The Accuracy Of Network Meta-Analysis Feasibility Predictions Based On Data Included Only In The Abstracts Of Trial Publications

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Objectives:

- Network meta-analysis (NMA) is an effective technique for comparing multiple treatments simultaneously but requires treatment regimens and outcomes to be reported consistently across trials and in a similar population.
- Time-consuming data extraction from full texts is needed to confirm whether a network can be created, with data often extracted for studies and outcomes that cannot be compared.
- We propose a time-saving method that uses data from publication abstracts to determine whether an NMA might be feasible, and to help focus data extraction on comparable interventions and outcomes.

Methodology:

- A recent systematic literature review (SLR) with NMA comparing efficacy and safety of two antiretroviral therapies for HIV was used as the gold standard¹.
- Using an Evidence Mapper tool (www.evidencemapper.co.uk), abstracts from the 206 studies included in the SLR were indexed by fields including each treatment comparison, trial name and reported outcomes.
- A network-feasibility tool assessed the possibility of creating a connected network including efavirenz and dolutegravir.
- The accuracy of the abstract-predicted networks for each outcome were compared to those in the published SLR.

Results:

- Viral suppression at 48 and 96 weeks, CD4 cell count at 48 and 96 weeks, discontinuations and treatment-related adverse event rates were the most commonly-reported outcomes in both the full texts and abstracts.
- The abstract-only sensitivity for predicting networks for four of these outcomes was 92% to 100%. The accuracy of less commonly reported outcomes was lower, with overall sensitivities of 25% to 100% and specificities of 33% to 100%. Specificity was 100% for 15 of the 23 outcomes (Figure 1).
- Time taken from identifying relevant publications to network prediction for the abstract-only method was 98 hours compared to an estimated 600 hours with full data extraction (Figure 5).

Outcome	Discontinuations	Viral suppression 96 wk	Viral suppression 48 wk	Viral suppression 12 wk	CD4 count 96 wk	CD4 count 48 wk	CD4 count 24 wk	TEAE	TE SAE	Weight change 48 wk
Sensitivity	100%	92%	92%	25%	73%	83%	45%	92%	100%	67%
Specificity	100%	100%	-	100%	50%	100%	100%	100%	100%	80%

Fig 1. Sensitivity and specificity of the Evidence Mapper predictions compared with outcomes that were included in full NMA¹

TEAE treatment-related adverse events; TE SAE Treatment-related severe adverse events; wk weeks

	1. CD4 cell count W48	2. CD4 cell count W96	3. Discontinuations due to AEs	4. Treatment- related AEs		6. Viral suppression W96	
EFV vs LPV/RTV	1	0	2	0	3	1	
FFV/ vs NV/P	2	0	1	1	4	1	
Efavirenz vs Raltegravi	1	0	0	0	1	0	$\overline{}$
EFV vs RAL	1	2	4	7	4	3	
EFV vs RPV	0	1	6	1	4	1	
EFV vs TMC278	1	0	1	1	1	0	
EFV vs ZDV	0	0	0	1	0	1	
FTC/NVP vs LPV/RTV	0	0	0	1	0	1	



Fig 2. Section of Evidence Map showing intervention comparisons against six different outcomes as indexed from abstracts



Fig 5. Comparison of workflow and estimated time taken between the standard process and process using the

Evidence Mapper

Conclusions:

- The accuracy of the Evidence Mapper approach varies by outcome and reflects how frequently different outcomes are reported in the abstracts.
- Although this method cannot confirm that an NMA is feasible, and so cannot replace the full NMA feasibility assessment, it could create a network of sufficient accuracy for commonly-reported outcomes to identify when an NMA is not likely to be feasible.
- Although developing the Evidence Map takes additional time that is not usually required for a systematic review, this is offset by efficiencies in subsequent data extraction. By identifying the main outcomes and timepoints at which they are reported before data extraction starts, researcher time can be focused on extracting data only for those interventions and outcomes that are likely to be comparable.

1. Kanters, S. et al. EClinicalMedicine 28 (2020) 100573

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