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## Risk of Harm in Synthetic & Biological Intervention Trials in Patients with Inflammatory Arthritis: Protocol for A Meta-Epidemiological Study with Focus on Contextual Factors

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# Risk of Harm in Synthetic & Biological Intervention Trials in Patients with Inflammatory Arthritis: Protocol for A Meta-Epidemiological Study with Focus on Contextual Factors

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Study concept and design: EM, SMN, ST, RC, JPAI, ST, PCT, JSS.

Drafting on the protocol: EM, JB, SMN, TE, RC, JPAI, ST, PCT, JSS.

Critical revision of the protocol for important intellectual content and final approval before submission: All authors.

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This study had no financial competing interests.

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### *Amendments*

Important deviations from the protocol will be reported in the peer-reviewed publication.

## ABSTRACT

**Introduction:** Inflammatory Arthritis (IA) conditions, including rheumatoid arthritis (RA), psoriatic arthritis (PsA), and axial spondyloarthritis (AxSpA), are characterised by inflammatory infiltration of the joints. Biologic and targeted synthetic disease-modifying antirheumatic drugs (bDMARDs and tsDMARDs, respectively) reduce the effects of proinflammatory cytokines and immune cells to ameliorate disease. However, immunosuppression can be associated with high rates of serious adverse events (SAEs), including serious infections, and maybe an increased risk of malignancies and cardiovascular events. Currently, there is no empirical evidence on the extent to which contextual factors and risk of bias (RoB) domains may modify these harm signals in randomised trials.

**Method and analysis:** We will search MEDLINE (via PubMed) for systematic reviews published since April 2015 and all Cochrane reviews. From these reviews, randomised trials will be eligible if they include patients with an IA condition (RA, PsA, or AxSpA) with at least one group randomly allocated to bDMARD and/or tsDMARD treatments. A predefined form will be used for extracting data on population characteristics (e.g., baseline characteristics or eligibility criteria, such as medication background), and specific harm outcome measures, such as number of withdrawals, numbers of patients discontinuing due to adverse events, and number of patients having SAEs. RoB in individual trials will be assessed using a modified Cochrane RoB tool. We will estimate the potentially causal harm effects related to the experimental intervention compared to control comparator as risk ratios, and heterogeneity across randomised comparisons will be assessed statistically and evaluated as inconsistency using the  $I^2$  Index. Our meta-regression analyses will designate population and trial characteristics, and each RoB domain as independent variables, whereas the three harm domains will serve as dependent variables.

**Ethics and dissemination:** Ethics approval is not required for this study. Results will be disseminated through publication in international peer-reviewed journals.

**Registration:** PROSPERO (CRD: 42020171124).

## Strengths and limitations of this study

- This will be an extensive and comprehensive risk of harm analysis of bDMARDs and tsDMARDs across multiple IA diagnoses unlike previous assessments that have been more circumscribed.
- A large array of contextual factors and risk of bias items will be assessed.
- Despite the comprehensive nature of the assessment, some analyses may be underpowered, especially for uncommon harms, and some meta-regression assessments may be affected by ecological bias.

For peer review only

# INTRODUCTION

## Background

Inflammatory Arthritis (IA) is a heterogeneous group of autoimmune diseases that includes rheumatoid arthritis (RA), psoriatic arthritis (PsA), axial spondyloarthritis (axSpA, including ankylosing spondylitis AS) (1, 2). These diseases are characterised by inflammatory infiltration of the joints (3), resulting in pain, swelling, stiffness and restricted movement (4). Ultimately, they can have a detrimental impact on quality of life, cause progressive disability and premature death (5, 6). Not only are the implications severe, also the diseases are a global concern; RA alone affects about 1% of the world's population (7).

Aside from conventional synthetic (cs) DMARDs including methotrexate, targeted therapies, consisting of biological disease-modifying antirheumatic drugs (bDMARDs) and targeted synthetic DMARDs (tsDMARDs) are considered effective for treating IA *per se* (8-10). Notably, bDMARDs work by targeting specific molecules or receptors (11), such as tumour necrosis factor alpha (TNF $\alpha$ ), which is a potent inflammatory cytokine produced by T-cells and macrophages (12, 13). In contrast, tsDMARDs target intracellular pathways and reduce the effect of cytokines known to drive the proinflammatory machinery of cellular immune response (14-16). As such, b- and tsDMARDs are Immunomodulatory; although effective in alleviating symptoms of IA, they also carry risk of harm (defined as: "*the totality of possible adverse consequences of an intervention or therapy*" (17)). Indeed, meta-analyses and an observational cohort study have shown that bDMARDs are associated with higher rates of serious infections (18-20) and potentially dose-dependent increased risk of malignancies (21). Some meta-studies and systematic literature reviews suggest that tsDMARD rates of serious infections and malignancies are no different from those of bDMARDs (16, 22, 23). Recent reviews report a possibly increased risk of venous thromboembolism with tsDMARDs (23, 24).

Randomised controlled trials (RCTs) inevitably vary with respect to eligibility criteria, patient characteristics, and internal validity, which may distort their results (i.e., the harm signal) and thus potentially bias their interpretation (25, 26). If evidence were available on which trial characteristics to adjust for when interpreting harm from meta-research, these covariates would be considered important contextual factors. Currently, a contextual factor is broadly defined as a "*...variable that is not an outcome of the study but needs to be recognized (and measured) to understand the study results. This*



1 *includes potential confounders and effect modifiers*" (27). However, we currently have no  
2 empirical evidence concerning the extent to which contextual factors, such as population  
3 and trial characteristics and risk of bias (RoB) domains, modify the harm signals from  
4 trials testing targeted therapies (i.e., bDMARDs and tsDMARDs) across IA diseases.  
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## 8 **Rationale**

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10 Designing, conducting, and reporting RCTs should incorporate methods—such as  
11 concealing randomised allocation, blinding participants and personnel, and  
12 appropriately engaging the intention-to-treat population—that avoid biases resulting  
13 from incompatibilities between the intervention and control groups. Empirical  
14 evidence suggests that the absence of rigorous methodology can lead to biased  
15 intervention effect estimates (i.e., net benefits) (28). Contextual factors, such as  
16 population and trial characteristics, also have been shown to be possible effect  
17 modifiers when assessing benefits (8, 29).  
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24 The effect on harms of RoB, trial characteristics and contextual factors (e.g.,  
25 population characteristics) has yet to be investigated, and using meta-epidemiology is  
26 the method of choice for doing so (30). Previous meta-epidemiological research  
27 within rheumatology has primarily investigated the effect of methodological quality  
28 (internal validity) on treatment effects (benefit) (8, 29, 31, 32). To our knowledge, no  
29 one has yet investigated the importance in IA therapies of contextual factors (i.e.,  
30 population and trial characteristics) and RoB when the outcome is harmful effects.  
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## 38 **Aims and objectives**

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40 This exploratory meta-epidemiological study aims to improve harm reporting by  
41 investigating the influence of RoB domains, trial characteristics, and contextual  
42 factors on three generic harm measures (17), as well as mortality among patients  
43 with IA who were treated with bDMARDs and/or tsDMARDs. Our objective is to  
44 explore whether specific participant and trial characteristics (i.e., contextual factors  
45 incl. RoB domains) have a quantitative influence in terms of effect modification and/or  
46 distortion due to biases on the observed likelihood of harm from an experimental  
47 intervention compared to control comparators in randomised trials. If contextual  
48 factors have such an influence, we hope to shed light on their importance to future  
49 trial reporting and interpretation of harm when reporting randomised trials (17).  
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## Protocol and registration

This protocol was developed in accordance with the v1.07 2018 Methodological Expectations for Cochrane Intervention Reviews (MECIR) recommendations of the Cochrane Collaboration (33) and reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Protocols (PRISMA-P) guidelines (34). The study protocol was pre-specified and registered in PROSPERO on 2020-03-27, CRD number: CRD42020171124.

## METHODS AND ANALYSIS

This (meta-epidemiological) study combines data from a large representative sample of available trials into a single database by assembling trials already included in published systematic reviews. Generic outcome measures that cover important harm domains (*i*: withdrawals, *ii*: withdrawals due to adverse events [WD d/t AEs], and *iii*: serious adverse events [SAEs] (17)) and mortality will constitute the dependent variable(s) in the database. Harm effects in relation to the use of targeted therapies will be analysed to determine whether they are affected by contextual factors among population and trial characteristics.

### Eligibility criteria

We will search MEDLINE (via PubMed) for trials included in published systematic reviews (published since April 2015) or Cochrane reviews. From these systematic reviews, randomised trials will be eligible if they fulfil our inclusion criteria (see table 1 for PICO framework), with at least one group randomly allocated to bDMARD and/or tsDMARD.

The interventions of interest are targeted therapies (i.e., bDMARDs and tsDMARDs) approved by either EMA or FDA to date, treating IA conditions in adult populations. These therapies will include bDMARDs: abatacept, adalimumab, anakinra, certolizumab, etanercept, golimumab, guselkumab, infliximab, ixekizumab, rituximab, sarilumab, secukinumab, tocilizumab, ustekinumab, and tsDMARDs: apremilast, baricitinib, filgotinib, tofacitinib and upadacitinib.

Only RCTs included in an existing systematic review of patients with inflammatory arthritis (RA, PsA, and AxSpA [incl. AS]) will be considered for eligibility. We will exclude reviews (i.e., not look for trials) that have been withdrawn. Furthermore, only RCTs from the eligible systematic reviews where the full text is available in

English will be included. There will be no restriction on publication year of the individual RCTs.

Table 1. Research objective described using PICO\*

<b>Participants</b>	<b>Adult patients with rheumatoid arthritis (RA), psoriatic arthritis (PsA), axial spondyloarthritis (axSpA) or ankylosing spondylitis (AS).</b>
<b>Intervention</b>	Targeted therapies (i.e., bDMARDs and tsDMARDs)
<b>Comparison</b>	Placebo, standard care or waiting list/no intervention, active comparator and unclear.
<b>Outcome(s)</b>	Number of withdrawals (WDs), number of WDs due to adverse events (WD d/t AEs), number of serious adverse events (SAEs) and number of patients who died.

\*PICO - participants, intervention, comparison, and outcome.

## Information sources and search strategy

We will search MEDLINE (via PubMed) for eligible meta-analyses or systematic reviews of trials published since April 2015 and eligible Cochrane reviews using the search algorithm shown in table 2:

Table 2. Search strategy

```
(arthritis[tiab] OR spondyloarthritis[tiab] OR ankylosing[tiab] OR psoriatic[tiab] OR
Spondylarthropathies[tiab] OR rheumatoid[tiab] OR Psoriasis[tiab])
AND
("disease-modifying antirheumatic drugs"[tiab] OR "biological agent"[tiab] OR biologics*[tiab] OR
DMARD[tiab] OR abatacept[tiab] OR adalimumab[tiab] OR anakinra[tiab] OR apremilast[tiab] OR
baricitinib[tiab] OR certolizumab[tiab] OR etanercept[tiab] OR filgotinib[tiab] OR golimumab[tiab] OR
guselkumab[tiab] OR infliximab[tiab] OR ixekizumab[tiab] OR rituximab[tiab] OR sarilumab[tiab] OR
secukinumab[tiab] OR tocilizumab[tiab] OR tofacitinib[tiab] OR upadacitinib[tiab] OR
ustekinumab[tiab])
AND
(("Systematic Review"[pt] OR Meta-Analysis[pt] OR meta-analysis[tiab] OR "systematic review"[tiab]
OR meta-analys*[pt] OR meta-analys*[ti] OR metaanalys*[ti] OR meta-regress*[tiab] OR
metaregress*[tiab])
AND ("2015/04/01"[Date - Publication]: "3000"[Date - Publication]))
```

OR "Cochrane Database Syst Rev" [jour])

## Study selection

Two independent reviewers (JB and EM, with support from SMN/RC) will screen the systematic reviews based on title and abstract, in accordance with eligibility criteria.

The same two reviewers will assess the full systematic review texts for eligibility of the reviews and subsequently select the RCTs from the reviews that are eligible, according to our objectives. We will obtain the full text if at least one of the reviewers considers an RCT to be potentially eligible during the screening process.

Disagreements will be resolved by consensus or by consulting a third reviewer (RC). EndNote X9.2 software will be used to manage the reviews and RCT records retrieved from the search.

## Data collection process

Two reviewers (JB and EM) will extract data using a predefined, standardised data extraction form, and in case of uncertainty a third reviewer (SMN/RC) will be consulted. If a trial is included in more than one review, the trial will be registered and counted/included once.

***Review Level:*** From the reviews, we will extract data on review registration number, year of publication, first author's name, number of RCTs eligible for our study, and the condition and intervention studied, according to the review title.

***Randomised Trial Level:*** From the trials, we will extract data on first author's name, publication ID, trial duration, duration until switch (e.g., relevant for adaptive trial designs), rescue, early escape or cross over, number of participants in each arm, and treatment given in the active and comparator arms (i.e., following the PICO framework). Treatment in the comparator arm will be grouped into the following predefined categories: (i) placebo; (ii) standard care or waiting list/no intervention; (iii) active comparator, or as an ultimate last option; (iv) unclear. Outcome measures and data extraction of trial and participant characteristics are specified below and listed in table 3.

## Participant characteristics in individual studies

*Data on the following trial eligibility criteria will be extracted:*

- Binary indicator (0 or 1) of inflammation scored as 1 with  $\geq 1$  of the following criteria: erythrocyte sedimentation rate (ESR)  $\geq 28$  mm/hour, CRP level  $\geq 0.3$  mg/dL, and/or morning stiffness lasting  $\geq 45$  minutes
- minimum AND maximum required number of swollen joint counts (SJC)
- minimum AND maximum required number of tender joint counts (TJC)
- minimum AND maximum allowed disease duration
- rheumatoid factor (RF) and/or anti-cyclic citrullinated peptide antibody (anti-CCP) and/or anti-cyclic citrullinated peptide antibody 2 (CCP2) status

In order to stratify trials according to the DMARD history of their included patients, we will ask the following signalling question: Had the participants, prior to inclusion, potentially exhausted the treatment potential of at least one class of DMARD—either conventional synthetic DMARDs (i.e., [csDMARD], bDMARD, or tsDMARD)?

- csDMARD-naïve (patients were either csDMARD naïve or had not exhausted the treatment potential of at least one csDMARD)
- csDMARD-IR (csDMARD inadequate responders), where patients had exhausted at least one csDMARD option previously
- bDMARD or tsDMARD-IR (bDMARD or tsDMARD inadequate responders), patients had inadequate response to at least one previous bDMARD or tsDMARD. Inclusion in this group entails exclusion from other DMARD history groups.

*Patients' concomitant medication (background) of DMARDs during the trial period will be ordered in the following three levels:*

- methotrexate (MTX)
- csDMARDs other than MTX
- bDMARDs or tsDMARDs

We will extract information about how the three groups were handled at randomisation, potentially enabling us to cluster the trials into one of the following five levels: (i) Naïve (i.e., patients had never used the drug[s] of interest); (ii) Not using (i.e., the study included only patients who were currently not using the drug[s] of interest); (iii) Discontinued (i.e., patients were not allowed to continue drug[s] of interest); (iv) Continued (i.e., patients were allowed to continue drug[s] of interest); and (v) Not reported (unclear: no information was reported on this matter). In the case of axSpa, NSAID will be extracted equivalent to csDMARDs.

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2 *Data on the following aggregate (average/median) patient baseline characteristics will*  
3 *be extracted:* age, female (proportion), disease duration (years), ESR (mm/hour),  
4 CRP (mg/dL), Disease activity score, RF positive (proportion), anti-CCP positive  
5 (proportion), anti-CCP2 positive (proportion), SJC, TJC, health assessment  
6 questionnaire—disability index (HAQ-DI), physician global assessment (e.g., Visual  
7 Analogue Scale [VAS]), patient global assessment (e.g., VAS), and patient-reported  
8 pain on visual analogue scales of 0–100 mm (e.g., VAS).  
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### 15 **Risk of bias and trial characteristics in individual studies**

16 Many published reviews include some form of RoB assessment (i.e., at least for the  
17 most frequently used RoB domains) for each individual trial; these assessments will  
18 be mapped to the best of our ability to correspond to the Cochrane RoB v.1 (35). The  
19 RoB will also be assessed by one of the two reviewers (JB and EM) and  
20 subsequently compared with the original bias and internal validity assessments' in the  
21 review, from which it was sampled.  
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28 Within each full-text trial report, we will apply the following domains of the original  
29 Cochrane RoB tool (i.e., RoB v.1.0) (35), which comprise methods for:  
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- 31 • sequence generation/maintaining allocation concealment (selection bias)
- 32 • blinding both patients and personnel (performance bias)
- 33 • management/analysis/reporting of incomplete outcome data (attrition bias)
- 34
- 35
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38 Each of these three domains will be rated as high risk, low risk, or unclear RoB (35).  
39 In case of uncertainty, another reviewer (SMN/RC) will be consulted. Any  
40 discrepancy between RoB assessment sources will be resolved by discussion among  
41 the authors.  
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46 The following additional bias sources will also be assessed, and data will be  
47 extracted from them:  
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- 49 • single vs. multi-site trials (36)
- 50 • small vs. large trials (where small will pragmatically be defined as <100 patients per  
51 arm) (37, 38)
- 52 • source of funding grouped into one of the following five categories: (i) 100% industry  
53 (pharmaceutical/device company) funded; (ii) mixed funding (e.g., non-industry and  
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1 industry; (iii) provision of drug only; (iv) 100% non-profit funded; and (v)  
2 unclear/undisclosed funding (39)  
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## 5 **Outcome measures**

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7 Data extraction for each RCT will include the number of patients who died, and the numbers  
8 of patients with any of the following “generic events”: (i) all withdrawals (WDs); (ii) WDs due  
9 to AEs; and (iii) SAEs (17). If the number of individual patients with SAEs is not reported, we will  
10 extract the number of reported SAEs instead.  
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14 Where reasons are provided to explain the SAEs, they will be categorised according to  
15 MedDRA v.23.0 [(i) Infections and infestations; (ii) Neoplasms benign, malignant and  
16 unspecified (incl. cysts and polyps); (iii) Cardiac and vascular disorders; or (iv) others]. If  
17 patients in the comparison group later are offered the intervention (i.e., switching to the  
18 intervention group), the number of events before the switch will be used as the endpoint of choice  
19 (i.e., before introducing adaptive trial designs).  
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## 25 **Summary measures**

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27 For each binary outcome, we will extract data corresponding to the 2×2 table,  
28 summarising the number of patients who experienced the outcome in each  
29 comparison group as reported in the randomised trial and the total number of patients  
30 randomly assigned in each group. For outcomes collected and reported  
31 corresponding to different time points, we will select the time point with the longest  
32 follow-up while still respecting the primary research design (e.g., before introducing  
33 an adaptive trial design, and/or open label extension) (40, 41).  
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40 Because all the outcome measures are dichotomous, the relative Risk Ratios  
41 (RRs) with 95% confidence intervals (95%CI) will be the preferred measure of  
42 relative effect, and these can subsequently be applied to the baseline or control  
43 group risks to generate absolute risks (42). When appropriate for the very rare  
44 adverse events, we will use a continuity correction (adding to all cells a factor  
45 proportional to the reciprocal of the size of the contrasting study group), as  
46 suggested by Sweeting and colleagues (43), to take into account zero cell counts in  
47 one group only. This continuity correction will be applied when no events are  
48 observed in one study arm of a trial. The correction is inversely proportional to the  
49 relative size of the opposite of the study (21, 43). Continuity correction for the  
50 experimental intervention arm is  $1/(R+1)$ ;  $R$  is the ratio of control group to  
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intervention group sizes (i.e.,  $R = n_C/n_I$ ). Similarly, the continuity correction for the control comparator arm is  $R/(R+1)$ . We expect that most trials will report only a few SAEs and deaths, so the odds ratios and 95%CI's will also (for the purpose of sensitivity analysis) be calculated with the use of the *Peto* method. Because the expected events are sparse and all trials will have similar durations of follow-up for their treatment groups, the use of both risk ratios and odds ratios should represent a valid approach to assessing the risk associated with the use of synthetic or biological intervention in patients with IA. We expect the search to bring around 175 eligible trials (RA: 117, PsA: 15, AxSpA: 43) (44-48). A random sample of 10 eligible studies (49-58) showed typical reported event rates in the placebo and intervention groups for all WD of 14,9% and 12,5%, for WDs due to AEs/TEAEs or SAE of 2,8% and 4,8% and for SAE of 5% and 6,5%, respectively. Simple power estimation showed that a sample group of 7,560 patients was required for a study power of 80%.

## Synthesis of results

Outcome events will be coded so that an RR direction of more than 1 indicates a potentially harmful effect of the experimental intervention (i.e.,  $RR = [r_I/n_I] / [r_C/n_C]$ ). Mixed effects Restricted Maximum Likelihood (REML) meta-analyses (59) will be used to combine the harm effects across RCTs (based on their log  $[RR]$ ) (60); we will apply the trial ID as a random effect, while applying the review ID (from which the trial was sampled) as a fixed effect in order to model the hierarchical structure of the data sampling (61).

Heterogeneity across randomised comparisons will be assessed by using the Cochrane Q test (62), interpreted based on the  $I^2$  inconsistency index (63), and quantified by the estimate for between-trial variance ( $\tau^2$ ), estimated as  $T^2$  (64). The effect of population and trial characteristics (listed below) on the between-trial variance will be calculated by univariably adding a factor for the specific characteristic in the model. If introducing a specific covariate into the meta-model reduces the observed between-trial variance ( $T^2$ ), this result will be considered an indication of a potentially important effect modifier (65).

*Table 3. Population and trial characteristics*

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### **Trial eligibility criteria:**

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1 Minimum and maximum required number of swollen joint counts  
 2 Minimum and maximum required number of tender joint counts  
 3 Minimum and maximum required C-reactive protein  
 4 Minimum and maximum required Erythrocyte sedimentation rate  
 5 Minimum and maximum allowed disease duration  
 6 Rheumatoid factor  
 7 Anti-cyclic citrullinated peptide antibody status  
 8 Anti-cyclic citrullinated peptide antibody 2 status

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13 **DMARD history:**

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15 csDMARD-naïve  
 16 csDMARD-IR (csDMARD inadequate responders)  
 17 bDMARD or tsDMARD-IR (bDMARD or tsDMARD inadequate responders)

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21 **Medication background of DMARDs:**

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23 Methotrexate  
 24 -Naïve  
 25 -Not using  
 26 -Discontinued  
 27 -Continued  
 28 -Not reported  
 29 csDMARDs other than methotrexate  
 30 -Naïve  
 31 -Not using  
 32 -Discontinued  
 33 -Continued  
 34 -Not reported  
 35 bDMARDs or tsDMARDs.  
 36 -Naïve  
 37 -Not using  
 38 -Discontinued  
 39 -Continued  
 40 -Not reported

---

50 **Aggregate (e.g., average/median) patient baseline characteristics:**

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52 Age  
 53 Female (%)  
 54 Disease duration  
 55 Erythrocyte sedimentation rate

1 C-reactive protein  
 2 Disease activity score  
 3 RF positive (%)  
 4 Anti-CCP positive (%)  
 5 CCP2 positive (%)  
 6 Swollen joint counts  
 7 Tender joint counts  
 8 Health assessment questionnaire—disability index  
 9 Physician global assessment of disease activity  
 10 Patient global assessment of disease activity  
 11 Patient-reported pain on visual analogue scales of 0–100 mm

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## 18 Risk of bias across studies

19 Stratified meta-analyses will be used for tests of interaction between harms and the  
 20 trial RoB (listed in Table 4) and trial characteristics collected as described above.  
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25 *Table 4. Risk of bias*

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### 28 **Cochrane risk of bias domains:**

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- 30 · Risk of selection bias
  - 31 · Risk of performance bias
  - 32 · Risk of attrition bias
  - 33 · Overall risk of bias\*
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### 38 **Additional bias sources:**

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- 40 · Single vs. multi-site trials
  - 41 · Small vs. large trials
  - 42 · Source of funding
- 

45 \*For each trial, the overall RoB will be classified as low (i.e., low RoB for all three domains); high (i.e., high  
 46 RoB for one or more domains); or unclear (i.e., unclear RoB for one or more domains in the absence of  
 47 high RoB).  
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 49  
 50

## 51 Perspectives

52 The Outcome Measures in Rheumatology (OMERACT) initiative established the Contextual  
 53 Factors Working Group to guide the understanding, identification and handling of contextual  
 54 factors for clinical trials, with most of the current emphasis' being on net benefit inferred from a  
 55  
 56  
 57

1 rheumatology trial (66). This meta-epidemiological study will work from the original definition of  
2 what constitutes a contextual factor, as defined in the introduction. We will explore and hope to  
3 reveal the possible impact of contextual factors (i.e., population and trial characteristics) and  
4 RoB domains of three different (but related) harm measures, as well as deaths (67). Knowing  
5 which factors are associated with a causal model for harms—either as effect modifiers or  
6 distortions of the outcome due to bias—is important for improving investigation and reporting of  
7 harms in future trials (68). Also, research in this area might identify subgroups among rheumatic  
8 disease patients that are at higher risk of experiencing harms. Such information would provide  
9 important evidence for future treatment guideline development. Ultimately the doctor will be able  
10 to differentiate the risk of intervention based on the patient’s characteristics. This has the potential  
11 to enhance informed decision-making and effect therapeutic interventions applied in practice,  
12 leading to safer treatment of individual patients and increase efficiency in the health care system.  
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### 23 **Patient and public involvement**

24 Patients and/or the public were not involved in designing study concept or drafting of the protocol.  
25  
26  
27

### 28 **ETHICS AND DISSEMINATION**

29 Because our study does not collect primary data, no formal ethical assessment and informed  
30 consent are required. First, second and third author (EM, JB and SMN) will draft the paper  
31 describing this meta-epidemiological study; the study will be disseminated in a peer-reviewed  
32 publication.  
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# Risk of Harm in Synthetic and Biological Intervention Trials in Patients with Inflammatory Arthritis: Protocol for A Meta-Epidemiological Study Focusing on Contextual Factors

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This study had no financial competing interests.

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### *Amendments*

Important deviations from the protocol will be reported in the peer-reviewed publication.

## ABSTRACT

**Introduction:** Inflammatory Arthritis (IA) conditions, including rheumatoid arthritis (RA), psoriatic arthritis (PsA), and axial spondyloarthritis (AxSpA), are characterised by inflammatory infiltration of the joints. Biologic and targeted synthetic disease-modifying antirheumatic drugs (bDMARDs and tsDMARDs, respectively) reduce the effects of proinflammatory cytokines and immune cells to ameliorate disease. However, immunosuppression can be associated with high rates of serious adverse events (SAEs), including serious infections, and maybe an increased risk of malignancies and cardiovascular events. Currently, there is no empirical evidence on the extent to which contextual factors and risk of bias (RoB) domains may modify these harm signals in randomised trials.

**Method and analysis:** We will search MEDLINE (via PubMed) for systematic reviews published since April 2015 and all Cochrane reviews. From these reviews, randomised trials will be eligible if they include patients with an IA condition (RA, PsA, or AxSpA) with at least one group randomly allocated to bDMARD and/or tsDMARD treatments. A predefined form will be used for extracting data on population characteristics (e.g., baseline characteristics or eligibility criteria, such as medication background), and specific harm outcome measures, such as number of withdrawals, numbers of patients discontinuing due to adverse events, and number of patients having SAEs. RoB in individual trials will be assessed using a modified Cochrane RoB tool. We will estimate the potentially causal harm effects related to the experimental intervention compared to control comparator as risk ratios, and heterogeneity across randomised comparisons will be assessed statistically and evaluated as inconsistency using the  $I^2$  Index. Our meta-regression analyses will designate population and trial characteristics, and each RoB domain as independent variables, whereas the three harm domains will serve as dependent variables.

**Ethics and dissemination:** Ethics approval is not required for this study. Results will be disseminated through publication in international peer-reviewed journals.

**Registration:** PROSPERO (CRD: 42020171124).

## Strengths and limitations of this study

For peer review only - <http://bmjopen.bmj.com/site/about/guidelines.xhtml>

- This will be an extensive and comprehensive risk of harm analysis of bDMARDs and tsDMARDs across multiple IA diagnoses unlike previous assessments that have been more circumscribed.
- A large array of contextual factors and risk of bias items will be assessed.
- The study selection will be done by two independent reviewers.
- Despite the comprehensive nature of the assessment, the study may be limited by poor reporting/lack of data for certain contextual factors and uncommon harms, and some meta-regression assessments may be affected by ecological bias due to the use of aggregated data, and meta-confounding.

# INTRODUCTION

## Background

Inflammatory Arthritis (IA) is a heterogeneous group of autoimmune diseases that includes rheumatoid arthritis (RA), psoriatic arthritis (PsA), axial spondyloarthritis (axSpA, including ankylosing spondylitis AS) (1, 2). These diseases are characterised by inflammatory infiltration of the joints (3), resulting in pain, swelling, stiffness and restricted movement (4). Ultimately, they can have a detrimental impact on quality of life, cause progressive disability and premature death (5, 6). Not only are the implications severe, also the diseases are a global concern; RA alone affects about 1% of the world's population (7).

Aside from conventional synthetic (cs) DMARDs including methotrexate, targeted therapies, consisting of biological disease-modifying antirheumatic drugs (bDMARDs) and targeted synthetic DMARDs (tsDMARDs) are considered effective for treating IA *per se* (8-10). Notably, bDMARDs work by targeting specific molecules or receptors (11), such as tumour necrosis factor alpha (TNF $\alpha$ ), which is a potent inflammatory cytokine produced by T-cells and macrophages (12, 13). In contrast, tsDMARDs target intracellular pathways and reduce the effect of cytokines known to drive the proinflammatory machinery of cellular immune response (14-16). As such, b- and tsDMARDs are Immunomodulatory; although effective in alleviating symptoms of IA, they also carry risk of harm (defined as: "*the totality of possible adverse consequences of an intervention or therapy*" (17)). Indeed, meta-analyses and an observational cohort study have shown that bDMARDs are associated with higher rates of serious infections (18-20) and potentially dose-dependent increased risk of malignancies (21). Some meta-studies and systematic literature reviews suggest that tsDMARD rates of serious infections and malignancies are no different from those of bDMARDs (16, 22, 23). Recent reviews report a possibly increased risk of venous thromboembolism with tsDMARDs (23, 24).

Randomised controlled trials (RCTs) inevitably vary with respect to eligibility criteria, patient characteristics, and internal validity, which may distort their results (i.e., the harm signal) and thus potentially bias their interpretation (25, 26). If evidence were available on which trial characteristics to adjust for when interpreting harm from meta-research, these covariates would be considered important contextual factors. Currently, a contextual factor is broadly defined as a "*...variable that is not an outcome of the study but needs to be recognized (and measured) to understand the study results. This*

1 *includes potential confounders and effect modifiers*" (27). However, we currently have no  
2 empirical evidence concerning the extent to which contextual factors, such as population  
3 and trial characteristics and risk of bias (RoB) domains, modify the harm signals from  
4 trials testing targeted therapies (i.e., bDMARDs and tsDMARDs) across IA diseases.  
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## 8 **Rationale**

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10 Designing, conducting, and reporting RCTs should incorporate methods—such as  
11 concealing randomised allocation, blinding participants and personnel, and  
12 appropriately engaging the intention-to-treat population—that avoid biases resulting  
13 from incompatibilities between the intervention and control groups. Empirical  
14 evidence suggests that the absence of rigorous methodology can lead to biased  
15 intervention effect estimates (i.e., net benefits) (28). Contextual factors, such as  
16 population and trial characteristics, also have been shown to be possible effect  
17 modifiers when assessing benefits (8, 29).  
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24 The effect on harms of RoB, trial characteristics and contextual factors (e.g.,  
25 population characteristics) has yet to be investigated, and using meta-epidemiology is  
26 the method of choice for doing so (30). Previous meta-epidemiological research  
27 within rheumatology has primarily investigated the effect of methodological quality  
28 (internal validity) on treatment effects (benefit) (8, 29, 31, 32). To our knowledge, no  
29 one has yet investigated the importance in IA therapies of contextual factors (i.e.,  
30 population and trial characteristics) and RoB when the outcome is harmful effects.  
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## 38 **Aims and objectives**

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40 This exploratory meta-epidemiological study aims to improve harm reporting by  
41 investigating the influence of RoB domains, trial characteristics, and contextual  
42 factors on the three harm measures: all withdrawals (WD), withdrawals due to  
43 adverse events (WD d/t AEs), and serious adverse events (SAEs) (17), as well as  
44 mortality among patients with IA who were treated with bDMARDs and/or tsDMARDs.  
45 Our objective is to explore whether specific participant and trial characteristics (i.e.,  
46 contextual factors including RoB domains) have a quantitative influence in terms of  
47 effect modification and/or distortion due to biases on the observed likelihood of harm  
48 from an experimental intervention compared to control comparators in randomised  
49 trials. If contextual factors have such an influence, we hope to shed light on their  
50 importance to future trial reporting and interpretation of harm when reporting  
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1 randomised trials (17).  
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#### 4 **Protocol and registration**

5 This protocol was developed in accordance with the v1.07 2018 Methodological  
6 Expectations for Cochrane Intervention Reviews (MECIR) recommendations of the  
7 Cochrane Collaboration (33) and reported according to the Preferred Reporting Items  
8 for Systematic Reviews and Meta-Analyses extension for Protocols (PRISMA-P)  
9 guidelines (34). The study protocol was pre-specified and registered in PROSPERO  
10 on 2020-03-27, CRD number: CRD42020171124.  
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### 18 **METHODS AND ANALYSIS**

19 This (meta-epidemiological) study combines data from a large representative sample  
20 of available trials into a single database by assembling trials already included in  
21 published systematic reviews. Generic outcome measures that cover important harm  
22 domains (*i*: WD, *ii*: WD d/t AEs and *iii*: SAEs (17)) and mortality will constitute the  
23 dependent variable(s) in the database. Harm effects in relation to the use of targeted  
24 therapies will be analysed to determine whether they are affected by contextual  
25 factors among population and trial characteristics.  
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#### 34 **Eligibility criteria**

35 We will search MEDLINE (via PubMed) for systematic reviews (published since April  
36 2015) or Cochrane reviews. From these systematic reviews, included randomised trials  
37 will (independent of publication year) be eligible if they fulfil our inclusion criteria (see  
38 table 1 for PICO framework), with at least one group randomly allocated to bDMARD  
39 and/or tsDMARD.  
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45 The interventions of interest are targeted therapies (i.e., bDMARDs and  
46 tsDMARDs) approved by either EMA or FDA to date, treating IA conditions in adult  
47 populations. These therapies will include bDMARDs: abatacept, adalimumab, anakinra,  
48 certolizumab, etanercept, golimumab, guselkumab, infliximab, ixekizumab, rituximab,  
49 sarilumab, secukinumab, tocilizumab, ustekinumab, and tsDMARDs: apremilast,  
50 baricitinib, filgotinib, tofacitinib and upadacitinib.  
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55 Only RCTs included in an existing systematic review of patients with  
56 inflammatory arthritis (RA, PsA, and AxSpA [including AS]) will be considered for  
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eligibility. We will exclude reviews (i.e., not look for trials) that have been withdrawn. Furthermore, only RCTs from the eligible systematic reviews where the full text is available in English will be included. There will be no restriction on publication year of the individual RCTs.

Table 1. Research objective described using PICO\*

<b>Participants</b>	<b>Adult patients with rheumatoid arthritis (RA), psoriatic arthritis (PsA), axial spondyloarthritis (axSpA) or ankylosing spondylitis (AS).</b>
<b>Intervention</b>	Targeted therapies (i.e., bDMARDs and tsDMARDs)
<b>Comparison</b>	Placebo, standard care or waiting list/no intervention, active comparator and unclear (i.e. comparison described in insufficient detail to fit within the other categories).
<b>Outcome(s)</b>	Number of withdrawals (WDs), number of WDs due to adverse events (WD d/t AEs), number of serious adverse events (SAEs) and number of patients who died.

\*PICO - participants, intervention, comparison, and outcome.

## Information sources and search strategy

We will search MEDLINE (via PubMed) for eligible meta-analyses or systematic reviews of trials published since April 2015 and eligible Cochrane reviews using the search algorithm shown in table 2:

Table 2. Search strategy

```
(arthritis[tiab] OR spondyloarthritis[tiab] OR ankylosing[tiab] OR psoriatic[tiab] OR
Spondylarthropathies[tiab] OR rheumatoid[tiab] OR Psoriasis[tiab])

AND

("disease-modifying antirheumatic drugs"[tiab] OR "biological agent"[tiab] OR biologics*[tiab] OR
DMARD[tiab] OR abatacept[tiab] OR adalimumab[tiab] OR anakinra[tiab] OR apremilast[tiab] OR
baricitinib[tiab] OR certolizumab[tiab] OR etanercept[tiab] OR filgotinib[tiab] OR golimumab[tiab] OR
guselkumab[tiab] OR infliximab[tiab] OR ixekizumab[tiab] OR rituximab[tiab] OR sarilumab[tiab] OR
secukinumab[tiab] OR tocilizumab[tiab] OR tofacitinib[tiab] OR upadacitinib[tiab] OR
ustekinumab[tiab])

AND

(("Systematic Review"[pt] OR Meta-Analysis[pt] OR meta-analysis[tiab] OR "systematic review"[tiab]
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OR meta-analys*[pt] OR meta-analys*[ti] OR metaanalys*[ti] OR meta-regress*[tiab] OR  
metaregress*[tiab]  
AND ("2015/04/01"[Date - Publication]: "3000"[Date - Publication])  
OR "Cochrane Database Syst Rev" [jour])
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## Study selection

Two independent reviewers (JB and EM, with support from SMN/RC) will screen the systematic reviews based on title and abstract, in accordance with eligibility criteria. The same two reviewers will assess the full systematic review texts for eligibility of the reviews and subsequently select the RCTs from the reviews that are eligible, according to our objectives. We will obtain the full text if at least one of the reviewers considers an RCT to be potentially eligible during the screening process. Disagreements will be resolved by consensus or by consulting a third reviewer (RC). EndNote X9.2 software will be used to manage the reviews and RCT records retrieved from the search.

## Data collection process

Two reviewers (JB and EM) will extract data using a predefined, standardised data extraction form, and in case of uncertainty a third reviewer (SMN/RC) will be consulted. If a trial is included in more than one review, the trial will be registered and counted/included once.

***Review Level:*** From the reviews, we will extract data on review registration number, year of publication, first author's name, number of RCTs eligible for our study, and the condition and intervention studied, according to the review title.

***Randomised Trial Level:*** From the trials, we will extract data on first author's name, publication ID, trial duration, duration until switch (e.g., relevant for adaptive trial designs), rescue, early escape or cross over, number of participants in each arm, and treatment given in the active and comparator arms (i.e., following the PICO framework). Treatment in the comparator arm will be grouped into the following predefined categories: (i) placebo; (ii) standard care or waiting list/no intervention; (iii) active comparator, or as an ultimate last option; (iv) unclear. Outcome measures and data extraction of trial and participant characteristics are specified below and listed in

1 table 3.

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4 **Participant characteristics in individual studies**

5 *Data on the following trial eligibility criteria will be extracted:*

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- Binary indicator (0 or 1) of inflammation scored as 1 with  $\geq 1$  of the following criteria: erythrocyte sedimentation rate (ESR)  $\geq 28$  mm/hour, CRP level  $\geq 0.3$  mg/dL, and/or morning stiffness lasting  $\geq 45$  minutes
  - minimum AND maximum required number of swollen joint counts (SJC)
  - minimum AND maximum required number of tender joint counts (TJC)
  - minimum AND maximum allowed disease duration
  - rheumatoid factor (RF) and/or anti-cyclic citrullinated peptide antibody (anti-CCP) and/or anti-cyclic citrullinated peptide antibody 2 (CCP2) status

22 In order to stratify trials according to the DMARD history of their included patients, we  
23 will ask the following signalling question: Had the participants, prior to inclusion,  
24 potentially exhausted the treatment potential of at least one class of DMARD—either  
25 conventional synthetic DMARDs (i.e., [csDMARD], bDMARD, or tsDMARD)?

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- csDMARD-naïve (patients were either csDMARD naïve or had not exhausted the treatment potential of at least one csDMARD)
  - csDMARD-IR (csDMARD inadequate responders), where patients had exhausted at least one csDMARD option previously
  - bDMARD or tsDMARD-IR (bDMARD or tsDMARD inadequate responders), patients had inadequate response to at least one previous bDMARD or tsDMARD. Inclusion in this group entails exclusion from other DMARD history groups.

42 *Patients' concomitant medication (background) of DMARDs during the trial period will*  
43 *be ordered in the following three levels:*

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- methotrexate (MTX)
  - csDMARDs other than MTX
  - bDMARDs or tsDMARDs

50 We will extract information about how the three groups were handled at  
51 randomisation, potentially enabling us to cluster the trials into one of the following five  
52 levels: (i) Naïve (i.e., patients had never used the drug[s] of interest); (ii) Not using  
53 (i.e., the study included only patients who were currently not using the drug[s] of  
54 interest); (iii) Discontinued (i.e., patients were not allowed to continue drug[s] of  
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1 interest; (iv) Continued (i.e., patients were allowed to continue drug[s] of interest);  
2 and (v) Not reported (unclear: no information was reported on this matter). In the  
3 case of axSpa, NSAID will be extracted equivalent to csDMARDs.  
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7 *Data on the following aggregate (average/median) patient baseline characteristics will*  
8 *be extracted:* age, female (proportion), disease duration (years), ESR (mm/hour),  
9 CRP (mg/dL), Disease activity score, RF positive (proportion), anti-CCP positive  
10 (proportion), anti-CCP2 positive (proportion), SJC, TJC, health assessment  
11 questionnaire—disability index (HAQ-DI), physician global assessment (e.g., Visual  
12 Analogue Scale [VAS]), patient global assessment (e.g., VAS), and patient-reported  
13 pain on visual analogue scales of 0–100 mm (e.g., VAS).  
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### 21 **Risk of bias and trial characteristics in individual studies**

22 Many published reviews include some form of RoB assessment (i.e., at least for the  
23 most frequently used RoB domains) for each individual trial; these assessments will  
24 be mapped to the best of our ability to correspond to the Cochrane RoB v.1 (35). The  
25 RoB will also be assessed by one of the two reviewers (JB or EM) and subsequently  
26 compared with the original bias and internal validity assessments' in the review, from  
27 which it was sampled.  
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33 Within each full-text trial report, we will apply the following domains of the original  
34 Cochrane RoB tool (i.e., RoB v.1.0) (35), which comprise methods for:  
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- 36 • sequence generation/maintaining allocation concealment (selection bias)
- 37 • blinding both patients and personnel (performance bias)
- 38 • management/analysis/reporting of incomplete outcome data (attrition bias)
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43 Each of these three domains will be rated as high risk, low risk, or unclear RoB (35).  
44 In case of uncertainty, another reviewer (SMN/RC) will be consulted. Any  
45 discrepancy between RoB assessment sources will be resolved by discussion among  
46 the authors.  
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51 The following additional bias sources will also be assessed, and data will be  
52 extracted from them:  
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- 54 • single vs. multi-site trials (36)
- 55 • small vs. large trials (where small will pragmatically be defined as <100 patients per
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arm) (37, 38)

- source of funding grouped into one of the following five categories: (i) 100% industry (pharmaceutical/device company) funded; (ii) mixed funding (e.g., non-industry and industry; (iii) provision of drug only; (iv) 100% non-profit funded; and (v) unclear/undisclosed funding (39)

## Outcome measures

Data extraction for each RCT will include the number of patients who died, and the numbers of patients with any of the following “generic events”: (i) all withdrawals (WDs); (ii) WDs due to AEs; and (iii) SAEs (17). If the number of individual patients with SAEs is not reported, we will extract the number of reported SAEs instead.

Where reasons are provided to explain the SAEs, they will be categorised according to MedDRA v.23.0 [(i) Infections and infestations; (ii) Neoplasms benign, malignant and unspecified (including cysts and polyps); (iii) Cardiac and vascular disorders; or (iv) others]. If patients in the comparison group later are offered the intervention (i.e., switching to the intervention group), the number of events before the switch will be used as the endpoint of choice (i.e., before introducing adaptive trial designs).

## Summary measures

For each binary outcome, we will extract data corresponding to the 2×2 table, summarising the number of patients who experienced the outcome in each comparison group as reported in the randomised trial and the total number of patients randomly assigned in each group. For outcomes collected and reported corresponding to different time points, we will select the time point with the longest follow-up while still respecting the primary research design (e.g., before introducing an adaptive trial design, and/or open label extension) (40, 41).

Because all the outcome measures are dichotomous, the relative Risk Ratios (RRs) with 95% confidence intervals (95%CI) will be the preferred measure of relative effect, and these can subsequently be applied to the baseline or control group risks to generate absolute risks (42). When appropriate for the very rare adverse events, we will use a continuity correction (adding to all cells a factor proportional to the reciprocal of the size of the contrasting study group), as suggested by Sweeting and colleagues (43), to take into account zero cell counts in one group only. This continuity correction will be applied when no events are

observed in one study arm of a trial. The correction is inversely proportional to the relative size of the opposite of the study (21, 43). Continuity correction for the experimental intervention arm is  $1/(R+1)$ ;  $R$  is the ratio of control group to intervention group sizes (i.e.,  $R = n_C/n_I$ ). Similarly, the continuity correction for the control comparator arm is  $R/(R+1)$ . We expect that most trials will report only a few SAEs and deaths, so the odds ratios and 95%CI's will also (for the purpose of sensitivity analysis) be calculated with the use of the *Peto* method. Because the expected events are sparse and all trials will have similar durations of follow-up for their treatment groups, the use of both risk ratios and odds ratios should represent a valid approach to assessing the risk associated with the use of synthetic or biological intervention in patients with IA. The number of studies to be included will be determined by the number of eligible trials available in the systematic reviews, hence a formal sample size calculation would not be meaningful. However, we expect the search to bring around 175 eligible trials (RA: 117, PsA: 15, AxSpA: 43) based on a few large systematic reviews within the field (44-48).

## Synthesis of results

Outcome events will be coded so that an RR direction of more than 1 indicates a potentially harmful effect of the experimental intervention (i.e.,  $RR = [r_I/n_I] / [r_C/n_C]$ ). Mixed effects Restricted Maximum Likelihood (REML) meta-analyses (49) will be used to combine the harm effects across RCTs (based on their log  $[RR]$ ) (50); we will apply the trial ID as a random effect, while applying the review ID (from which the trial was sampled) as a fixed effect in order to model the hierarchical structure of the data sampling (51).

Heterogeneity across randomised comparisons will be assessed by using the Cochran Q test (52), interpreted based on the  $I^2$  inconsistency index (53), and quantified by the estimate for between-trial variance ( $\tau^2$ ), estimated as  $T^2$  (54). The effect of population and trial characteristics (listed below) on the between-trial variance will be calculated by univariably adding a factor for the specific characteristic in the model. If introducing a specific covariate into the meta-model reduces the observed between-trial variance ( $T^2$ ), this result will be considered an indication of a potentially important effect modifier (55).

Further analyses might (if possible) include multivariable models (56).

Observational by nature, meta-epidemiological studies like the present should be

1 expected to have some degree of meta-confounding because prognostic factors  
 2 might be unequally distributed between studies exposed (trial characteristic positive)  
 3 or not. We will attempt to adjust for possible confounding covariates (i.e. “de-  
 4 confound”) the inference. That is, we will explore the ability to adjust for any important  
 5 preexposure covariate ‘ C ’ (i.e., something that happened before the “*study design*  
 6 *variable of interest was generated*”) that is potentially unequally distributed between  
 7 the meta-epidemiological exposure groups (E: Exposed vs. Unexposed), which is  
 8 ALSO an ancestor (i.e., likely cause) of the trial outcome (i.e., a more exaggerated  
 9 risk of harm):  $M_E \leftarrow C \rightarrow Y_E$  (56).  
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17 *Table 3. Population and trial characteristics*

<b>Trial eligibility criteria:</b>	
	Minimum and maximum required number of swollen joint counts
	Minimum and maximum required number of tender joint counts
	Minimum and maximum required C-reactive protein
	Minimum and maximum required Erythrocyte sedimentation rate
	Minimum and maximum allowed disease duration
	Rheumatoid factor
	Anti-cyclic citrullinated peptide antibody status
	Anti-cyclic citrullinated peptide antibody 2 status
<b>DMARD history:</b>	
	csDMARD-naïve
	csDMARD-IR (csDMARD inadequate responders)
	bDMARD or tsDMARD-IR (bDMARD or tsDMARD inadequate responders)
<b>Medication background of DMARDs:</b>	
	Methotrexate
	-Naïve
	-Not using
	-Discontinued
	-Continued
	-Not reported
	csDMARDs other than methotrexate
	-Naïve
	-Not using
	-Discontinued

1 -Continued  
 2 -Not reported  
 3  
 4 bDMARDs or tsDMARDs.  
 5 -Naïve  
 6 -Not using  
 7  
 8 -Discontinued  
 9 -Continued  
 10  
 11 -Not reported  
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13 **Aggregate (e.g., average/median) patient baseline characteristics:**  
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15 Age  
 16 Female (%)  
 17 Disease duration  
 18 Erythrocyte sedimentation rate  
 19 C-reactive protein  
 20 Disease activity score  
 21 RF positive (%)  
 22 Anti-CCP positive (%)  
 23 CCP2 positive (%)  
 24 Swollen joint counts  
 25 Tender joint counts  
 26 Health assessment questionnaire—disability index  
 27 Physician global assessment of disease activity  
 28 Patient global assessment of disease activity  
 29 Patient-reported pain on visual analogue scales of 0–100 mm  
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 39 **Risk of bias across studies**  
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41 Stratified meta-analyses will be used for tests of interaction between harms and the  
 42 trial RoB (listed in Table 4) and trial characteristics collected as described above.  
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46 *Table 4. Risk of bias*  
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48 **Cochrane risk of bias domains:**  
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- 50 · Risk of selection bias
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  - 52 · Risk of performance bias
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  - 54 · Risk of attrition bias
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  - 56 · Overall risk of bias\*
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**Additional bias sources:**

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- Single vs. multi-site trials
  - Small vs. large trials
  - Source of funding
- 

\*For each trial, the overall RoB will be classified as low (i.e., low RoB for all three domains); high (i.e., high RoB for one or more domains); or unclear (i.e., unclear RoB for one or more domains in the absence of high RoB).

## Perspectives

The Outcome Measures in Rheumatology (OMERACT) initiative established the Contextual Factors Working Group to guide the understanding, identification and handling of contextual factors for clinical trials, with most of the current emphasis' being on net benefit inferred from a rheumatology trial (57). This meta-epidemiological study will work from the original definition of what constitutes a contextual factor, as defined in the introduction. We will explore and hope to reveal the possible impact of contextual factors (i.e., population and trial characteristics) and RoB domains of three different (but related) harm measures, as well as deaths (58). Knowing which factors are associated with a causal model for harms—either as effect modifiers or distortions of the outcome due to bias—is important for improving investigation and reporting of harms in future trials (59). If future trials report harms according to important contextual factors, meta-analyses would be able to investigate contextual factors for harms without relying on getting access to individual patient data. Such meta-research might identify subgroups among rheumatic disease patients that are at higher risk of experiencing harms. Such information would provide important evidence for future treatment guideline development. Ultimately the doctor will be able to differentiate the risk of intervention based on the patient's characteristics. This has the potential to enhance informed decision-making and effect therapeutic interventions applied in practice, leading to safer treatment of individual patients and increase efficiency in the health care system.

## Patient and public involvement

Patients and/or the public were not involved in designing study concept or drafting of the protocol.

## ETHICS AND DISSEMINATION

Because our study does not collect primary data, no formal ethical assessment and informed consent are required. First, second and third author (EM, JB and SMN) will draft the paper

describing this meta-epidemiological study; the study will be disseminated in a peer-reviewed publication.

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**PRISMA-P (Preferred Reporting Items for Systematic review and Meta-Analysis Protocols) 2015 checklist: recommended items to address in a systematic review protocol\***

Section and topic	Item No	Checklist item
<b>ADMINISTRATIVE INFORMATION</b>		
Title:		
Identification	1a	Identify the report as a protocol of a systematic review
Update	1b	If the protocol is for an update of a previous systematic review, identify as such
Registration	2	If registered, provide the name of the registry (such as PROSPERO) and registration number
Authors:		
Contact	3a	Provide name, institutional affiliation, e-mail address of all protocol authors; provide physical mailing address of corresponding author
Contributions	3b	Describe contributions of protocol authors and identify the guarantor of the review
Amendments	4	If the protocol represents an amendment of a previously completed or published protocol, identify as such and list changes; otherwise, state plan for documenting important protocol amendments
Support:		
Sources	5a	Indicate sources of financial or other support for the review
Sponsor	5b	Provide name for the review funder and/or sponsor
Role of sponsor or funder	5c	Describe roles of funder(s), sponsor(s), and/or institution(s), if any, in developing the protocol
<b>INTRODUCTION</b>		
Rationale	6	Describe the rationale for the review in the context of what is already known
Objectives	7	Provide an explicit statement of the question(s) the review will address with reference to participants, interventions, comparators, and outcomes (PICO)
<b>METHODS</b>		
Eligibility criteria	8	Specify the study characteristics (such as PICO, study design, setting, time frame) and report characteristics (such as years considered, language, publication status) to be used as criteria for eligibility for the review
Information sources	9	Describe all intended information sources (such as electronic databases, contact with study authors, trial registers or other grey literature sources) with planned dates of coverage
Search strategy	10	Present draft of search strategy to be used for at least one electronic database, including planned limits, such that it could be repeated
Study records:		
Data management	11a	Describe the mechanism(s) that will be used to manage records and data throughout the review

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3	Selection process	11b	State the process that will be used for selecting studies (such as two independent reviewers) through each phase of the review (that is, screening, eligibility and inclusion in meta-analysis)
4			
5	Data collection process	11c	Describe planned method of extracting data from reports (such as piloting forms, done independently, in duplicate), any processes for obtaining and confirming data from investigators
6			
7	Data items	12	List and define all variables for which data will be sought (such as PICO items, funding sources), any pre-planned data assumptions and simplifications
8			
9	Outcomes and prioritization	13	List and define all outcomes for which data will be sought, including prioritization of main and additional outcomes, with rationale
10			
11	Risk of bias in individual studies	14	Describe anticipated methods for assessing risk of bias of individual studies, including whether this will be done at the outcome or study level, or both; state how this information will be used in data synthesis
12			
13	Data synthesis	15a	Describe criteria under which study data will be quantitatively synthesised
14		15b	If data are appropriate for quantitative synthesis, describe planned summary measures, methods of handling data and methods of combining data from studies, including any planned exploration of consistency (such as $I^2$ , Kendall's $\tau$ )
15		15c	Describe any proposed additional analyses (such as sensitivity or subgroup analyses, meta-regression)
16		15d	If quantitative synthesis is not appropriate, describe the type of summary planned
17			
18	Meta-bias(es)	16	Specify any planned assessment of meta-bias(es) (such as publication bias across studies, selective reporting within studies)
19			
20	Confidence in cumulative evidence	17	Describe how the strength of the body of evidence will be assessed (such as GRADE)
21			

**\* It is strongly recommended that this checklist be read in conjunction with the PRISMA-P Explanation and Elaboration (cite when available) for important clarification on the items. Amendments to a review protocol should be tracked and dated. The copyright for PRISMA-P (including checklist) is held by the PRISMA-P Group and is distributed under a Creative Commons Attribution Licence 4.0.**

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# BMJ Open

## Risk of Harm in Synthetic and Biological Intervention Trials in Patients with Inflammatory Arthritis: Protocol for A Meta-Epidemiological Study Focusing on Contextual Factors

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# Risk of Harm in Synthetic and Biological Intervention Trials in Patients with Inflammatory Arthritis: Protocol for A Meta-Epidemiological Study Focusing on Contextual Factors

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### 56 *Disclaimers*

57 The views expressed in the submitted protocol are the authors' own and not an official position of  
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### 62 *Contributions*

63 Study concept and design: EM, JB, SMN, TE, LEK, RC, JPAI, ST, DF, JSS, PCT.

64 Drafting on the protocol: EM, JB, SMN, TE, LEK, RC, JPAI, ST, DF, JSS, PCT.

65 Critical revision of the protocol for important intellectual content and final approval before submission: All authors.

66 Guarantor of the protocol: RC.

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### 68 *Competing interests*

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### 75 *Amendments*

76 Important deviations from the protocol will be reported in the peer-reviewed publication.

## ABSTRACT

**Introduction:** Inflammatory Arthritis (IA) conditions, including rheumatoid arthritis (RA), psoriatic arthritis (PsA), and axial spondyloarthritis (AxSpA), are characterised by inflammatory infiltration of the joints. Biologic and targeted synthetic disease-modifying antirheumatic drugs (bDMARDs and tsDMARDs, respectively) reduce the effects of proinflammatory cytokines and immune cells to ameliorate disease. However, immunosuppression can be associated with high rates of serious adverse events (SAEs), including serious infections, and maybe an increased risk of malignancies and cardiovascular events. Currently, there is no empirical evidence on the extent to which contextual factors and risk of bias (RoB) domains may modify these harm signals in randomised trials.

**Method and analysis:** We will search MEDLINE (via PubMed) for systematic reviews published since April 2015 and all Cochrane reviews. From these reviews, randomised trials will be eligible if they include patients with an IA condition with at least one group randomly allocated to bDMARD and/or tsDMARD treatments. A predefined form will be used for extracting data on population characteristics (e.g., baseline characteristics or eligibility criteria, such as medication background), and specific harm outcome measures, such as number of withdrawals, numbers of patients discontinuing due to adverse events, and number of patients having SAEs. RoB in individual trials will be assessed using a modified Cochrane RoB tool. We will estimate the potentially causal harm effects related to the experimental intervention compared to control comparator as risk ratios, and heterogeneity across randomised comparisons will be assessed statistically and evaluated as inconsistency using the  $I^2$  Index. Our meta-regression analyses will designate population and trial characteristics, and each RoB domain as independent variables, whereas the three harm domains will serve as dependent variables.

**Ethics and dissemination:** Ethics approval is not required for this study. Results will be disseminated through publication in international peer-reviewed journals.

**Registration:** PROSPERO (CRD: 42020171124).

## Strengths and limitations of this study

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- This will be an extensive and comprehensive risk of harm analysis of bDMARDs and tsDMARDs across multiple IA diagnoses unlike previous assessments that have been more circumscribed.
- A large array of contextual factors and risk of bias items will be assessed.
- The study selection will be done by two independent reviewers.
- Despite the comprehensive nature of the assessment, the study may be limited by poor reporting (i.e., lack of data/information for certain contextual factors and uncommon harms), and some meta-regression assessments may be affected by ecological bias due to the use of aggregated data, and meta-confounding.

## INTRODUCTION

### Background

Inflammatory Arthritis (IA) is a heterogeneous group of autoimmune diseases that includes rheumatoid arthritis (RA), psoriatic arthritis (PsA), axial spondyloarthritis (axSpA, including ankylosing spondylitis AS) (1, 2). These diseases are characterised by inflammatory infiltration of the joints (3), resulting in pain, swelling, stiffness and restricted movement (4). Ultimately, they can have a detrimental impact on quality of life, cause progressive disability and premature death (5, 6). Not only are the implications severe, also the diseases are a global concern; RA alone affects about 1% of the world's population (7).

Aside from conventional synthetic (cs) DMARDs including methotrexate, targeted therapies, consisting of biological disease-modifying antirheumatic drugs (bDMARDs) and targeted synthetic DMARDs (tsDMARDs) are considered effective for treating IA *per se* (8-10). Notably, bDMARDs work by targeting specific molecules or receptors (11), such as tumour necrosis factor alpha (TNF $\alpha$ ), which is a potent inflammatory cytokine produced by T-cells and macrophages (12, 13). In contrast, tsDMARDs target intracellular pathways and reduce the effect of cytokines known to drive the proinflammatory machinery of cellular immune response (14-16). As such, b- and tsDMARDs are Immunomodulatory; although effective in alleviating symptoms of IA, they also carry risk of harm (defined as: "*the totality of possible adverse consequences of an intervention or therapy*" (17)). Indeed, meta-analyses and an observational cohort study have shown that bDMARDs are associated with higher rates of serious infections (18-20) and potentially dose-dependent increased risk of malignancies (21). Some meta-studies and systematic literature reviews suggest that tsDMARD rates of serious infections and malignancies are no different from those of bDMARDs (16, 22, 23). Recent reviews report a possibly increased risk of venous thromboembolism with tsDMARDs (23, 24).

Randomised controlled trials (RCTs) inevitably vary with respect to eligibility criteria, patient characteristics, and internal validity, which may distort their results (i.e., the harm signal) and thus potentially bias their interpretation (25, 26). If evidence were available on which trial characteristics to adjust for when interpreting harm from meta-research, these covariates would be considered important contextual factors. Currently, a contextual factor is broadly defined as a "*...variable that is not an outcome of the study but needs to be recognized (and measured) to understand the study results. This*

160 *includes potential confounders and effect modifiers*" (27). However, we currently have no  
161 empirical evidence concerning the extent to which contextual factors, such as population  
162 and trial characteristics and risk of bias (RoB) domains, modify the harm signals from  
163 trials testing targeted therapies (i.e., bDMARDs and tsDMARDs) across IA diseases.  
164

## 165 **Rationale**

166 Designing, conducting, and reporting RCTs should incorporate methods—such as  
167 concealing randomised allocation, blinding participants and personnel, and  
168 appropriately engaging the intention-to-treat population—that avoid biases resulting  
169 from incompatibilities between the intervention and control groups. Empirical  
170 evidence suggests that the absence of rigorous methodology can lead to biased  
171 intervention effect estimates (i.e., net benefits) (28). Contextual factors, such as  
172 population and trial characteristics, also have been shown to be possible effect  
173 modifiers when assessing benefits (8, 29).

174 The effect on harms of RoB, trial characteristics and contextual factors (e.g.,  
175 population characteristics) has yet to be investigated, and using meta-epidemiology is  
176 the method of choice for doing so (30). Previous meta-epidemiological research  
177 within rheumatology has primarily investigated the effect of methodological quality  
178 (internal validity) on treatment effects (benefit) (8, 29, 31, 32). To our knowledge, no  
179 one has yet investigated the importance in IA therapies of contextual factors (i.e.,  
180 population and trial characteristics) and RoB when the outcome is harmful effects.  
181

## 182 **Aims and objectives**

183 This exploratory meta-epidemiological study aims to improve harm reporting by  
184 investigating the influence of RoB domains, trial characteristics, and contextual  
185 factors on the three harm measures: all withdrawals (WD), withdrawals due to  
186 adverse events (WD d/t AEs), and serious adverse events (SAEs) (17), as well as  
187 mortality among patients with IA who were treated with bDMARDs and/or tsDMARDs.  
188 Our objective is to explore whether specific participant, drug classes, and trial  
189 characteristics (i.e., contextual factors including RoB domains) have a quantitative  
190 influence in terms of effect modification and/or distortion due to biases on the  
191 observed likelihood of harm from an experimental intervention compared to control  
192 comparators in randomised trials. If contextual factors have such an influence, we  
193 hope to shed light on their importance to future trial reporting and interpretation of

194 harm when reporting randomised trials (17).  
195

## 196 **Protocol and registration**

197 This protocol was developed in accordance with the v1.07 2018 Methodological  
198 Expectations for Cochrane Intervention Reviews (MECIR) recommendations of the  
199 Cochrane Collaboration (33) and reported according to the Preferred Reporting Items  
200 for Systematic Reviews and Meta-Analyses extension for Protocols (PRISMA-P)  
201 guidelines (34). The study protocol was pre-specified and registered in PROSPERO  
202 on 2020-03-27, CRD number: CRD42020171124.  
203

## 204 **METHODS AND ANALYSIS**

205 This meta-epidemiological study combines data from a large representative sample  
206 of available trials into a single database by assembling trials already included in  
207 published systematic reviews. Generic outcome measures that cover important  
208 harm domains (*i*: WD, *ii*: WD d/t AEs and *iii*: SAEs (17)) and mortality will constitute  
209 the dependent variable(s) in the database. Harm effects in relation to the use of  
210 targeted therapies will be analysed to determine whether they are affected by  
211 contextual factors among population, drug classes (e.g., biologics vs small  
212 molecules) and trial characteristics.  
213

### 214 **Eligibility criteria**

215 We will search MEDLINE (via PubMed) for systematic reviews (published since April  
216 2015) or Cochrane reviews. From these systematic reviews, included randomised trials  
217 will (independent of publication year) be eligible if they fulfil our inclusion criteria (see  
218 table 1 for PICO framework), with at least one group randomly allocated to bDMARD  
219 and/or tsDMARD.  
220

221 The interventions of interest are targeted therapies (i.e., bDMARDs and  
222 tsDMARDs) approved by either EMA or FDA to date, treating IA conditions in adult  
223 populations; this pharmacological distinction will also be used for separate stratified  
224 analyses. These therapies will include bDMARDs: abatacept, adalimumab, anakinra,  
225 certolizumab, etanercept, golimumab, guselkumab, infliximab, ixekizumab, rituximab,  
226 sarilumab, secukinumab, tocilizumab, ustekinumab, and tsDMARDs: apremilast,  
227 baricitinib, filgotinib, tofacitinib and upadacitinib.  
228



Only RCTs included in an existing systematic review of patients with inflammatory arthritis (RA, PsA, and AxSpA [including AS]) will be considered for eligibility. We will exclude reviews (i.e., not look for trials) that have been withdrawn. Furthermore, only RCTs from the eligible systematic reviews where the full text is available in English will be included. There will be no restriction on publication year of the individual RCTs.

Table 1. Research objective described using PICO\*

<b>Participants</b>	<b>Adult patients with rheumatoid arthritis (RA), psoriatic arthritis (PsA), axial spondyloarthritis (axSpA) or ankylosing spondylitis (AS).</b>
<b>Intervention</b>	Targeted therapies (i.e., bDMARDs and tsDMARDs)
<b>Comparison</b>	Placebo, standard care or waiting list/no intervention, active comparator and unclear (i.e. comparison described in insufficient detail to fit within the other categories).
<b>Outcome(s)</b>	Number of withdrawals (WDs), number of WDs due to adverse events (WD d/t AEs), number of serious adverse events (SAEs) and number of patients who died.

\*PICO - participants, intervention, comparison, and outcome.

## Information sources and search strategy

We will search MEDLINE (via PubMed) for eligible meta-analyses or systematic reviews of trials published since April 2015 and eligible Cochrane reviews using the search algorithm shown in table 2:

Table 2. Search strategy

```
(arthritis[tiab] OR spondyloarthritis[tiab] OR ankylosing[tiab] OR psoriatic[tiab] OR
Spondylarthropathies[tiab] OR rheumatoid[tiab] OR Psoriasis[tiab])

AND

("disease-modifying antirheumatic drugs"[tiab] OR "biological agent"[tiab] OR biologics*[tiab] OR
DMARD[tiab] OR abatacept[tiab] OR adalimumab[tiab] OR anakinra[tiab] OR apremilast[tiab] OR
baricitinib[tiab] OR certolizumab[tiab] OR etanercept[tiab] OR filgotinib[tiab] OR golimumab[tiab] OR
guselkumab[tiab] OR infliximab[tiab] OR ixekizumab[tiab] OR rituximab[tiab] OR sarilumab[tiab] OR
secukinumab[tiab] OR tocilizumab[tiab] OR tofacitinib[tiab] OR upadacitinib[tiab] OR
ustekinumab[tiab])
```

```

1 AND
2 ((“Systematic Review”[pt] OR Meta-Analysis[pt] OR meta-analysis[tiab] OR “systematic review”[tiab]
3 OR meta-analys*[pt] OR meta-analys*[ti] OR metaanalys*[ti] OR meta-regress*[tiab] OR
4 metaregress*[tiab]
5
6 AND (“2015/04/01”[Date - Publication]: “3000”[Date - Publication]))
7
8 OR “Cochrane Database Syst Rev” [jour])
9

```

## Study selection

Two independent reviewers (JB and EM, with support from SMN/RC) will screen the systematic reviews based on title and abstract, in accordance with eligibility criteria. The same two reviewers will assess the full systematic review texts for eligibility of the reviews and subsequently select the RCTs from the reviews that are eligible, according to our objectives. We will obtain the full text if at least one of the reviewers considers an RCT to be potentially eligible during the screening process. Disagreements will be resolved by consensus or by consulting a third reviewer (RC). EndNote X9.2 software will be used to manage the reviews and RCT records retrieved from the search.

## Data collection process

Two reviewers (JB and EM) will extract data using a predefined, standardised data extraction form, and in case of uncertainty a third reviewer (SMN/RC) will be consulted. If a trial is included in more than one review, the trial will be registered and counted/included once.

**Review Level:** From the reviews, we will extract data on review registration number, year of publication, first author’s name, number of RCTs eligible for our study, and the condition and intervention studied, according to the review title.

**Randomised Trial Level:** From the trials, we will extract data on first author’s name, publication ID, trial duration, duration until switch (e.g., relevant for adaptive trial designs), rescue, early escape or cross over, number of participants in each arm, and treatment given in the active and comparator arms (i.e., following the PICO framework). Treatment in the comparator arm will be grouped into the following predefined categories: (i) placebo; (ii) standard care or waiting list/no intervention; (iii)

active comparator, or as an ultimate last option (*iv*) unclear. Outcome measures and data extraction of trial and participant characteristics are specified below and listed in table 3.

### Participant characteristics in individual studies

Data on the following trial eligibility criteria will be extracted:

- Binary indicator (0 or 1) of inflammation scored as 1 with  $\geq 1$  of the following criteria: erythrocyte sedimentation rate (ESR)  $\geq 28$  mm/hour, CRP level  $\geq 0.3$  mg/dL, and/or morning stiffness lasting  $\geq 45$  minutes
- minimum AND maximum required number of swollen joint counts (SJC)
- minimum AND maximum required number of tender joint counts (TJC)
- minimum AND maximum allowed disease duration
- rheumatoid factor (RF) and/or anti-cyclic citrullinated peptide antibody (anti-CCP) and/or anti-cyclic citrullinated peptide antibody 2 (CCP2) status

In order to stratify trials according to the DMARD history of their included patients, we will ask the following signalling question: Had the participants, prior to inclusion, potentially exhausted the treatment potential of at least one class of DMARD—either conventional synthetic DMARDs (i.e., [csDMARD], bDMARD, or tsDMARD)?

- csDMARD-naïve (patients were either csDMARD naïve or had not exhausted the treatment potential of at least one csDMARD)
- csDMARD-IR (csDMARD inadequate responders), where patients had exhausted at least one csDMARD option previously
- bDMARD or tsDMARD-IR (bDMARD or tsDMARD inadequate responders), patients had inadequate response to at least one previous bDMARD or tsDMARD. Inclusion in this group entails exclusion from other DMARD history groups.

Patients' concomitant medication (background) of DMARDs during the trial period will be ordered in the following three levels:

- methotrexate (MTX)
- csDMARDs other than MTX
- bDMARDs or tsDMARDs

We will extract information about how the three groups were handled at randomisation, potentially enabling us to cluster the trials into one of the following five levels: (*i*) Naïve (i.e., patients had never used the drug[s] of interest); (*ii*) Not using

(i.e., the study included only patients who were currently not using the drug[s] of interest); (iii) Discontinued (i.e., patients were not allowed to continue drug[s] of interest); (iv) Continued (i.e., patients were allowed to continue drug[s] of interest); and (v) Not reported (unclear: no information was reported on this matter). In the case of axSpa, NSAID will be extracted and considered equivalent to csDMARDs.

*Data on the following aggregate (average/median) patient baseline characteristics will be extracted: age, female (proportion), disease duration (years), ESR (mm/hour), CRP (mg/dL), Disease activity score, RF positive (proportion), anti-CCP positive (proportion), anti-CCP2 positive (proportion), SJC, TJC, health assessment questionnaire—disability index (HAQ-DI), physician global assessment (e.g., Visual Analogue Scale [VAS]), patient global assessment (e.g., VAS), and patient-reported pain on visual analogue scales of 0–100 mm (e.g., VAS).*

### **Risk of bias and trial characteristics in individual studies**

Many published reviews include some form of RoB assessment (i.e., at least for the most frequently used RoB domains) for each individual trial; these assessments will be mapped to the best of our ability to correspond to the Cochrane RoB v.1 (35). The RoB will also be assessed by one of the two reviewers (JB or EM) and subsequently compared with the original bias and internal validity assessments' in the review, from which it was sampled.

Within each full-text trial report, we will apply the following domains of the original Cochrane RoB tool (i.e., RoB v.1.0) (35), which comprise methods for:

- sequence generation/maintaining allocation concealment (selection bias)
- blinding both patients and personnel (performance bias)
- management/analysis/reporting of incomplete outcome data (attrition bias)

Each of these three domains will be rated as high risk, low risk, or unclear RoB (35). In case of uncertainty, another reviewer (SMN/RC) will be consulted. Any discrepancy between RoB assessment sources will be resolved by discussion among the authors.

The following additional bias sources will also be assessed, and data will be extracted from them:

- single vs. multi-site trials (36)
- small vs. large trials (where small will pragmatically be defined as <100 patients per arm) (37, 38)
- source of funding grouped into one of the following five categories: (i) 100% industry (pharmaceutical/device company) funded; (ii) mixed funding (e.g., non-industry and industry; (iii) provision of drug only; (iv) 100% non-profit funded; and (v) unclear/undisclosed funding (39)

## Outcome measures

Data extraction for each RCT will include the number of patients who died, and the numbers of patients with any of the following “generic events”: (i) all withdrawals (WDs); (ii) WDs due to AEs; and (iii) SAEs (17). If the number of individual patients with SAEs is not reported, we will extract the number of reported SAEs instead.

Where reasons are provided to explain the SAEs, they will be categorised according to MedDRA v.23.0 [(i) Infections and infestations; (ii) Neoplasms benign, malignant and unspecified (including cysts and polyps); (iii) Cardiac and vascular disorders; or (iv) others]. If patients in the comparison group later are offered the intervention (i.e., switching to the intervention group), the number of events before the switch will be used as the endpoint of choice (i.e., before introducing adaptive trial designs).

## Summary measures

For each binary outcome, we will extract data corresponding to the 2×2 table, summarising the number of patients who experienced the outcome in each comparison group as reported in the randomised trial and the total number of patients randomly assigned in each group. For outcomes collected and reported corresponding to different time points, we will select the time point with the longest follow-up while still respecting the primary research design (e.g., before introducing an adaptive trial design, and/or open label extension) (40, 41).

Because all the outcome measures are dichotomous, the relative Risk Ratios (RRs) with 95% confidence intervals (95%CI) will be the preferred measure of relative effect, and these can subsequently be applied to the baseline or control group risks to generate absolute risks (42). When appropriate for the very rare adverse events, we will use a continuity correction (adding to all cells a factor proportional to the reciprocal of the size of the contrasting study group), as

suggested by Sweeting and colleagues (43), to take into account zero cell counts in one group only. This continuity correction will be applied when no events are observed in one study arm of a trial. The correction is inversely proportional to the relative size of the opposite of the study (21, 43). Continuity correction for the experimental intervention arm is  $1/(R+1)$ ;  $R$  is the ratio of control group to intervention group sizes (i.e.,  $R = n_C/n_I$ ). Similarly, the continuity correction for the control comparator arm is  $R/(R+1)$ . We expect that most trials will report only a few SAEs and deaths, so the odds ratios and 95%CI's will also (for the purpose of sensitivity analysis) be calculated with the use of the *Peto* method. Because the expected events are sparse and all trials will have similar durations of follow-up for their treatment groups, the use of both risk ratios and odds ratios should represent a valid approach to assessing the "risk" associated with the use of synthetic or biological intervention in patients with IA. The number of studies to be included will be determined by the number of eligible trials available in the systematic reviews, hence a formal sample size calculation would not be meaningful. However, we expect the search to bring around 175 eligible trials (RA: 117, PsA: 15, AxSpA: 43) based on a few large systematic reviews within the field (44-48).

## Synthesis of results

Outcome events will be coded so that an RR direction of more than 1 indicates a potentially harmful effect of the experimental intervention (i.e.,  $RR = [r_I/n_I] / [r_C/n_C]$ ). Mixed effects Restricted Maximum Likelihood (REML) meta-analyses (49) will be used to combine the harm effects across RCTs (based on their log [RR]) (50); we will apply the trial ID as a random effect, while applying the review ID (from which the trial was sampled) as a fixed effect in order to model the hierarchical structure of the data sampling (51).

Heterogeneity across randomised comparisons will be assessed by using the Cochrane Q test (52), interpreted based on the  $I^2$  inconsistency index (53), and quantified by the estimate for between-trial variance ( $\tau^2$ ), estimated as  $T^2$  (54). The effect of population and trial characteristics (listed below) on the between-trial variance will be calculated by univariably adding a fixed factor for the specific characteristic in the model. If introducing a specific covariate into the meta-model reduces the observed between-trial variance ( $T^2$ ), this result will be considered an indication of a potentially important effect modifier (55).

Further analyses might (if possible) include multivariable models (56).  
Observational by nature, meta-epidemiological studies like the present should be expected to have some degree of meta-confounding because prognostic factors might be unequally distributed between studies exposed (trial characteristic positive) or not. We will attempt to adjust for possible confounding covariates (i.e. “de-confound”) the inference. That is, we will explore the ability to adjust for any important preexposure covariate ‘ *C* ’ (i.e., something that happened before the “*study design variable of interest was generated*”) that is potentially unequally distributed between the meta-epidemiological exposure groups (E: Exposed vs. Unexposed), which is ALSO an ancestor (i.e., likely cause) of the trial outcome (i.e., a more exaggerated risk of harm):  $M_E \leftarrow C \rightarrow Y_E$  (56).

### Power and sample size considerations

Although the number of trials being eligible in the synthesis is fixed based on the premises, there are several factors that can influence the statistical power in meta-analyses, such as the total number of eligible RCTs ( $k$ ), their individual sample sizes ( $N_1, N_2, \dots, N_k$ ), and the number of harm events observed in each of the trials ( $e_1, e_2, \dots, e_k$ ). Since we want to study harmful effects of various experimental interventions, even very small effect sizes would be informative. Substantial heterogeneity – between exposed vs unexposed subgroups will affect the precision of our meta-analytic estimates, and thus our potential to find significant differences between strata. Thus, on an *ad hoc* basis, we performed some analyses exploring how large the difference between two strata had to be in order for us to be able to detect it, given the expected number of studies at our disposal (say, at least 200 trials across conditions) (8, 29, 57, 58). An *ad hoc* subgroup power analysis was conducted in R using the `power.analysis.subgroup` function, based on the approach described by Hedges and Pigott (59, 60): Assuming that we want to compare two independent Odds Ratios,  $OR_1 = 2$  vs  $OR_2 = 1$ , with a conservative guesstimate of the standard error of the log(OR) values of 0.15 (61), we would have a good statistical power to detect a difference between strata (90.4%). The output also tells us that, all else being equal, the effect size difference ( $\log[OR_1]$  vs  $\log[OR_2]$ ) needs to be at least 0.595 in order to reach sufficient power.

Table 3. Population and trial characteristics

<b>Trial eligibility criteria:</b>	
	Minimum and maximum required number of swollen joint counts
	Minimum and maximum required number of tender joint counts
	Minimum and maximum required C-reactive protein
	Minimum and maximum required Erythrocyte sedimentation rate
	Minimum and maximum allowed disease duration
	Rheumatoid factor
	Anti-cyclic citrullinated peptide antibody status
	Anti-cyclic citrullinated peptide antibody 2 status
<b>DMARD history:</b>	
	csDMARD-naïve
	csDMARD-IR (csDMARD inadequate responders)
	bDMARD or tsDMARD-IR (bDMARD or tsDMARD inadequate responders)
<b>Medication background of DMARDs:</b>	
	Methotrexate
	-Naïve
	-Not using
	-Discontinued
	-Continued
	-Not reported
	csDMARDs other than methotrexate
	-Naïve
	-Not using
	-Discontinued
	-Continued
	-Not reported
	bDMARDs or tsDMARDs.
	-Naïve
	-Not using
	-Discontinued
	-Continued
	-Not reported
<b>Aggregate (e.g., average/median) patient baseline characteristics:</b>	
	Age



---

1 Female (%)

---

2 Disease duration

---

3 Erythrocyte sedimentation rate

---

4 C-reactive protein

---

5 Disease activity score

6 RF positive (%)

7 Anti-CCP positive (%)

8 CCP2 positive (%)

9 Swollen joint counts

10 Tender joint counts

11 Health assessment questionnaire—disability index

12 Physician global assessment of disease activity

13 Patient global assessment of disease activity

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14 Patient-reported pain on visual analogue scales of 0–100 mm

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## 21 Risk of bias across studies

22 Stratified meta-analyses will be used for tests of interaction between harms and the  
 23 trial RoB (listed in Table 4) and trial characteristics collected as described above.  
 24

25 *Table 4. Risk of bias*

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### 26 **Cochrane risk of bias domains:**

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- 27 · Risk of selection bias
  - 28 · Risk of performance bias
  - 29 · Risk of attrition bias
  - 30 · Overall risk of bias\*
- 

### 31 **Additional bias sources:**

---

- 32 · Single vs. multi-site trials
  - 33 · Small vs. large trials
  - 34 · Source of funding
- 

35 \*For each trial, the overall RoB will be classified as low (i.e., low RoB for all three domains); high (i.e., high  
 36 RoB for one or more domains); or unclear (i.e., unclear RoB for one or more domains in the absence of  
 37 high RoB).  
 38

## 39 DISCUSSION

The Outcome Measures in Rheumatology (OMERACT) initiative established the Contextual Factors Working Group to guide the understanding, identification and handling of contextual factors for clinical trials, with most of the current emphasis' being on net benefit inferred from a rheumatology trial (62). This meta-epidemiological study will work from the original definition of what constitutes a contextual factor, as defined in the introduction. We will explore and hope to reveal the possible impact of contextual factors (i.e., population and trial characteristics) and RoB domains of three different (but related) harm measures, as well as deaths (63). Knowing which factors are associated with a causal model for harms—either as effect modifiers or distortions of the outcome due to bias—is important for improving investigation and reporting of harms in future trials (64). If future trials report harms according to important contextual factors, meta-analyses would be able to investigate contextual factors for harms without relying on getting access to individual patient data. Such meta-research might identify subgroups among rheumatic disease patients that are at higher risk of experiencing harms. Such information would provide important evidence for future treatment guideline development. Ultimately the doctor will be able to differentiate the risk of intervention based on the patient's characteristics. This has the potential to enhance informed decision-making and effect therapeutic interventions applied in practice, leading to safer treatment of individual patients and increase efficiency in the health care system.

This study has several strengths. This will be a comprehensive risk of harm analysis of bDMARDs and tsDMARDs across multiple IA diagnoses unlike previous assessments. The study selection, data extraction and RoB assessment will be done by two independent reviewers, the data extraction will be extensive as it will include data on many different contextual factors and risk of bias items. Finally, we will only include RCTs to avoid inherent problems when investigating potential effect modifiers from non-RCT evidence.

Nevertheless, several limitations should be considered. First, the analyses may be limited by poor reporting, and data is likely to be lacking for certain contextual factors (i.e., exposures) and uncommon harms (i.e. outcomes). Second, by relying on the search results of published reviews, we assume that we retrieve a representative sample for our analysis, however, it is possible that potentially useful trials may be omitted, e.g. due to very specific eligibility criteria in the reviews or very recent trials that has not yet been included in a systematic review, which could theoretically influence our results. Third, other characteristics that we do not consider may be relevant. Fourth, meta-regression assessments, despite including only RCTs, are observational by nature and their results may by themselves be confounded by other factors(65). Finally, the meta-regression assessments involving aggregated data may be affected by ecological fallacy and could potentially be misleading(66).

## Patient and public involvement

Patients and/or the public were not involved in designing study concept or drafting of the protocol.

## ETHICS AND DISSEMINATION

Because our study does not collect primary data, no formal ethical assessment and informed consent are required. The study will be disseminated in a peer-reviewed publication.

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60**PRISMA-P (preferred reporting items for systematic review and meta-analysis protocols) 2015 checklist: recommended items to address in a systematic review protocol**

Section and topic	Item No	Checklist item
<b>Administrative information</b>		
Title:		
Identification	1a	Identify the report as a protocol of a systematic review (Line 3)
Update	1b	If the protocol is for an update of a previous systematic review, identify as such (n/a)
Registration	2	If registered, provide the name of the registry (such as PROSPERO) and registration number (Line 111)
Authors:		
Contact	3a	Provide name, institutional affiliation, e-mail address of all protocol authors; provide physical mailing address of corresponding author (Line 11-55)
Contributions	3b	Describe contributions of protocol authors and identify the guarantor of the review (Line 65-70)
Amendments	4	If the protocol represents an amendment of a previously completed or published protocol, identify as such and list changes; otherwise, state plan for documenting important protocol amendments (n/a)
Support:		
Sources	5a	Indicate sources of financial or other support for the review (Line 73)
Sponsor	5b	Provide name for the review funder and/or sponsor (Line 76-79)
Role of sponsor or funder	5c	Describe roles of funder(s), sponsor(s), and/or institution(s), if any, in developing the protocol (n/a)
<b>Introduction</b>		
Rationale	6	Describe the rationale for the review in the context of what is already known (Line 166-181)
Objectives	7	Provide an explicit statement of the question(s) the review will address with reference to participants, interventions, comparators, and outcomes (PICO) (Table 1, line 235)
<b>Methods</b>		
Eligibility criteria	8	Specify the study characteristics (such as PICO, study design, setting, time frame) and report characteristics (such as years considered, language, publication status) to be used as criteria for eligibility for the review (Line 215-233)
Information sources	9	Describe all intended information sources (such as electronic databases, contact with study authors, trial registers or other grey literature sources) with planned dates of coverage (238-241)
Search strategy	10	Present draft of search strategy to be used for at least one electronic database, including planned limits, such that it could be repeated (Table 2, Line 243)
Study records:		
Data management	11a	Describe the mechanism(s) that will be used to manage records and data throughout the review (Line 253)
Selection process	11b	State the process that will be used for selecting studies (such as two independent reviewers) through each phase of the review (that is, screening, eligibility and inclusion in meta-analysis) (Line 245-254)
Data collection process	11c	Describe planned method of extracting data from reports (such as piloting forms, done independently, in duplicate), any processes for obtaining and confirming data from investigators (Line 257-260)
Data items	12	List and define all variables for which data will be sought (such as PICO items, funding sources), any pre-planned data assumptions and simplifications (Line 262-358)
Outcomes and prioritization	13	List and define all outcomes for which data will be sought, including prioritization of main and additional outcomes, with rationale (Line 262-358)
Risk of bias in individual studies	14	Describe anticipated methods for assessing risk of bias of individual studies, including whether this will be done at the outcome or study level, or both; state how this information will be used in data synthesis (Line 321-346)
Data synthesis	15a	Describe criteria under which study data will be quantitatively synthesized (Line 392-418 and line 443-450)
	15b	If data are appropriate for quantitative synthesis, describe planned summary measures, methods of handling data and methods of combining data from studies, including any planned exploration of consistency (such as $I^2$ , Kendall's $\tau$ ) (Line 360-407)

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	15c	Describe any proposed additional analyses (such as sensitivity or subgroup analyses, meta-regression) (Line 408-418)
	15d	If quantitative synthesis is not appropriate, describe the type of summary planned (n/a)
Meta-bias(es)	16	Specify any planned assessment of meta-bias(es) (such as publication bias across studies, selective reporting within studies) (n/a)
Confidence in cumulative evidence	17	Describe how the strength of the body of evidence will be assessed (such as GRADE) (n/a)

For peer review only