL respectively. For the second low level sample performed on IU#2, the 2 SD range was 0.30 to 0.65 ng/mL. The result for one point was 0.7 ng/mL. For the remaining points, the results were 0.4 ng/mL, 0.5 ng/mL, and 0.6 ng/mL for 45%, 40%, and 10% of the time, respectively. CSF Glucose was analyzed for precision at IU and WF, and had CVs ranging from 0% to 1.8% for 8 data sets. Interestingly, NMH had no analytes with CVs ≥10%. For all analytes at three sites on four systems at all QC levels, 97% had CV ≤10% while 80.3% having CVs ≤5%.

A summary of the precision data for this study is shown in Table 1. In comparison to manufacturer's claims, 4 analytes — DBIL, TBIL, acetaminophen, and digoxin showed CVs exceeding the manufacturer's claims by 2 .0–7.5%. Two analytes showed CVs >10%. — DBIL, 14.6% and digoxin, 17.9%, as compared to manufacturer's claims of <8% and <10.4% respectively.

Linearity/AMR

For the 66 analytes studied all were found to be linear, as determined using 4 to 7 concentrations of standards material that covered the AMR specified by the manufacturer, and within allowable limits for each institution. Supplemental Table 2 showed the DxC and AU reference ranges and AMRs. In comparison to manufacturer's claims, the upper limits of the AMRs were within the claims: for HDLD, lactate, prealbumin and U creatinine for 1 center, and for U Ca, U Mg, and U uric acid for 2 centers, and greater than the claim for U amylase for 1 center.

Method comparison

Supplemental Table 3 showed the DxC 800 and AU5822 method comparisons. For the 66 analytes, 63.6% utilized different methodologies: 21 of 40 serum/plasma chemistry analytes, and 8 of 12 urine chemistry analytes. All TDMs changed to EMIT methods while CSF Glucose remained the same for both instruments. Even for methods with the same methodology, the precise formulations may differ. Therefore, for many analytes, a bias between instruments might result in different slopes or intercepts. In these cases, new reference ranges might need to be established as described in the reference ranges previously, or at least the current reference ranges verified.

Deming regression, performed on data from both the individual sites and the aggregate data, are shown in the Supplemental Table 4, showing the correlation, bias plot and other statistics. Using the combined data for the samples analyzed on both the DxC800 and AU5822 systems, Deming regression showed 87.9% of the analytes with slopes between 0.900–1.100. Of the 19 chemistry analytes with unchanged methodology, Rs were >0.9735. Fig. 1 (c,d) showed the regression plots and statistics for representative analytes albumin and BUN. For the chemistry analytes with methodology changed between the DxC and AU platforms, Rs for the aggregate data ranged between 0.9217 (Na) to 0.9998 (AST). Among the chemistry analytes, the most notable slope changes were: amylase, which individually and when aggregated, had decreased slopes <0.8, and lipase, which individually and when aggregated had increased slopes >1.7, as shown by Fig. 1 (a,b). Urine amylase also showed comparable slopes ≤0.8 for the individual and aggregated data sets. Again, these changes were due to different methodologies. IgG showed a decreased slope of 0.844, resulting in a minor change in reference range.

Supplemental Table 4 showed that positive biases were evident for GGT, UCa, and UCl, and negative biases for AST, C4 and CSF glucose, and iron in one IU analyzer. Negative biases were observed for high concentrations of ALT, lactate and Mg. With the exception of urine amylase, Rs were ≥0.9930 for all urine analytes regardless of methodology change. Urine amylase R, with methodology changes between analyzers, was 0.9856 in addition to a decreased slope.

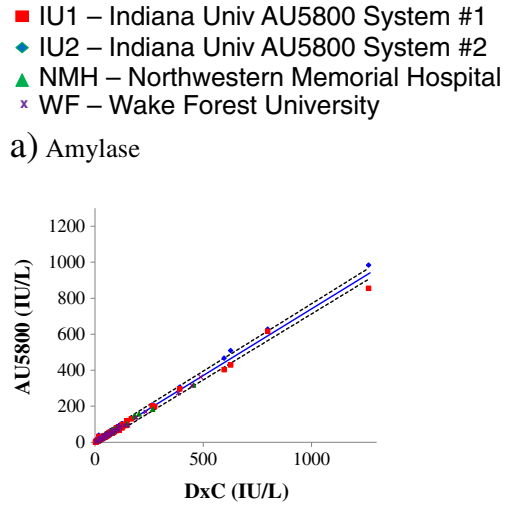
For the AU5822 analyzer, the drug assay method was an EMIT, homogeneous enzymatic immunoassay, while particle enhanced turbidimetric inhibition immunoassays were used in DxC. The exception was salicylate, utilizing salicylate hydroxylase. The aggregated drug assay data showed some scatter around the regression lines. Rs were ≥0.9689 for all TDMs except digoxin (R = 0.9492). Digoxin's slope was >1.1 for 2 analyzers, resulting in 1.135 for the combined data set. As previously noted, tobramycin also showed a decreased slope of 0.733 with R = 0.9866. Table 2 summarized the correlation statistics for those 8 analytes with slopes outside the range 0.900–1.100. These are all tests with either methodology (e.g., amylase, lipase) or standardization (e.g., tobramycin) differences between the DxC800 and AU5822 instruments and those results were expected.

Reference ranges

For most of the 66 analytes studied, the reference ranges at each institution needed only minor or no adjustments. In some cases, no

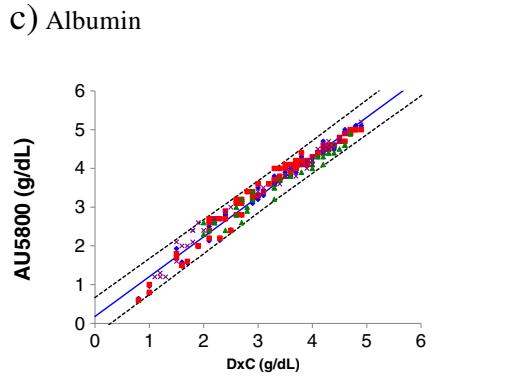
Table 1
Precision summary of assays on AU5800.

	# Analytes	# Data sets per Analyte	CV range (%)	≤5% CV	≤10% CV
Chemistries	40	4–18	0.0–14.6	37 (92.5%)	39 (97.5%)
Urines	12	8–14	0.3–2.2	12 (100%)	12 (100%)
TDMs	13	11–15	0.6–17.9	3 (23.1%)	12 (92.3%)
CSF	1	8	0.0–1.8	1 (100%)	1 (100%)
Total	66	4–18	0.0–17.9	53 (80.3%)	64 (97.0%)



	IU1	IU2	NMH	WF	All
Mean (DxC)	100.1250	100.1250	91.9500	76.6765	93.3592
Mean (AU5800)	79.2568	71.5227	69.1250	54.6324	69.5373
R	0.9994	0.9974	0.9969	0.9985	0.9965
N	88	88	40	68	284
Slope	0,783	0.702	0.704	0.720	0.741
Intercept	0.809	1.256	4.412	0.537	0.368

	IU1	IU2	NMH	WF	All
Mean (DxC)	57.9130	51.0154	41.0250	38.1600	48.3111
Mean (AU5800)	81.3133	73.7692	48.0500	49.4600	65.7850
R	0.9482	0.9763	0.9801	0.9839	0.9600
N	69	65	40	50	225
Slope	1.735	1.968	2.032	2.194	1.874
Intercept	-19.168	-26.620	-35.312	-34.257	-24.766



	IU1	IU2	NMH	WF	All
Mean (DxC)	3.2976	3.2976	3.4600	3.3054	3.3239
Mean (AU5800)	3.5688	3.5976	3.6500	3.5964	3.5961
R	o.9880	0.9849	0.9825	0.9907	0.9852
N	84	84	40	56	264
Slope	1.064	1.061	0.905	0.987	1.028
Intercept	0.059	0.100	0.520	0.333	0.180

	IU1	IU2	NMH	WF	All
Mean (DxC)	32.1078	32.1078	20.5250	23.3830	29.1065
Mean (AU5800)	33.0882	33.2255	22.2000	25.4681	30.4227
R	0.9993	0.9991	0.9979	0.9961	0.9984
N	102	102	40	47	291
Slope	0.988	1.001	0.939	0.943	0.981
Intercept	1.372	1.098	3.025	3.409	1.857

Fig. 1. Method correlation plots and statistics for selected assays. Fig. 1a amylase and b lipase are examples of analyte correlations that required modifications to reference ranges due to expected differences in methodology or standardization. Fig. 1c albumin and d ALT are examples of the many analytes that showed good correlation and did not require modifications to reference ranges.

change in reference range was required despite changes in methodology. This can be attributed to the common standardization and traceability schemes used by the developers. The exceptions were those analytes that showed slopes beyond 0.900–1.100 between platforms.

Table 2
Analytes with method comparison slopes <0.9 or >1.1.

Analyte	Slope	Intercept	R
Amylase	0.741	0.368	0.9965
CRP	1.293	−0.253	0.9912
IgG	0.844	113.169	0.9960
Lipase	1.874	−24.766	0.9600
U-Amylase	0.763	−3.661	0.9856
Amikacin	0.883	0.535	0.9933
Digoxin	1.135	0.051	0.9492
Tobramycin	0.733	0.144	0.9866

These included serum amylase and lipase, and urine lipase in NMH that required reference range changes. Urine amylase was changed in NMH but not in IU. Tobramycin also showed slope difference but the reference range was not changed. With aminoglycosides such as tobramycin, the clinical concern is two-fold, treating the infection with concurrent signs of patient improvement and avoiding ototoxicity whenever possible. Reference ranges for these analytes, as established on the DxC and AU platforms, at each institution are shown in Table 3. Reference Range data for all 66 analytes both on Synchron DxC and on AU5800 are shown in the online Supplemental Table 2.

Limitations included the comparison studies not performed on the same sample sets. They were collected at different time period with possible different patient demographic. As previously noted, the study was conceptualized after the validation studies were completed.

As shown by the above sections, we compared the precision, AMR, and reference interval results to the manufacturer's claims in the

Table 3
Reference ranges for analytes, listed in Table 2, with differing methodology and slopes.

Analyte	Site	DxC reference range	AU reference range	Reference range change
Amylase	IU	25–161 U/L	19–86 U/L	Yes
	NMH	20–115 U/L	29–103 U/L	Yes
	WF	30–122 U/L	29–103 U/L	Yes
Lipase	IU	22–51 U/L	7–59 U/L	Yes
	NMH	7–60 U/L	11–82 U/L	Yes
	WF	20–50 U/L	11–82 U/L	Yes
Urine–amylase	IU	1–17 (U/L)/h	1–17 (U/L)/h	No
	NMH	1–17 (U/L)/h	5–27 (U/L)/h	Yes
	WF	NA	NA	NA
Tobramycin	IU	TR = 0.0–2.0 μg/mL PK = 4.0–10.0 μg/mL	TR = 0.0–2.0 μg/mL PK = 4.0–10.0 μg/mL	No
	NMH	TR = <2.0 μg/mL PK = 5.0–10.0 μg/mL	TR = <2.0 μg/mL PK = 5.0–10.0 μg/mL	No
	WF	5.0–80.0 μg/mL	10.0–30.0 μg/mL	Yes

Instructions for Use. All the AMRs met the claims though Supplemental Table 2 shows some minor differences, based on variations in testing and in local implementations. Reference intervals were similarly validated though again with some differences in local implementation and within the institution's policies on changes of reference intervals. Precision data shown in Supplemental Table 1 in general were well within the claims with minor differences. Apparent exceptions for high CVs for DBIL and TBIL are actually within the SD claims for low analyte levels. Other precision exceptions with apparent high CVs for lithium, acetaminophen, digoxin, and tobramycin are all instances of a single QC level at a single institution showing a high CV but with an acceptable SD at a low analyte concentration and that were not reproducible at other sites. The analytes with well-established and clinically relevant performance criteria were well accepted by clinicians in all three institutions.

Conclusions

Four AU5822 analyzers independently evaluated at three separate institutions provided consistent results for precision, linearity/analytical measurement range, method comparison and reference ranges such that the data could be merged for aggregate analysis. The merged data of 12,064 samples provided a substantially larger data set than those of previously published studies. A total of 66 analytes, each with at least one site providing all elements of the performance data, were included in our study. Precision CVs were <10% for almost all analytes studied and the majority of linearity/AMRs were within the limits specified by the manufacturer and established by the individual laboratories separately. Deming regression analysis on the aggregate data set showed that 87.9% of the analytes studied had slopes of 0.900–1.100. Slopes outside this range were found for 6 analytes with changes in methodology or standardization between the instruments, and for 2 analytes with no change in methodology or standardization. Changes in methodology required changes in reference ranges at all sites for 2 analytes, amylase and lipase, as was not unexpected. Many analytes, however, despite methodology change, only required minor or no adjustments. When there was no methodology change, the DxC and AU platforms yielded similar results.

This large multi-center study demonstrates that the AU5822 analyzer offered very consistent results among individual laboratories even in geographically separated locations with diverse patient populations. We also concluded that, despite methodology or standardization changes on the AU5822 analyzer relative to the Synchron DxC, the impact of changing analyzers in our laboratories created few challenges while allowing us to update and enhance our analytical and workflow processes. Since installations, the test results had been well received by clinicians from all three institutions.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.clinbiochem.2015.06.010.

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References

[1] CAP Today. Chemistry Analyzers for Mid- and High-Volume Laboratories. http://www.cap.org/apps/docs/cap_today/0713/chemistry_analyzers.pdf; July 2013.
[2] Cattozzo G, Albeni C, Calonaci A, De Luca G. Evaluation of the analytical performance of the Beckman Coulter AU680 automated analytical system based on quality specifications for allowable performance derived from biological variation. Clin Chem Lab Med 2011;49(9):1563–7. http://dx.doi.org/10.1515/CCLM.2011.629.
[3] Lippi G, Dipalo M, Musa R, Avanzini P, Ferrarini C, Pattini A, et al. Evaluation of the analytical performances of the novel Beckman Coulter AU5800. Clin Biochem 2012; 45:502–4. http://dx.doi.org/10.1016/j.clinbiochem.2012.01.015.
[4] Zimmerman MK, Friesen LR, Nice A, Vollmer PA, Dockery EA, Rankin JD, et al. Multicenter evaluation of analytical performance of Beckman Coulter AU5822 analyzer (Abstract/Poster). AACC; 2013.
[5] CLSI. Evaluation of precision performance of quantitative measurement methods; approved guideline—second edition. CLSI document EP05-A2. Wayne, PA: Clinical and Laboratory Standards Institute; 2004.
[6] CLSI. Evaluation of the linearity of quantitative measurement procedures: a statistical approach; approved guideline. CLSI document EP06-A. Wayne, PA: Clinical and Laboratory Standards Institute; 2003.
[7] CLSI. Measurement procedure comparison and bias estimation using patient samples; approved guideline — third edition. CLSI document EP09-A3. Wayne PA: Clinical and Laboratory Standards Institute; 2013.
[8] CLSI. Defining, establishing, and verifying reference intervals in the clinical laboratory; approved guideline—third edition. CLSI document EP28-A3c. Wayne, PA: Clinical and Laboratory Standards Institute; 2008.