was determined by a Random Forest to define the relative importance of variables for disease prediction.

Results: AdaptiveNet predicted active disease defined as DAS28-BSR >2.6 at the next visit with an overall accuracy of 75.6% (SD $\pm$ 0.7%) and a sensitivity and specificity of 84.2% (SD $\pm$ 1.6%) and 61.5% (SD $\pm$ 3.6%), respectively. The performance of the prediction for correct disease status was significantly higher in patients with a disease duration >3 years and positive rheumatoid factor. Regression allowed forecasting individual DAS28-BSR values with a Mean Squared Error (MSE) of 0.9 (SD $\pm$ 0.05). Compared to Linear Regression, Random Forests and Support Vector Machines, AdaptiveNet showed an increased performance of 7% in MSE. MSE was significantly lower in patients with disease duration >3 years and with positive anti-CCP antibodies. Feature importance identified number of painful joints, longer disease duration and age as most relevant factors for prediction of remission, whereas medication played a smaller role.

Conclusion: Predictability of disease activity in RA by this deep neural network was stronger in patients with a longer disease history and a positive auto-antibody status, potentially due to a more stable disease course. Generally, AdaptiveNet had a superior capacity to predict numeric RA disease activity compared to classical machine learning architectures, however all investigated models had limitations in low specificity.

REFERENCES:

- [1] Hügler M, Kalweit G, Hügler T, Boedecker J. Dynamic Deep Neural Network For Multimodal Clinical Data Analysis. *Stud Comput Intell*: Springer Verl. 2020.

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A list of rheumatology practices and hospitals that are contributing to the SCQM registries can be found on <http://www.scqm.ch/institutions>.

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POS0469

FALL RISK ASSESSMENT IN RHEUMATOID ARTHRITIS PATIENTS

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Background: Rheumatoid arthritis patients may have an increased risk of falls due to changes caused by the disease such as muscle weakness, joint impairment, reduced mobility and postural instability.

Objectives: The aim of this study was to analyze the occurrence of falls in RA patients and its risk factors.

Methods: Between January 2020 and July 2020, 51 patients with RA were included in the study. Fall history, and the number of falls within the past 12 months were questioned. All participants were assessed with Timed Up and Go Test (TUGT), One-Leg Stand Test (OLST), Walking and Talking Test (WTT), Sternal Push Test (SPT), Tinetti Test (TT), Four Test Balance Scale (FTBS), The Short Falls Efficacy Scale-International (FES-I), Pain Severity and Patient Global Assessment (PGA) by Visual Analog Scale (VAS), disability by the Health Assessment Questionnaire (HAQ), and disease activity by Disease Activity Score in 28 joints (DAS28) were evaluated in for each patient. The Kolmogorov-Smirnov, Mann-Whitney and chi-square tests were performed with a significance level of $P \leq 0.05$.

Results: 22 patients had at least one or more falls. The average age was 54.9 ± 11.5 years with a female predominance (sex ratio = 0.13). Comparing the two groups of patients: those with a history of falls and those without, patients with previous falls were mainly married women ($p=0.57$), with a low intellectual level ($p=0.63$). The body mass index in this group was higher ($p=0.01$) with respectively a higher number of painful and swollen joints ($p=0.16$, $p=0.07$); the mean HAQ was higher ($p=0.03$), and the mean VAS was more important ($p=0.05$). 12/22 patients had co-morbidities and were poly-medicated. 20/22 had joint foot deformities (hallux valgus was the most common deformity). 21/22 were on low dosage corticosteroid therapy. The mean TUGT was 18.5 seconds (>14 seconds). The OLST was less than 5 seconds in 12/22, the sternal push test was positive in 9/22, WTT was positive in 6/22 and the mean tinetti test was 22.4 ± 5.4 suggesting a high risk of falls. The average Short FES-I was 14.6 ± 4.4 reflecting a high fear of falls in this group of patients.

Conclusion: Knowledge about risk factors can help to identify high-risk patients in order to decrease their risk of falling, thus preventing fall-related injuries.

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POS0470

GLUCOCORTICOID DISCONTINUATION IN EARLY RHEUMATOID AND UNDIFFERENTIATED ARTHRITIS PATIENTS. A SUB-ANALYSIS OF THE BeSt AND IMPROVED STUDIES

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Background: Discontinuation of glucocorticoids (GC) as bridging therapy in rheumatoid arthritis (RA) treatment is recommended as rapidly as clinically feasible. Little is known about the rate of, and possible characteristics associated with successful GC discontinuation.

Objectives: To evaluate the success rate of GC discontinuation, and to study which factors are associated with successful GC discontinuation.

Methods: Data from two treat-to-target studies; BeSt (target DAS ≤ 2.4 , LDA), and IMPROVED (target DAS <1.6 , remission) were evaluated for all patients initially treated with a tapered high-dose of oral GC with conventional DMARD(s). GCs were discontinued when DAS ≤ 2.4 was maintained for 28 weeks in BeSt, and as soon as DAS was <1.6 in IMPROVED. GC discontinuation could be attempted twice: first attempt called 'primary', second attempt after GC restart called 'secondary'. Discontinuation was considered successful if the treatment target was maintained at the next visit. Univariable, and exploratory forward and backward multivariable logistic regression analyses were performed to identify potential characteristics associated with successful discontinuation (p -value <0.2 included in final model).

Results: From the 131 patients initiating combination therapy with prednisone in the BeSt study, 93 attempted discontinuation. Primary discontinuation was successful in 60% (56/93) and secondary discontinuation in 54% (19/35). A lower DAS at the visit prior to GC discontinuation and ACPA negativity were associated with successful discontinuation (table 1). Of the 610 patients in the IMPROVED, 400 attempted discontinuation. Primary discontinuation was successful in 61% (242/400), and secondary in 51% (71/139). A lower DAS both at baseline and at the visit prior to GC discontinuation were associated with successful discontinuation (table 1).

Conclusion: Primary GCs discontinuation was successful in approximately 60% and secondary in 50% of patients, independent of the treatment target and associated threshold for GC discontinuation. Most baseline characteristics were not predictive of successful GC discontinuation, but ACPA negativity (only in BeSt), baseline DAS (only in IMPROVED) and in both studies DAS prior to GC discontinuation were predictive for successful discontinuation. Based on this data it seems that 'standard' baseline characteristics are insufficient to 'personalize' the duration of temporary GC bridging but the DAS at the moment of GC discontinuation might give guidance.

Table 1. Results logistic regression analyses

	Univariable		Multivariable ^a	
	OR (95% CI)	p-value	OR (95% CI)	p-value
BeSt				
Age, year	1.00 (0.98; 1.03)	0.98		
Gender, female	0.51 (0.24; 1.09)	0.08		
Symptom duration BL, weeks	1.00 (0.99; 1.01)	0.61		
DAS at BL	0.92 (0.61; 1.40)	0.70		
DAS prior to discontinuation	0.13 (0.05; 0.33)	<0.01	0.11 (0.04; 0.30)	<0.01
RF, positive	1.28 (0.62; 2.69)	0.50	2.24 (0.81; 6.17)	0.12
ACPA, positive	0.70 (0.34; 1.43)	0.32	0.32 (0.12; 0.86)	0.02
Erosions, present at BL	0.65 (0.28; 1.49)	0.31		
Univariable				
Multivariable ^a				
IMPROVED				
Age, year	1.00 (0.99; 1.02)	0.64		
Gender, female	0.62 (0.43; 0.89)	0.01	0.75 (0.51; 1.11)	0.15
Symptom duration BL, weeks	1.00 (0.99; 1.00)	0.43	0.99 (0.99; 1.00)	0.08
DAS at BL	0.80 (0.65; 0.98)	0.03	0.78 (0.62; 0.98)	0.03
DAS prior to discontinuation	0.24 (0.15; 0.38)	<0.01	0.24 (0.14; 0.40)	<0.01
RF, positive	0.82 (0.57; 1.17)	0.27		
ACPA, positive	0.95 (0.66; 1.35)	0.76		
Erosions, present at BL	0.80 (0.49; 1.29)	0.35		
Univariable				
Multivariable ^a				

ACPA: anti-citrullinated protein antibodies; BL: baseline; DAS: disease activity score; RF: rheumatoid factor. ^a The final multivariable logistic regression model was based on stepwise forward and backward selection of predictors, both resulting in the same final model.

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POS0471

ASSOCIATION OF HLA-DRB1 HAPLOTYPES WITH CARDIOVASCULAR MORTALITY IN INFLAMMATORY POLYARTHRITIS: RESULTS FROM THE NORFOLK ARTHRITIS REGISTER

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Background: Haplotypes defined by amino acids at HLA-DRB1 positions 11, 71 and 74 associated with susceptibility to rheumatoid arthritis (RA), are associated with radiological outcome, anti-TNF response and all cause-mortality in RA. (1, 2) RA is associated with cardiovascular (CV) morbidity and mortality, but the increased prevalence of risk factors of CV disease in RA only partially explains this association.

Objectives: The aim was to investigate whether haplotypes associated with RA disease susceptibility and disease severity are also associated with CV mortality.

Methods: The Norfolk Arthritis register (NOAR) is a primary care-based inception cohort of patients with inflammatory polyarthritis (IP). (1, 2) NOAR patients with at least 2 years of follow-up and available mortality and genetic data were included in this study. Mortality data was provided by the Office for National Statistics.

Univariate Cox proportional hazard models were applied using STATA/IC 14.0. Models for CV mortality were adjusted for CV risk factors selected using stepwise regression: namely obesity, gender and hypertension. Hazard models were applied to the entire cohort of patients with inflammatory polyarthritis (IP). When calculating differences between highest and lowest risk genetic factors, bivariate analysis was used.

Results: HLA-DRB1 amino acids, haplotypes or haplotype groups associated with RA susceptibility are also associated with CV mortality as shown in the table 1. HLA-DRB1 polymorphisms encoding amino-acid haplotypes associated with an increased or decreased susceptibility to RA consistently show the same magnitude and direction of association for overall and CV mortality in IP. For example, the SEA-haplotype, associated with the lowest susceptibility to RA, and the best radiographic outcome, was found to be associated with decreased CV mortality (HR 0.67, 95% CI 0.47, 0.91, $p=0.023$). The relative difference in CV mortality between carriers of the high susceptibility VKA haplotype and carriers of the SEA haplotype was significant (HR 1.67, 95% CI 1.13, 2.48, $p=0.01$).

Table 1. Hazard ratios for CV mortality by genetic factors among patients with IP. Total number (n) of deaths are also displayed alongside the total number (n) of patients included in each analysis.

Amino acid / Haplotype /Group	Hazard Ratio (95% CI)	N
valine 11	1.10 (0.93, 1.30)	343 (2514)
serine 11	0.82 (0.70, 0.96)*	343 (2514)
Difference	1.23 (1.01, 1.49)*	
VKA haplotype	1.16 (0.94, 1.43)	310 (2328)
SEA haplotype	0.67 (0.47, 0.94)*	310 (2328)
Difference	1.67 (1.13, 2.48)*	
Group 1 †	1.10 (0.93, 1.31)	319 (2328)
Group 4 †	0.73 (0.60, 0.89)*	319 (2328)
Difference	1.37 (1.09, 1.72)*	

* $p<0.05$ † Haplotype groups as defined previously (2)

HLA-DRB1 haplotypes can be ranked according to the magnitude of their association with RA susceptibility and this hierarchy is conserved for various measures of disease outcome and overall mortality. (2, 3) The figure 1 shows that this risk hierarchy is also conserved for CV mortality: HLA-DRB1 haplotypes that

predispose to RA also predispose to increased CV mortality, independent of known CV risk factors.

Figure 1. Haplotypes with frequency >12% in NOAR are shown. X axis: susceptibility to ACPA-positive RA as ORs. (2) Y axis: CV mortality risk in IP as HRs, derived from multi-variate cox-proportional hazard models adjusted for CV risk factors. Values are on a logarithmic scale. A one-tailed p value was calculated using linear regression to determine the association between β coefficients of susceptibility and CV mortality.

Conclusion: The originally reported genetic associations between HLA-DRB1 polymorphisms and overall mortality were likely driven by associations with CV mortality.

REFERENCES:

- [1] S. Viatte *et al.*, *JAMA* **313**, 1645-1656 (2015).
- [2] S. Raychaudhuri *et al.*, *Nat Genet* **44**, 291-296 (2012).
- [3] D. P. Symmons, A. J. Silman, *Clin Exp Rheumatol* **21**, S94-99 (2003).

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POS0472

COMPARATIVE METABOLOMIC ANALYSIS OF SERUM SAMPLES FROM PATIENTS WITH COINCIDENTAL RHEUMATOLOGICAL AND MALIGNANT DISEASES

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Background: Rheumatic and musculoskeletal diseases (RMDs) and malignancies are both caused by a dysfunctional immune system and the probability of their coincidence in one individual is rising due to advances in cancer treatment and demographic changes. However, the lack of understanding of the complex interrelationship of both conditions often leads to undertreatment and high level of suffering in affected patients. Herein, the Malheur project breaks new ground by systematic analysis of concomitant malignant and rheumatic diseases and closes the knowledge gaps on the clinical and molecular level.

Objectives: To enable early diagnosis of concomitant malignancy and/or identification of patients at risk in the future, changes in serum metabolome were explored in order to create a diagnostic classification model.

Methods: Serum samples from patients with concomitant RMD and cancer or obligate precancerous lesions (n=78, breast cancer (23), melanoma (14), MGUS (12), prostate cancer (8) and others (21)) were collected as a pilot study within the Malheur project, a registry-based study initiated in 2018 at the university hospital Heidelberg, Germany. The following groups were defined by the underlying RMD: rheumatoid arthritis (n=42), psoriasis arthritis (n=23), spondylarthritis (n=9) and systemic lupus erythematosus (n=4). RMD patients without any malignancies were used as controls (n=280: 122 RA, 81 PsA, 46 SpA, 31 SLE).

Samples were analyzed by 1H NMR spectroscopy. For all samples, regular 1H acquisition with presaturation and Carr-Purcell-Meiboom-Gill (CPMG) spectra were acquired using a 600 MHz Bruker NMR spectrometer. Spectra were processed with TopSpin using 0.2 Hz of line broadening and manual phasing. Molar concentrations of 26 metabolites were acquired by integration of NMR spectra. With GraphPad Prism, univariate and ANOVA statistical analysis was performed to find significant differences between each malignant group and their control group as well as between all four malignant groups.