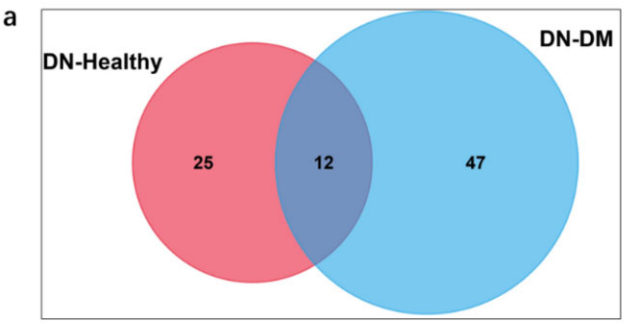
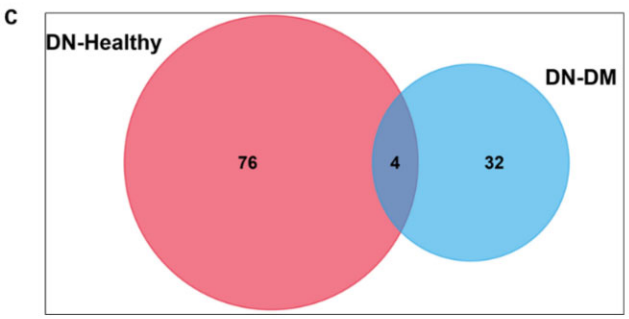


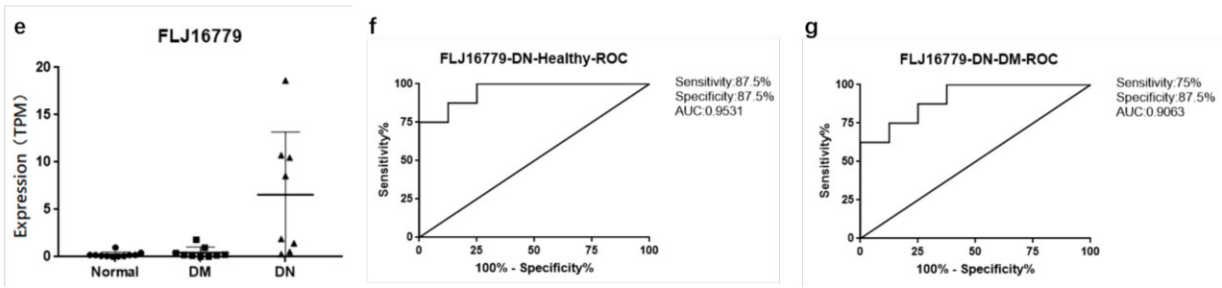
b

Gene_name	DN-Healthy FC.mean	DN-Healthy pvalue	DN-Diabetic FC.mean	DN-Diabetic pvalue
FLJ16779	20.775	0.030	12.552	0.034
AC099550.1	9.394	0.019	5.447	0.028
LINC01094	5.036	0.020	4.594	0.022
LINC01600	4.189	0.036	5.102	0.029
AC005076.1	4.077	0.038	5.391	0.028
AC025580.1	4.051	0.015	10.747	0.005
AC007638.2	3.039	0.049	4.179	0.030
AL049629.1	2.747	0.017	3.993	0.009
AL359710.1	2.587	0.047	3.129	0.029
AL031595.3	2.470	0.012	2.185	0.020
AP000787.1	2.370	0.031	2.328	0.036
AC073346.1	2.208	0.016	3.618	0.003



d

Gene_name	DN-Healthy FC.mean	DN-Healthy pvalue	DN-Diabetic FC.mean	DN-Diabetic pvalue
AC015912.3	-10.575	0.031	-5.443	0.046
AP003068.3	-33.494	0.031	-12.239	0.038
AP005432.2	-2.641	0.021	-2.900	0.016
LINC01144	-3.947	0.012	-4.238	0.017



MO385 **PERFORMANCE OF CREATININE-BASED EQUATIONS TO ESTIMATE GLOMERULAR FILTRATION RATE IN WHITE AND BLACK SUBJECTS FROM EUROPE, BRAZIL AND AFRICA**

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BACKGROUND AND AIMS: Current Glomerular filtration rate (GFR) estimating equations based on serum creatinine are facing increased criticism due to the inclusion of a race correction in black Americans with the CKD-EPI equation (CKD-EPI$_{ASR}$, A = Age, S = Sex, R = Race). A new equation without race (CKD-EPI$_{AS}$) has been proposed. However, this equation was developed mainly from US cohorts. The performance of this new equation has been poorly compared with current European-developed creatinine-based equations, i.e. the Lund-Malmö Revised (LMR), and the new European Kidney Function Consortium (EKFC)

METHOD: Data from subjects over 18 years, representing 11 cohorts from Europe (previously described as the EKFC dataset, $n = 13\,856$), and enhanced with data from Brazil ($n = 100$), France ($n = 4429$) and Africa [Democratic Republic of Congo (DRC) and Côte d'Ivoire, $n = 508$] were considered ($n = 18\,893$ for the whole cohort). The EKFC cohort was considered as non-black population. All data from Africa derived from black individuals. From France, 964 subjects were self-reported as black (=Blacks from Paris). Measured GFR as a reference method and IDMS creatinine results were available. Median bias (eGFR—mGFR) with 95% confidence intervals (CI), imprecision (interquartile range: IQR), and P30 accuracy (percentage of eGFR-values within ± 30% of mGFR) with 95% CI were calculated.

RESULTS: Results are summarized in Table.

CONCLUSION: The new CKD-EPI$_{AS}$ has been launched in the USA for societal reasons and is now recommended by US guidelines. However, in Europe and Africa, its performance was suboptimal. The EKFC equation, using the usual Q values, or population-specific Q values (when available), displays the best performance over the whole age range for populations in Europe and Africa.

Table 1. Median bias [95%CI] (mL/min/1.73 m²), imprecision (interquartile range, IQR) and P30(%) [95%CI] accuracy for six different creatinine-based equations (in green the best results, in red the worse)

European Whites (EKFC + Paris) $n = 17\,321$ age: 56.7 [42.0; 67.8] mGFR: 74.0 [46.2; 95.0]	CKD-EPI$_{ASR}$	CKD-EPI$_{ASR-NB}$	CKD-EPI$_{AS}$	LMR	EKFC	EKFC Q specific
Bias	3.0 [2.7; 3.2]	3.0 [2.7; 3.2]	6.0 [5.8; 6.3]	−3.2 [−3.4; −3.0]		
IQR [Pct25; Pct75]	16.8 [−4.4; 12.3]	16.8 [−4.4; 12.3]	17.2 [−1.5; 15.7]			
P30	82.5 [82.0; 83.1]	82.5 [82.0; 83.1]	78.5 [77.9; 79.1]			
Blacks from Paris $n = 964$ age: 51.2 [41.3; 60.2] mGFR: 59.3 [43.4; 76.9]						
Bias		−6.1 [−7.0; −5.4]	−3.6 [−4.7; −2.9]	−9.1 [−10.2; −8.5]	−6.3 [−7.0; −5.5]	
IQR [Pct25; Pct75]	19.1 [−6.8; 12.3]	15.5 [−13.2; 2.3]	16.3 [−11.1; 5.2]			15.5 [−8.5;7.0]
P30	77.4 [74.7; 80.0]	78.3 [75.7; 80.9]	81.0 [78.5; 83.5]	74.2 [71.4; 76.9]	80.5 [78.0; 83.0]	
Africans $n = 508$ age: 39.0 [30.0; 53.0] mGFR: 86.8 [71.7; 99.2]						
Bias	12.2 [10.7; 15.0]		2.5 [0.7; 4.2]	−9.0 [−10.5; −7.6]	−4.4 [−5.3; −3.3]	
IQR [Pct25; Pct75]	30.0 [−3.2; 26.8]	22.6 [−11.4; 11.2]	23.3 [−9.0; 14.3]			
P30	63.6 [59.4; 67.8]					
Brazilians $n = 100$ age: 59.5 [51.8; 66.0] mGFR: 42.0 [24.3; 61.3]						
Bias	2.4 [0.6; 5.3]	−0.0 [−3.0; 0.8]	1.0 [−0.3; 3.0]	−2.4 [−5.5; 0.7]	−0.1 [−2.9; 1.4]	NA
IQR [Pct25; Pct75]	13.0 [−2.1; 10.9]	13.6 [−6.6; 7.0]	13.9 [−4.6; 9.3]	13.7 [−9.5; 4.3]	13.2 [−7.2; 6.0]	NA
P30	74.0 [65.3; 82.7]	79.0 [70.9; 87.1]	76.0 [67.5; 84.5]	79.0 [70.9; 87.1]	78.0 [69.7; 86.3]	NA

CKD-EPI$_{ASR}$: Chronic Kidney Disease Epidemiology with variables age, sex and race. CKD-EPI$_{ASR-NB}$: Chronic Kidney Disease Epidemiology with variables age, sex and race but without applying the race coefficient. CKD-EPI$_{AS}$: Chronic Kidney Disease Epidemiology with variables age and sex. EKFC: European Kidney Function Consortium. IQR: interquartile range. LMR: Lund Malmö Revised. NA: not available. P30: accuracy within 30%.

MO386 **VISUALISING AND DIFFERENTIATING KIDNEY DISORDERS BY URINARY PEPTIDOMICS USING A MACHINE LEARNING APPROACH**

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BACKGROUND AND AIMS: Currently >20 000 native peptides in urine are known that are highly dynamic and able to display the status of different organs, especially the kidney. The characterization of urinary peptide profiles (UPP) enables the depiction of kidney disease severity, progression, fibrosis, and informs about the disease etiology. Advanced machine learning algorithms enable combining the changes in the very complex UPP associated with specific disease etiologies and reducing the dataspace to only few dimensions. Here, we show the application of a supervised machine learning pipeline for the visualization of different CKD etiologies based on high-dimensional peptidomics data, toward non-invasive disease classification.

METHOD: The Uniform Manifold Approximation and Projection (UMAP) algorithm was used as a novel nonlinear dimensionality-reduction technique to visualize and differentiate the UPP of patients with CKD of different etiologies. UPP of individual CKD patients (with diabetic kidney disease DKD, ($n = 386$), IgA nephropathy ($n = 743$) and vasculitis ($n = 150$)) and 369 healthy controls were extracted from the Human Urinary Proteome Database which contains >85 000 proteomics datasets analyzed using capillary electrophoresis coupled mass spectrometry. About 80% of the extracted datasets were used as a training and 20% as validation set.

RESULTS: When applying supervised-UMAP to the DKD patient and control datasets, excellent separation with an F1 score of 99.5% ± 0.9% in the training set, and 93.1% ± 3.3% in the independent test set could be observed. Subsequently, this approach was applied to differentiate controls and three kidney diseases (DKD, IgA nephropathy and vasculitis) simultaneously. In the training set an accuracy of up to 98% in DN and controls, and an overall F1 score of 93.7% ± 2.3% (Figure) was