and males (Example in Figure 1). An online calculator of the percentiles of skin ultrasound measures was also developed. A radar chart showing these values and the percentile for each site is automatically drawn, allowing the clinician to export the results obtained.

Results: A total of 140 Caucasian participants, i.e., 80 females, mean (SD) age of 47.2 (16.0) years; and, 60 males, 49.5 (17.3) years were included. Ultrasound dermal thickness and stiffness measures were higher in males than females, in all Rodnan skin sites (except in chest for ultrasound-dermal thickness). Age had also a significant impact in both ultrasound measures, but only in some skin sites. Gender and age percentile curves (97.5th, 95th, 75th, 50th, 25th, 5th, 2.5th) were plotted for each of the measures in each skin site.

Conclusion: Gender and age are strongly associated with skin ultrasound parameters, imposing the need for gender- and age-specific reference values. Normal reference percentile curves for skin ultrasound measures are promising tools to support earlier diagnosis and refine sensitivity to time- or drug-induced changes. These reference percentile curves are provided as a basis for future cooperative work to strengthen its evidence-base, representativeness and refinement regarding potentially influential factors.

REFERENCES:


Acknowledgements: NIL.

Disclosure of Interests: None Declared.

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POS0880 ASSESSMENT OF MYOSITIS-RELATED INTERSTITIAL LUNG DISEASE BY 68GA-DATA.SA.FAPI PET-CT

Keywords: Lungs, Myositis, Imaging

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Background: Idiopathic inflammatory myopathies (IIM) are a group of heterogeneous autoimmune disorders marked by skeletal muscle inflammation and extra-muscular complications including pulmonary involvement. Interstitial lung disease (ILD) is a common manifestation affecting up to 78% in IIM patients. Normal reference percentile curves for skin ultrasound measures are promising tools to support earlier diagnosis and refine sensitivity to time- or drug-induced changes. These reference percentile curves are provided as a basis for future cooperative work to strengthen its evidence-base, representativeness and refinement regarding potentially influential factors.

Methods: Patients with IIM recruited prospectively from the rheumatology outpatient clinic, and control subjects without rheumatic conditions or ILD recruited from the cardiology outpatient clinic underwent 68Ga-FAPI PET-CT imaging. Pulmonary FAPI accumulation was assessed by measuring the maximal standardized uptake value (SUVmax) and mean SUV (SUVmean) over the whole lung (wI), respectively. Values of SUV were compared across IIM patients with and without ILD and controls using analysis of variance (ANOVA) test and displayed as mean ±standard deviation (SD).

Results: The clinical characteristics of patients with IIM (15 patients with ILD confirmed by CT and 4 non-ILD patients with primary muscular affection) and control subjects (n=17) are displayed in the Table 1. Subtypes of IIM included anti-synthetase syndrome (57.9%), dermatomyositis (15.8%), overlap myositis (15.8%), and immune-mediated-necrotizing-myositis (10.5%). In individuals with IIM-related ILD, whole-lung 68Ga-DATA.SA.FAPI uptake was significantly increased as compared to both, the non-ILD IIM patients and the control group: wISUVmax (6.6 ±[2.05] vs. 3.74 ±[0.71] and 4.74 ±[1.24]) respectively, both p<0.001 (Figure 1A) and wISUVmean (1.50 ±[0.48] vs. 0.94 ±[0.22] and 1.11 ±[0.34]) respectively, both p<0.05 (Figure 1B). No differences of wISUVmax or wISUVmean were observed between non-ILD IIM patients and the control group.

Conclusion: This study demonstrates enhanced tracer uptake in 68Ga-DATA.SA.FAPI PET-CT in patients with IIM. Thus, FAPI PET-CT may provide a useful tool for the assessment of lung disease in IIM. Further discriminatory and diagnostic testing approaches are needed to integrate this novel imaging method into clinical decision making.

Table 1. Demographic and clinical characteristics of participants at baseline.

<table>
<thead>
<tr>
<th>Disease subtype</th>
<th>IIM patients Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>NSIP and OP</td>
<td>Yes</td>
</tr>
<tr>
<td>ILD-Subtype</td>
<td>Yes; No/NS</td>
</tr>
<tr>
<td>UIP</td>
<td>Yes</td>
</tr>
<tr>
<td>MDAS</td>
<td>Yes</td>
</tr>
<tr>
<td>Ml-2</td>
<td>Yes</td>
</tr>
<tr>
<td>Seronegative</td>
<td>Yes</td>
</tr>
<tr>
<td>Pulmonary function tests</td>
<td>Yes</td>
</tr>
<tr>
<td>FVC % (mean ± SD)</td>
<td>81.9 ± 21.4</td>
</tr>
<tr>
<td>DLCO % (mean ± SD)</td>
<td>66.1 ± 21.3</td>
</tr>
</tbody>
</table>

Abbreviations: No./n, number; SD, standard deviation; NSIP, nonspecific interstitial pneumonia; UIP, usual interstitial pneumonia; OP, organizing pneumonia; FVC, forced vital capacity; DLCO, diffusion capacity of the lungs for carbon monoxide.

Figure 1. 68Ga-FAPi-04 uptake in the lungs of IIM-patients and controls. A) whole lung maximal standardized uptake value; B) whole lung mean standardized uptake value in myositis patients with or without interstitial lung disease and control subjects. P-values <0.05 were considered statistically significant. Abbreviations: wISUVmax, whole-lung maximal standardized uptake value; wISUVmean, whole-lung mean standardized uptake value; ILD, interstitial lung disease; ns, not significant. P-values <0.05 are marked with one asterisk; p-values <0.001 are marked with two asterisks.

REFERENCES: NIL.

Acknowledgements: NIL.

Disclosure of Interests: None Declared.

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POS0880 USING POLYGENIC RISK SCORES TO AID DIAGNOSIS OF PATIENTS WITH EARLY INFLAMMATORY ARTHRITIS: RESULTS FROM THE NORFOLK ARTHRITIS REGISTER

Keywords: Epidemiology, Inflammatory arthritides, Genetics/epigenetics

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Background: There is growing evidence that genetic information can offer valuable information to a clinician in a diagnostic setting, and that it is feasible that
genetic data would be of benefit to the rheumatology outpatient setting by aiding early diagnosis. A genetic probability tool (G-PROB) has recently been developed to aid diagnosis using existing knowledge of disease-associated genetic variants but has only been tested in a limited capacity.

**Objectives:** Our aim was to assess whether G-PROB could aid diagnosis in the rheumatology outpatient setting using data from the Norfolk Arthritis Register (NOAR), a large prospective observational cohort of patients presenting with early inflammatory arthritis where diagnosis at baseline is unclear.

**Methods:** Genotypes and follow-up clinician diagnoses were obtained from patients from NOAR. Six G-probabilities (0-100%) were created for each patient based on known disease-associated odds ratios (ORs) of published genetic risk variants, each corresponding to one disease of rheumatoid arthritis (RA), systemic lupus erythematosus (SLE), psoriatic arthritis (PsA), spondyloarthropathy (SpA), gout or “other rheumatological diseases.” Performance of the G-probabilities were estimated using the area under the receiver operating characteristic curve (AUC). Calibration of G-probabilities with clinician diagnosis was high, with regression coefficients of 1.03, where 1.00 represents perfect calibration. G-probabilities discriminated clinician diagnosis with an AUC of 0.84 (0.81-0.86). G-probabilities <5% corresponded to a negative predictive value (NPV) of 96% where it was possible to suggest at least one unlikely diagnosis for 99.9% of patients, two or more diagnoses for 94% of patients, and three or more diagnoses for 54% of patients. G-probabilities >50% corresponded to a positive predictive value (PPV) of 74%. In 57% of patients, the disease with the highest G-probability corresponded to clinician diagnosis.

**Conclusion:** G-PROB successfully converts complex genetic information into meaningful, and interpretable conditional probabilities which may be especially helpful in suggesting unlikely diagnoses in the rheumatology outpatient setting.

**References:**


**Figure 1.** (A) Distribution of G-probabilities which match and those which do not match clinician diagnosis. Ideally the correct diagnosis should have higher probabilities, and the distribution should be skewed to the left, with incorrect diagnoses having lower probabilities with a distribution skewed to the right. (B) Linear regression without intercept showing concordance of G-probabilities with clinician diagnosis match, where x-axis shows G-probabilities, and y-axis shows the proportion of instances where predicted diagnosis is concordant with clinician diagnosis. (C) ROC analysis of correspondence of G-probabilities with clinician diagnosis, where AUC shows pooled data for all diseases (microAUC).

**Table 1.** Performance of G-probabilities in suggesting likely and unlikely diagnoses at different thresholds

<table>
<thead>
<tr>
<th>G-probability threshold</th>
<th># of patients with at least one G-probability at the given threshold (n=972) (%)</th>
<th># of G-probabilities at the given threshold (n=5,832) (%)</th>
<th>NPV or PPV at the given threshold in %</th>
</tr>
</thead>
<tbody>
<tr>
<td>A) Thresholds suggesting unlikely diagnoses</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;5%</td>
<td>971 (100)</td>
<td>2410 (41)</td>
<td>NPV 96</td>
</tr>
<tr>
<td>&gt;50%</td>
<td>972 (100)</td>
<td>3857 (66)</td>
<td>NPV 96</td>
</tr>
<tr>
<td>B) Thresholds suggesting likely diagnosis</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≥20%</td>
<td>572 (100)</td>
<td>1975 (34)</td>
<td>PPV 41</td>
</tr>
<tr>
<td>&gt;50%</td>
<td>470 (48)</td>
<td>470 (8)</td>
<td>PPV 74</td>
</tr>
</tbody>
</table>

**Acknowledgements:** RMH and SS are joint first authors, JB and AB are joint last authors. The authors would like to thank the patients involved in NOAR and all supporting staff involved in its implementation. The authors also thank Prof Deborah Symmons for her involvement in the inception of the NOAR cohort. RMH is supported by an Academic Clinical Fellowship awarded by the National Institute for Health Research as part of the Integrated Academic Training (IAT) programme.

**Disclosure of Interests:** None Declared.

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**POS0891**

**AUTOMATIC COMPUTATION OF KNEE OSTEOARTHRITIS SEVERITY USING KNEE X-RAYS AND CONVOLUTIONAL NEURAL NETWORKS**

**Keywords:** Imaging, Artificial intelligence, Osteoarthritis

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**Background:** Knee osteoarthritis is a heterogeneous and complex degenerative disease, characterized by a progressive deterioration of bone cartilage and structural modifications of the joint [1]. The precision of the diagnosis and the rating of the severity are major criteria for the therapeutic management and its follow-up. They are based on three criteria: the assessment of the pain, of the functional impairment and of the structural modifications. For this last criterion, the standard protocol in routine care remains the interpretation of X-ray images using standardized scales. The Kellgren-Lawrence (KL) score, which assesses both the joint space and the presence of osteophytes, allows a classification of the stages of osteoarthritis, but it relies on subjective manual interpretation and is time consuming for practitioners [2].

**Objectives:** In this study, we have developed artificial intelligence algorithms to automatically measure the tibia-femur joint space (or joint space width JSW) and determine the Kellgren-Lawrence (KL) score.

**Methods:** We constituted a retrospective cohort of 19,560 patients. Using all their images, we trained different neural networks in order to select just knee AP X-rays without prosthesis nor artifacts. Our work explores two approaches: the prediction of the stage of osteoarthritis according to the KL scale and the measurement of the JSW. For the prediction of the KL score, 2,081 X-rays annotated by 3 radiologists were used to train a convolutional neural network (CNN). The measurement of the JSW required the realization of 3 different annotations: the positioning of the joint, of the two condyles (medial and lateral) and the contouring of tibia and femur. Three neural networks were optimized to reproduce these annotations before calculating the JSW for each condyle. For each individual task, we decomposed the datasets into training, validation, and test sets, used different data augmentation techniques, and researched the best possible architecture.

**Results:** The Kellgren-Lawrence score prediction obtained the following performances: an accuracy of 0.92, a sensitivity of 0.84 and an area under the ROC curve (AUC) of 0.97. To evaluate the measurement of the JSW, we calculated the correlation between the area measured by the annotators and the area predicted by the algorithms, obtaining a Pearson correlation of 0.84.

**Conclusion:** This study highlights the relevance of the use of artificial neural networks for the assessment of osteoarthritis. Their performance opens the way to a tool assisting in the precise and standardized gradation of the severity of joint degradation.

**References:**


**Disclosure of Interests:** None Declared.

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**POS0892**

**AN END-TO-END MACHINE LEARNING PIPELINE FOR THE AUTOMATED DETECTION OF RADIOGRAPHIC HAND OSTEOARTHRITIS: A NO-CODING PLATFORM EXPERIENCE**

**Keywords:** Osteoarthritis, Artificial intelligence, Imaging

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**Background:** Machine learning’s performances in the field of radiology have been constantly increasing in recent years such that nowadays many algorithms outperform human performances and are FDA approved.[1,2] Non-coding platforms have recently emerged and allow healthcare professionals with no programming experience to play an active role in the development of machine learning (ML) algorithms according to existing or emerging clinical needs.