

Supplement for: Multicentre validation of the CamGFR model for estimated glomerular filtration rate

Abstract

This document is a supplemental file for the paper “Multicentre validation of the CamGFR model for estimated glomerular filtration rate” and provides additional methods, results, figures and tables. The .Rmd file format contains the R code used for this manuscript and is available at github.com/EdwardHWilliams/CamGFRValidationNonIDMS.

Data description and filtering

Raw data that were received from the seven different centres, which are identified by their location (Cambridge, Edinburgh, London-Barts, Manchester, Melbourne, Southampton and Wales). Data were individually processed and cleaned prior to being used for analyses. This step involved exploring the data for manual transcription errors such as the height and weight variable being swapped and removing unrealistic values for some variables. During this process all data were converted to the same units to enable data pooling and analyses across the different centres and subgroup categories.

Next, patients with data outside the inclusion criteria were removed. The inclusion criteria were:

- Serum creatinine value between 18 $\mu\text{mol/L}$ (0.2 mg/dL) and 400 $\mu\text{mol/L}$ (4.5 mg/dL)
- Age of 18 years or older
- Creatinine and GFR measurements performed within 30 days of each other

The creatinine cut-off values were chosen because the lower value is the typical detection threshold on the measurement assay and the upper value is 3-4 times the upper limit of normal in most centres, thus corresponding to a value at which most clinicians would consider kidney function severely impaired.

All creatinine data were either measured using a non-IDMS traceable measurement or the measurement procedure was not known. Table S1 summarises the information on the creatinine measurement for each centre.

Table S1: Creatinine methods used at each centre

Centre	Date range	Creatinine measurement method
Cambridge	2013	Dimension RxL compensated Jaffe, not IDMS-traceable
Edinburgh	2011 - 2017	An Abbott Architect assay using the Jaffe method; not IDMS-traceable
London-Barts	2010 - 2017	Unknown method; IDMS usage not known
Manchester	2012 - 2016	Jaffe method using O'Leary reagent; not IDMS-traceable
Melbourne	2000 - 2005	Jaffe method; not IDMS-traceable
Southampton	1999 - 2012	Jaffe method; given the date range, most, if not all, not IDMS-traceable
Wales	2005 - 2011, not all dates known	Different centres used either Jaffe or enzymatic methods; IDMS usage not known

Table 1 in the main manuscript provides the number of patients in different categorical groups and the summary statistics for the continuous variables (GFR, age, serum creatinine, body surface area (BSA), height and weight) for all patients. Here we provide the summary statistics for patients split into different centres (Table S2).

Table S2: Summary characteristics for patients from each centre separately

	Mean	SD	Minimum	Q1	Median	Q3	Maximum
Cambridge							
GFR [ml/min]	86	29	9	65	85	105	211
Creatinine [$\mu\text{mol/L}$]	87	27	40	70	83	97	258
Age [years]	55	16	18	44	56	67	86
Weight [kg]	77	19	39	64	74	87	184
Height [cm]	169	10	146	161	168	177	200
BSA [m^2]	1.86	0.24	1.34	1.69	1.85	2.01	2.87
Edinburgh							
GFR [ml/min]	83.7	34.9	9.1	54.6	83	110.2	206
Creatinine [$\mu\text{mol/L}$]	90	32	45	70	81	102	393
Age [years]	56	16	18	43	58	68	87
Weight [kg]	79	19	38	66	78	90	197
Height [cm]	171	10	144	164	171	179	202
BSA [m^2]	1.91	0.24	1.27	1.73	1.91	2.06	3.17
London-Barts							
GFR [ml/min]	110	20	46	98	111	122	166
Creatinine [$\mu\text{mol/L}$]	81	14	52	73	82	88	141
Age [years]	39.2	9.2	22.4	32.7	38.7	45.1	70.8
Weight [kg]	85	17	57	73	82	90	150
Height [cm]	177.9	7.8	160	172.8	177.8	182	200

Table S2: Summary characteristics for patients from each centre separately (*continued*)

	Mean	SD	Minimum	Q1	Median	Q3	Maximum
BSA [m ²]	2	0.2	1.6	1.9	2	2.1	2.6
Manchester							
GFR [ml/min]	77	29	14	56	74	94	194
Creatinine [μ mol/L]	88	22	46	74	83	96	235
Age [years]	62	14	18	54	65	72	91
Weight [kg]	72	19	33	59	70	83	164
Height [cm]	164.6	9.8	137	157	164	171	200
BSA [m ²]	1.78	0.24	1.17	1.6	1.76	1.93	2.79
Melbourne							
GFR [ml/min]	85	31	17	64	83	104	205
Creatinine [μ mol/L]	96	30	60	80	90	110	290
Age [years]	63	13	18	56	65	72	87
Weight [kg]	73	15	37	62	72	80	145
Height [cm]	169.4	9.3	148	163	170	176.6	194
BSA [m ²]	1.83	0.21	1.31	1.69	1.83	1.96	2.62
Southampton							
GFR [ml/min]	119	21	51	104	118	132	209
Creatinine [μ mol/L]	89	12	54	80	89	97	136
Age [years]	39.9	9.5	19	33	39	46	75
Weight [kg]	86	16	54	76	85	95	200
Height [cm]	179	7	156	174	179	183	204
BSA [m ²]	2.05	0.19	1.62	1.92	2.03	2.16	3.09
Wales							
GFR [ml/min]	89	31	23	65	90	111	169
Creatinine [μ mol/L]	74	19	38	61	74	84	164
Age [years]	57	18	22	42	58	72	90
Weight [kg]	77	18	45	63	76	88	155
Height [cm]	168	11	145	160	166	177	192
BSA [m ²]	1.86	0.24	1.41	1.67	1.83	2.04	2.57

To facilitate data comparison graphically, Figure S1 displays the data from Table S2 in several boxplots. Patients from Southampton and London-Barts have a higher GFR, height and weight and a lower age than patients from other centres. This is attributable to the fact that the data from these centres were from patients with seminoma only and hence were typically from young men. The panel of log(creatinine) illustrates the inter-centre variability.

Figure S2 show boxplots for log(creatinine) split by centre for all patients and patients with selected diagnoses respectively. As patients with similar diagnoses should be approximately matched for the other variables, the plots facilitate further comparison of serum creatinine differences between centres.

Table S3: Number of patients with given diagnoses in each centre

Diagnosis	Manchester	Edinburgh	Cambridge	Southampton	Melbourne	Wales	London-Barts	Total
Cancer								
GCT	35	118	58	436	0	67	108	822
Unknown	437	8	48	0	308	0	0	801
Gynae	251	54	104	0	0	89	0	498
Bladder/TCC	88	138	26	0	0	0	0	252
Thoracic	219	13	4	0	0	0	0	236
Gastro-oesophageal	203	19	5	0	0	0	0	227
Head and Neck	192	3	6	0	0	0	0	201
Endometrial	104	21	0	0	0	0	0	125
Uterus/Cervix	83	15	1	0	0	0	0	99
Sarcoma	31	36	12	0	0	0	0	79
Breast	29	6	2	0	0	0	0	37
HPB	26	6	0	0	0	0	0	32
Colorectal	17	10	0	0	0	0	0	27
CUP	26	1	0	0	0	0	0	27
RCC	12	6	0	0	0	0	0	18
Prostate	5	8	0	0	0	0	0	13
Neuroendocrine	1	11	0	0	0	0	0	12
Anal	6	1	0	0	0	0	0	7
CNS	6	0	0	0	0	0	0	6
Skin	5	0	0	0	0	0	0	5
Melanoma	1	0	0	0	0	0	0	1
Haematological								
Haematological	0	22	114	0	0	0	0	136
Non-cancer								
Kidney donor	0	94	35	0	0	0	0	129
Transplant	0	0	28	0	0	0	0	28
Unknown	0	9	0	0	0	0	0	9

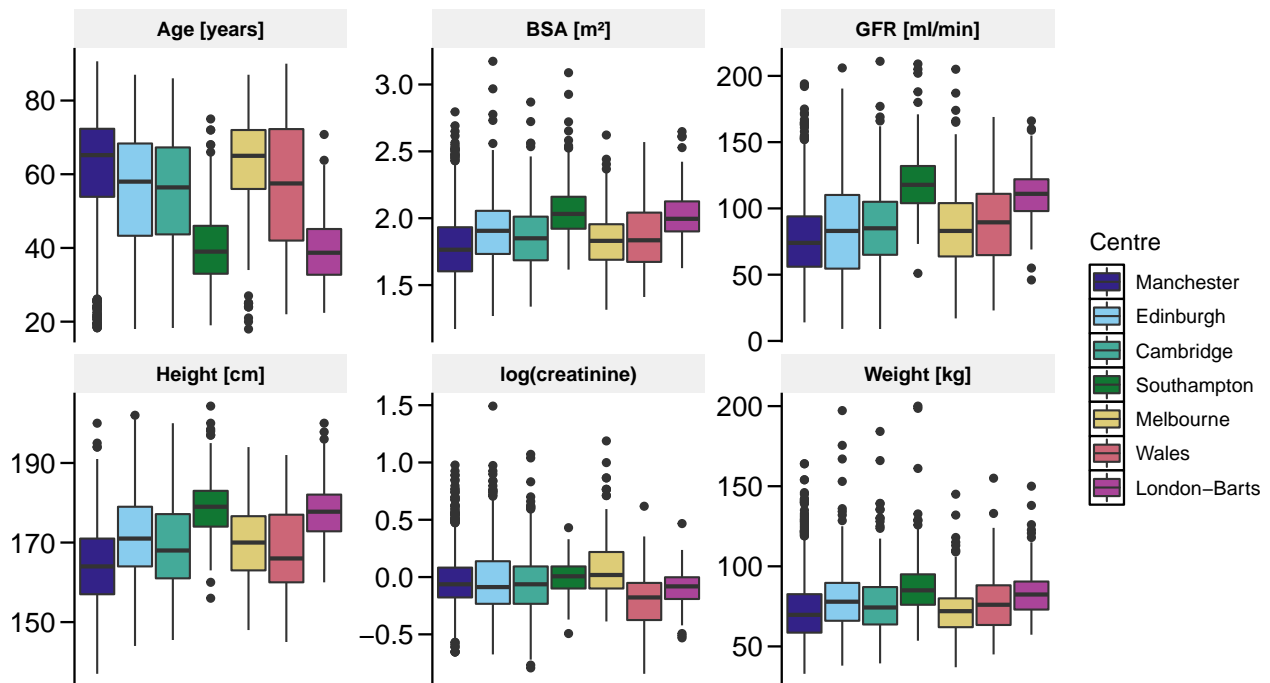


Figure S1: Boxplot of the continuous variables split by centre. Creatinine has been log transformed.

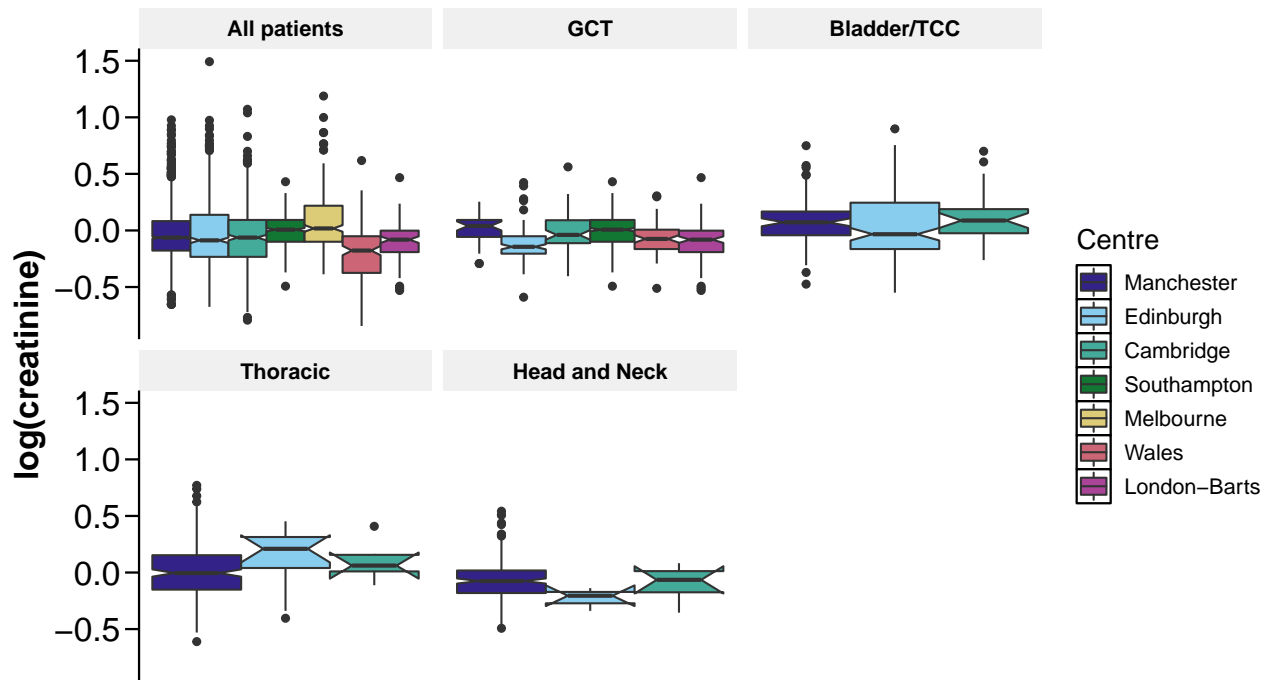


Figure S2: Boxplots of the serum creatinine of patients from different centres. Boxplots are shown for all patients combined and for patients with Germ Cell Tumours (GCT), Bladder or Transitional cell cancer (TCC), Thoracic cancer, Gastro-oesophageal cancer and Head and Neck cancer. The notches in the boxplots are $1.58\text{IQR}/\sqrt{n}$ (where n is the number of patient used for the given boxplot and IQR is the inter quartile range); they provide both an approximate 95% confidence interval for the median and an indication of the number of patients used for the given boxplot.

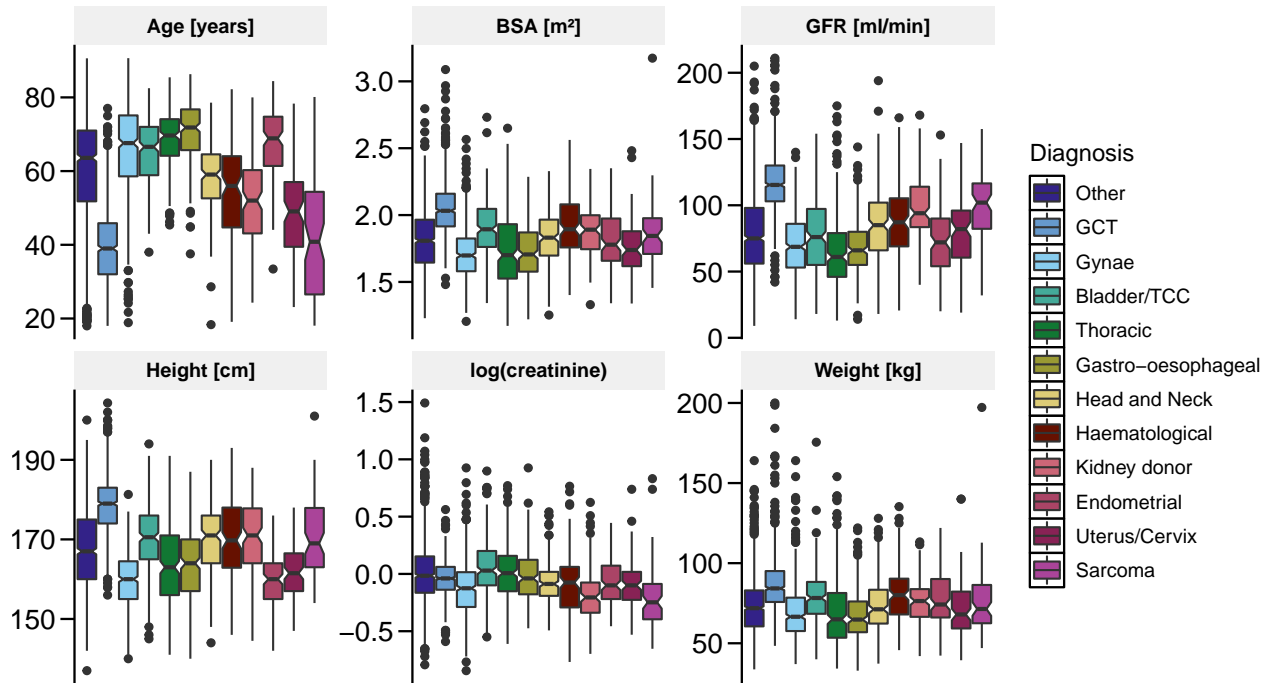


Figure S3: Boxplot of the continuous variables split by diagnosis. Subgroups with more than 50 patients are displayed. Subgroups with fewer than 50 patients have been combined with patients with an unknown diagnosis into the group Other. Boxplots are arranged by decreasing patient numbers from left to right. Serum creatinine has been log transformed.

Figure S3 takes the same format as Figure S1 but displays subgroups of patients based on diagnosis. Subgroups with more than 50 patients were included.

Information on ethnicity was available for patients from Cambridge and Manchester, who comprised the majority of patients. From a total of 2,055 patients with known ethnicity, 1,947 were White (either White British, White Irish, White other), 71 were Asian (Asian Indian, Asian Pakistani, Asian Bangladeshi, Asian other, Chinese, Other Chinese, Mixed White and Asian), 22 were Black (Black African, Black Caribbean, Black other, Mixed White and Black Caribbean, Mixed White and Black African) and 15 were of other ethnicity (other ethnic group, other mixed). Figure S4 shows boxplots for age, BSA, mGFR and log(creatinine) for patients from the ethnic subgroups. As white patients were the largest subgroup, t-tests were performed to look for differences between this subgroup and each other subgroup. There were no significant differences in the serum creatinine levels for patients from different ethnicities. However, there were significant differences in the other variables and therefore the subgroups were not matched. Given the correlations between these variables, it is difficult to interpret the creatinine comparisons precisely. To determine whether the average creatinine values differ between white and black patients when the other variables are similar, we sampled 22 white patients from the population that matched the set of black patients with regards to sex and age ten times. We then performed t-tests for these ten samples for log(creatinine), measured GFR and BSA. No significant differences were found (Table S4).

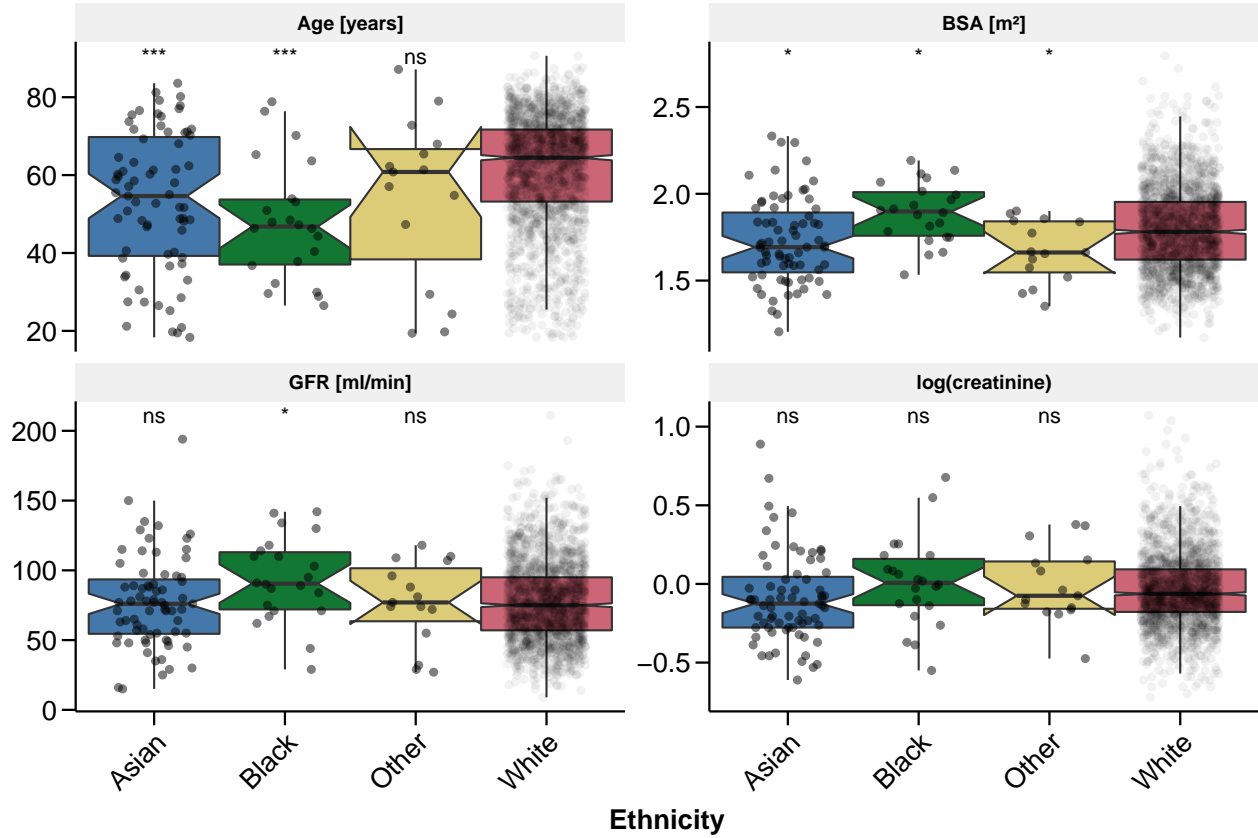


Figure S4: Boxplots of age, BSA, GFR and log(creatinine) and Age where patients are split by ethnicity. The '*' or 'ns' at the top of the boxplot represents the p-value from a t-test between the largest subgroup of white patients and each other ethnic subgroups, where 'ns' represents a p-value greater than 0.05 and '*', '**' and '***' represent p-values less than 0.05, 0.01 and 0.001 respectively.

Table S4: t-test p-values for comparing the mean age, log(creatinine), GFR and BSA between 22 patients who were ethnically black and 22 random patients who were ethnically white and matched by mean age (mean age within 1 year) and the same gender distribution (12 females and 10 males).

Age [years]	log(creatinine)	GFR [ml/min]	BSA [m²]
0.98	0.39	0.72	0.88
0.92	0.29	0.61	0.16
0.93	0.01	0.98	0.06
0.89	0.89	0.91	0.93
0.91	0.51	0.92	0.57
0.90	0.53	0.59	0.83
0.85	0.67	0.79	0.88
0.86	0.44	0.74	0.78
0.97	0.31	0.65	0.68
0.94	0.38	0.10	0.19

Comparison of models

We compared the CamGFR¹ model with the the following published models: CKD-EPI², MDRD (186 version)³, Wright⁴, Cockcroft-Gault⁵, Jelliffe⁶, Mayo⁷ and Martin⁸. If these equations estimated BSA-normalised GFR (CKD-EPI, MDRD, Jelliffe and Mayo), the estimated value was subsequently unnormalised by multiplying the estimated value by 1.73/BSA, where BSA is the patient's body surface area estimated using the DuBois-DuBois equation:

$$\text{BSA} = 0.20247 \times \text{Height}^{0.725} \times \text{Weight}^{0.425}$$

where height is measured in metres and weight is measured in kg. Some of these models (Cockcroft-Gault and Jelliffe) were developed to estimate creatinine clearance and not GFR, where creatinine clearance is itself a biased estimator of GFR. These models are included as they are still used to estimate GFR by some centres, clinical trial groups, and in other settings.

The equations were compared using three metrics: the root-mean-squared-error (RMSE), median residual value, and the residual interquartile range (IQR). These three metrics are estimators for a model's accuracy, bias and precision respectively. A 95% confidence interval was calculated for each of these metrics using the bootstrap resampling procedure. Specifically, 2,000 resamples with replacement (where the sample size was the same as the number of data points) were taken from the data used to calculate the metric. The metric was then calculated for each of these 2,000 samples and using the normal approximation a confidence interval was constructed⁹. The seed was reset to be the same when sampling the 2,000 replicates for the different metrics.

The main results of this analysis are reported in Figure 1 (results for patients split by centre) in the main manuscript along with Figures S5 (results for patients split by diagnosis), S6 (results for patients split by age) and S7 (results for patients split by BSA). Additionally, all numerical results are reported in Table S5 (an additional file). Table S5 gives the results for all equations above whereas the Figures only compare the performance of CamGFR, CKD-EPI, MDRD, Wright and Cockcroft-Gault.

We analysed performance when patients were split into groups by their age or BSA. Figures S6 and S7 show the performance of each model for equally sized subgroups of age and BSA, respectively. The accuracy of all models tends to increase with increasing age and tends to increase with increasing BSA. These observations can be largely explained by the fact that GFR is modelled on the square root scale in the CamGFR model and on the log scale for the CKD-EPI or MDRD models. Patients who are young or have a large BSA also tend to have a higher GFR and patients with a higher GFR will have a less accurate estimated GFR due to modelling on a square-root or log scale.

P-values for the differences between a statistic for a pair of equations were calculated using a bootstrap procedure described by Efron¹⁰. In this procedure we have two samples \mathbf{z} and \mathbf{y} of lengths n and m respectively, from possibly different probability distributions F and G . In our case F and G were the probability distributions of the residuals for the two equations of interest. We tested the null hypothesis $H_0 : F = G$, against the alternative hypothesis $H_0 : F \neq G$. Let $\mathbf{x} = [\mathbf{z}, \mathbf{y}]$, and chose a test statistic $t(\mathbf{x})$, which had the form $t(\mathbf{x}) = f(\mathbf{z}) - f(\mathbf{y})$, where the function $f(\mathbf{w})$ was either RMSE, median or IQR. Using the following procedure an approximate p-value was calculated by:

- For $r = 1, \dots, R$ let \mathbf{x}_r^* be a sample with replacement of size $n + m$ from the pooled vector $\mathbf{x} = [\mathbf{z}, \mathbf{y}]$. Let \mathbf{z}_r^* be the first n observations of \mathbf{x}_r^* and \mathbf{y}_r^* the remaining m observations.

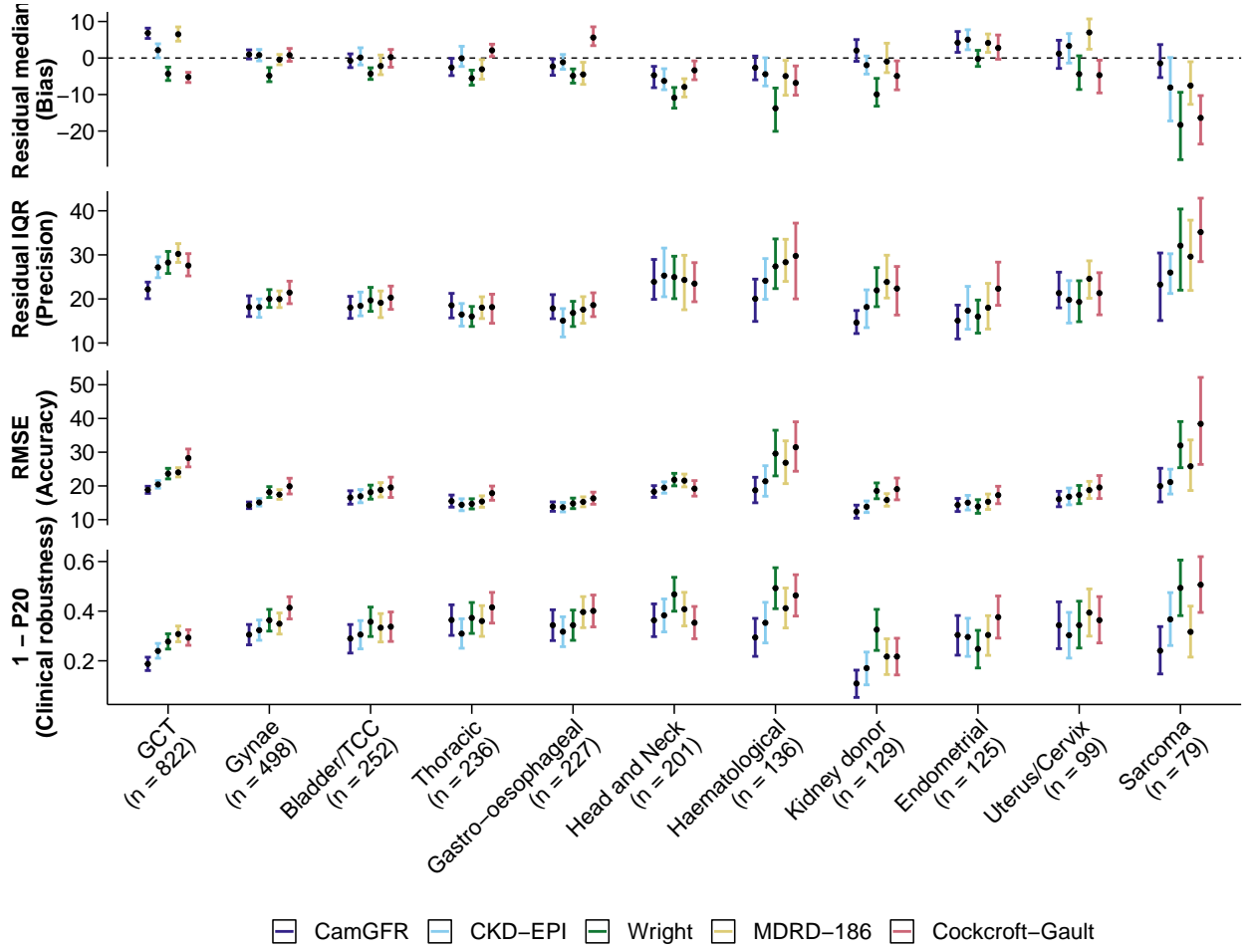


Figure S5: Performance of GFR models for patients from different diagnostic subgroups. The results for the CamGFR model and four other commonly used other models (CKD-EPI, Wright, MDRD-186 and Cockcroft-Gault) are displayed. Results for those diagnostic subgroups that had more than 50 patients are shown. (first row) The residual (measured GFR - estimated GFR) median, which is a measure of a model's bias, is displayed. (second row) The residual interquartile range (IQR), which is a measure of a model's precision, is displayed. (third row) The root-mean-squared error (RMSE), which is a measure of a model's accuracy, is displayed. Accuracy is a combination metric of bias and precision. (fourth row) The proportion of patients who have an absolute percentage error more than 20% (1-P20), which reflects clinical robustness by illustrating the proportion of patients with a clinically relevant error, is displayed. The best result would be closest to zero for the residual median, and the smallest value for IQR, RMSE, and 1-P20. All error bars are 95% confidence intervals calculated using bootstrap resampling with 2,000 repetitions and a normal distribution approximation.

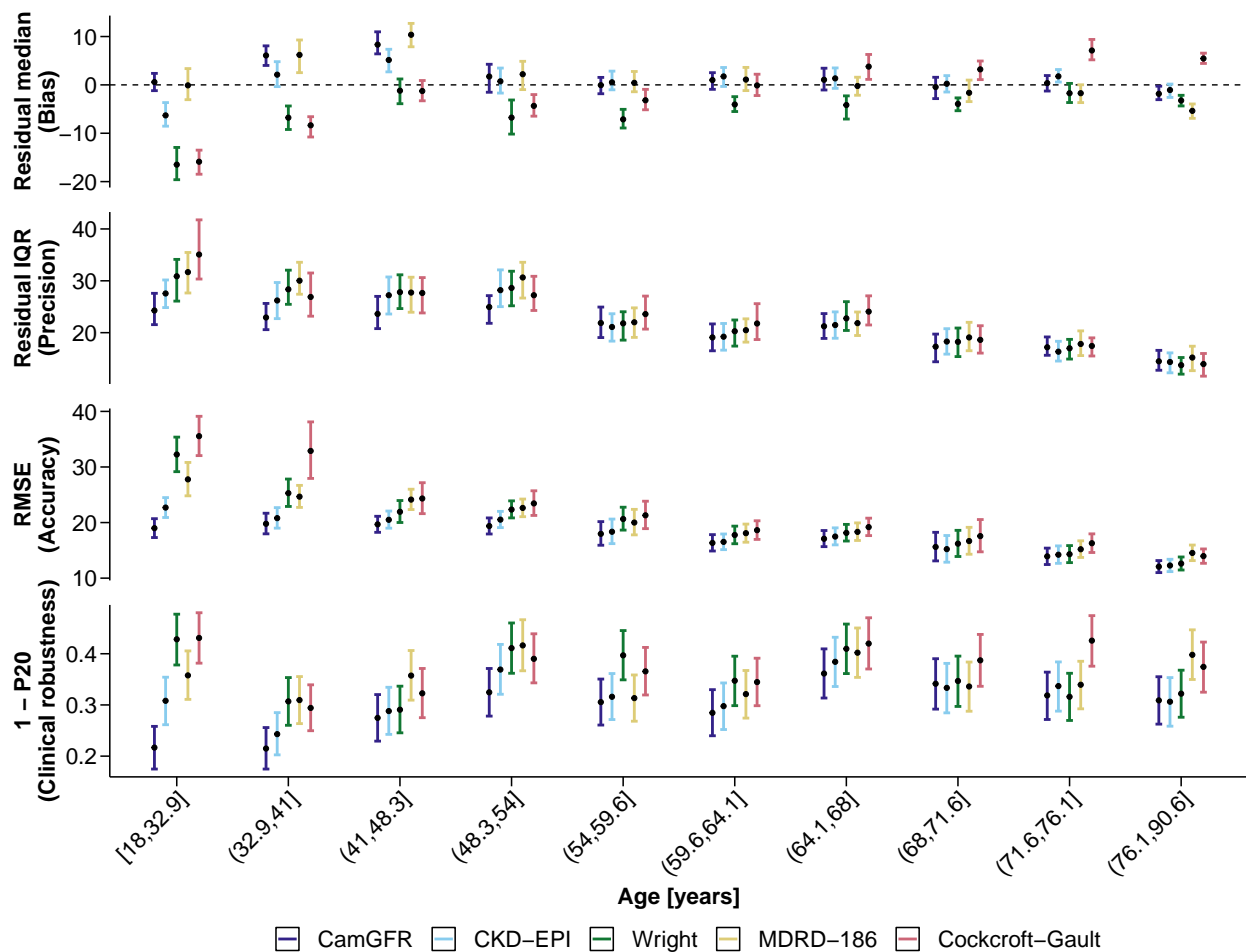


Figure S6: Comparison of model performance in different age groups. The results for five published models are shown. Patients were split into 10 equally sized groups by their age. $(a,b]$ denotes the interval a to b which is exclusive of the lower and inclusive of the higher age.

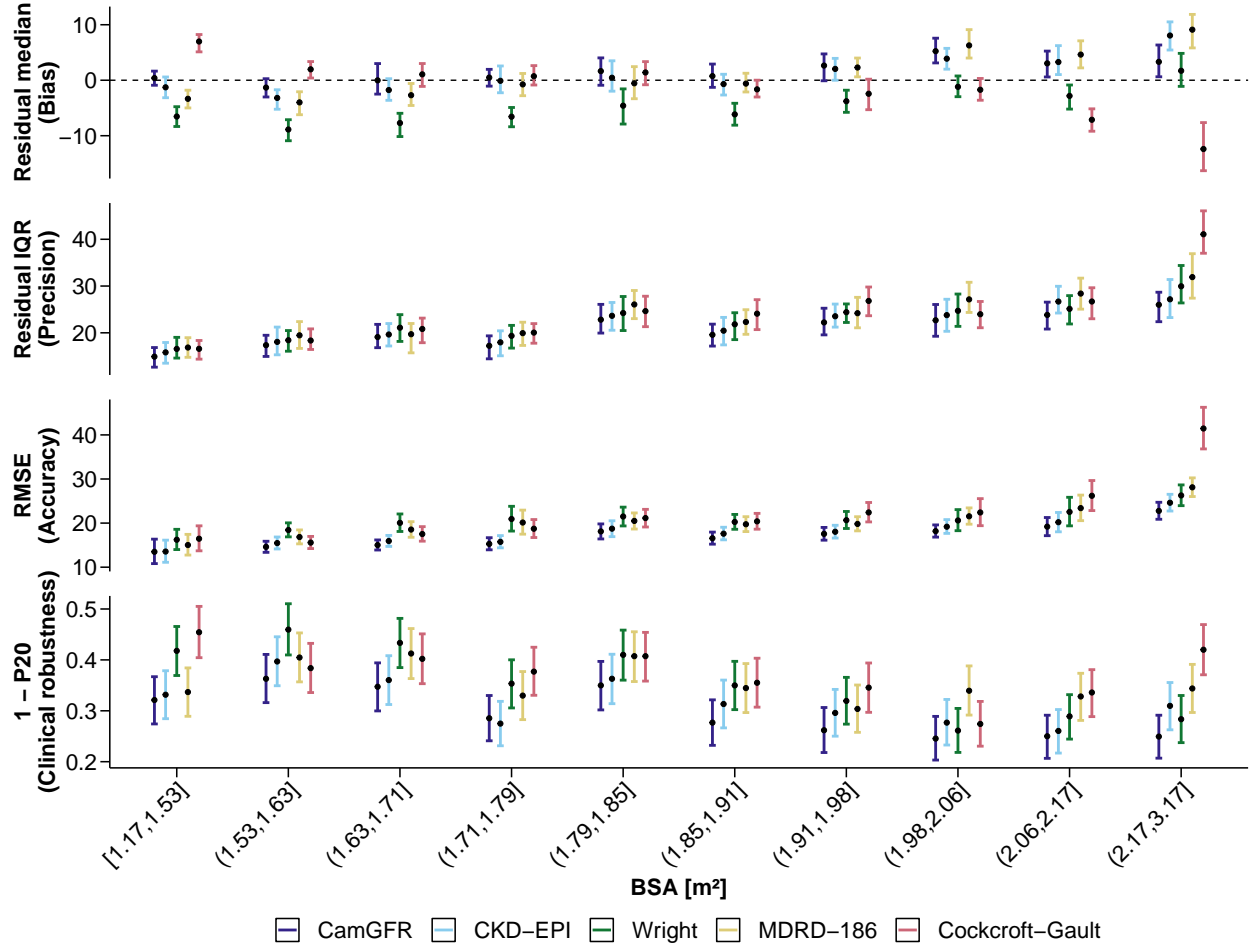


Figure S7: Comparison of model performance in different BSA groups. The results for five published models are shown. Patients were split into 10 equally sized groups by their BSA. $(a,b]$ denotes the interval a to b which is exclusive of the lower and inclusive of the higher BSA.

- Let

$$t_r^* = t(x_r^*) = f(z_r^*) - f(y_r^*), \quad r = 1, 2, \dots, R$$

- Calculate the approximate p-value for the hypothesis test as:

$$\hat{p} = \frac{1 + \sum_{r=1}^R \mathbb{1}_{|t_r^*| \geq |t_{obs}|}}{R + 1}$$

where $t_{obs} = t(x) = f(z) - f(y)$ is the observed value of the statistic and $\mathbb{1}_A$ is the indicator function which returns 1 if A is true and 0 otherwise. The absolute values of t are considered so as to perform a two-sided test.

It should be noted that the hypothesis test is strictly testing the null hypothesis $H_0 : F = G$ and not the null hypothesis $H_0 : f(Z) = f(G)$. When the approximate p-values are calculated with the statistic 1-P20 (the proportion of patients with an absolute percentage error more than 20%), z and y would be the vectors of percentage differences between the fitted and measured dose values. Approximate p-values (with $R = 10,000$) are given in Tabel S5 (an additional file).

Published models

This section gives the published models used in this manuscript. In the following equations:

- *Age* is the patient's Age in years
- *BSA* is the patient's body surface area in m^2 , if is estimated for the patients weight and weight using the DuBois DuBois equation [Janowitz2017a]
- *Scr* is the patient's blood serum cratinine in mg/dL
- *Wt* is the patient's weight is kg

CamGFR¹

$$GFR = \left(1.81395 + 0.01914 \times Age + 4.73278 \times BSA - 0.02970 \times Age \times BSA - 3.71619 \times \log(Scr) + 1.06284 \times \log(Scr)^2 - 0.91420 \times \log(Scr)^3 + (0.02020 + 0.01247 \times Age) [\text{if male}] \right)^2$$

CKD-EPI²

$$GFR = \begin{cases} 141 \times \min\left(\frac{Scr}{0.7}, 1\right)^{-0.329} \times \max\left(\frac{Scr}{0.7}, 1\right)^{-1.209} \times Age^{0.993} \times 1.018 & \text{if Sex} = F \\ 141 \times \min\left(\frac{Scr}{0.9}, 1\right)^{-0.411} \times \max\left(\frac{Scr}{0.9}, 1\right)^{-1.209} \times Age^{0.993} & \text{if Sex} = M \end{cases}$$

Cockcroft Gault⁵

$$GFR = \frac{(140 - Age) \times Wt \times (1 - 0.15[\text{if female}])}{72 \times Scr}$$

MDRD-186³

$$GFR = 186 \times Scr^{-1.154} \times Age^{-0.203} \times 0.742[\text{if female}]$$

Jelliffe⁶

$$GFR = \frac{(98 - 0.8(Age - 20)) \times (1 - 0.1[\text{if female}]) \times \frac{BSA}{1.73}}{Scr}$$

Wright⁴

$$GFR = \frac{(6580 - 38.8 \times Age) \times (1 - 0.168[\text{if female}]) \times BSA}{88.42 \times Scr}$$

Mayo Quadratic⁷

$$GFR = \exp \left(1.911 + 5.249 \frac{1}{Scr} - 2.114 \frac{1}{Scr^2} - 0.00686 Age - 0.205[\text{if female}] \right)$$

if $Scr < 0.8\text{mg/dL}$ then use 0.8 for Scr

Martin⁸

$$GFR = \frac{163 \times Wt \times (1 - 0.00496 \times Age) \times (1 - 0.252[\text{if female}])}{88.42 \times Scr}$$

References

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