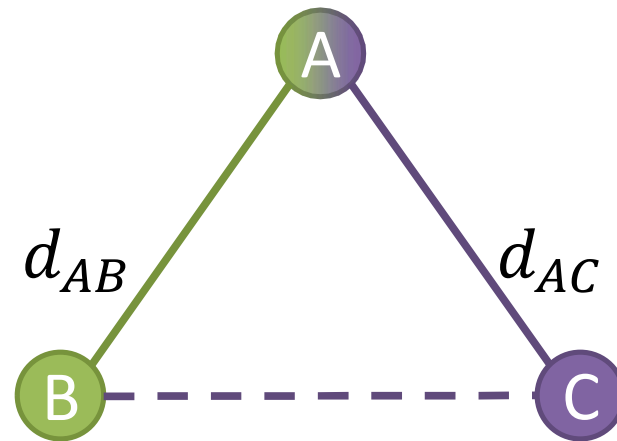

To Adjust or Not to Adjust for Effect Modifiers in HTA Submissions; Considerations in Population-Adjusted Indirect Treatment Comparisons

Multi-Level Network Meta-Regression

Nicky J. Welton (University of Bristol)

Thanks to: David Phillippo (University of Bristol)

Indirect Comparisons: Assumption

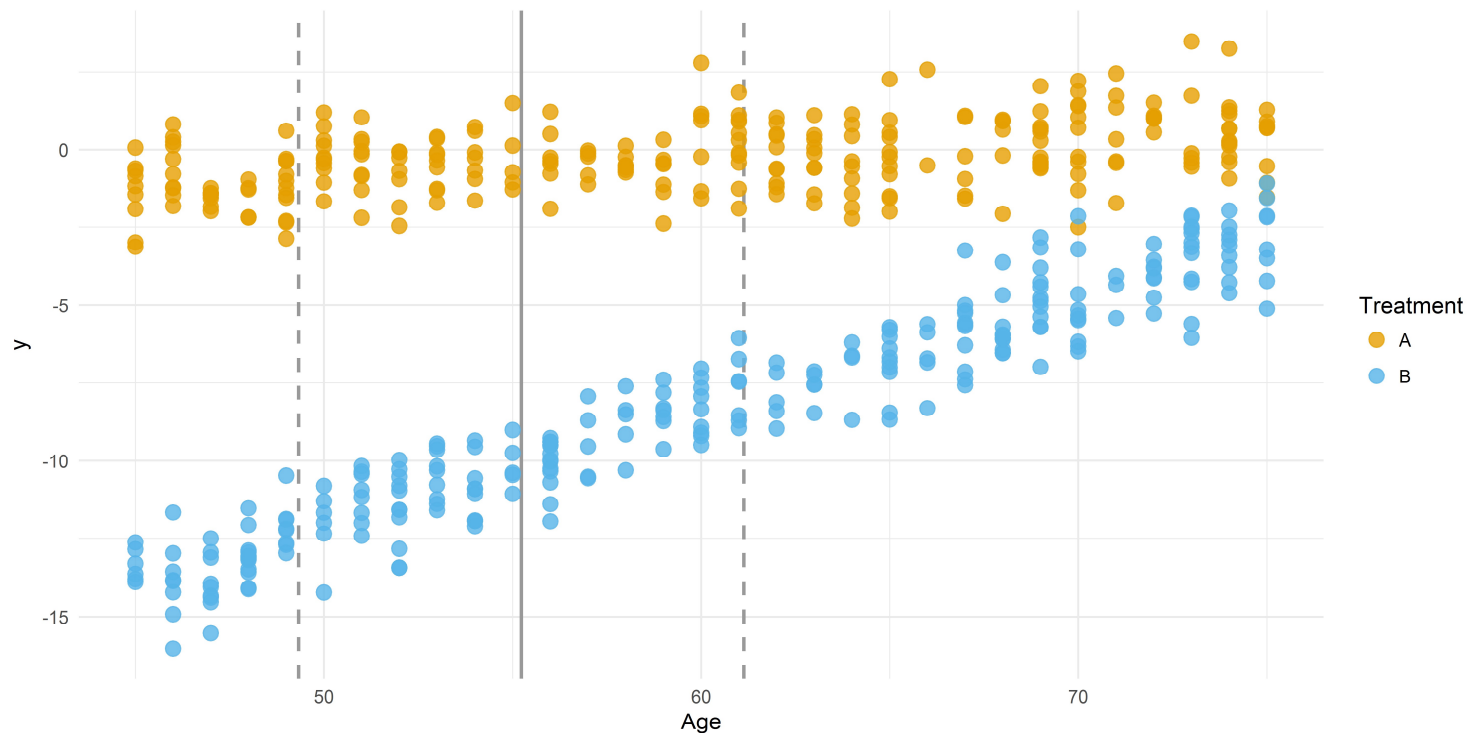


- Biased if there are imbalances in effect modifiers between AB and AC
- Population Adjusted Indirect Comparisons have been proposed to adjust for this
 - when there is IPD for AB study and aggregate data for the AC study

Matching-Adjusted Indirect Comparison (MAIC)

Signorovitch et al. (2010)

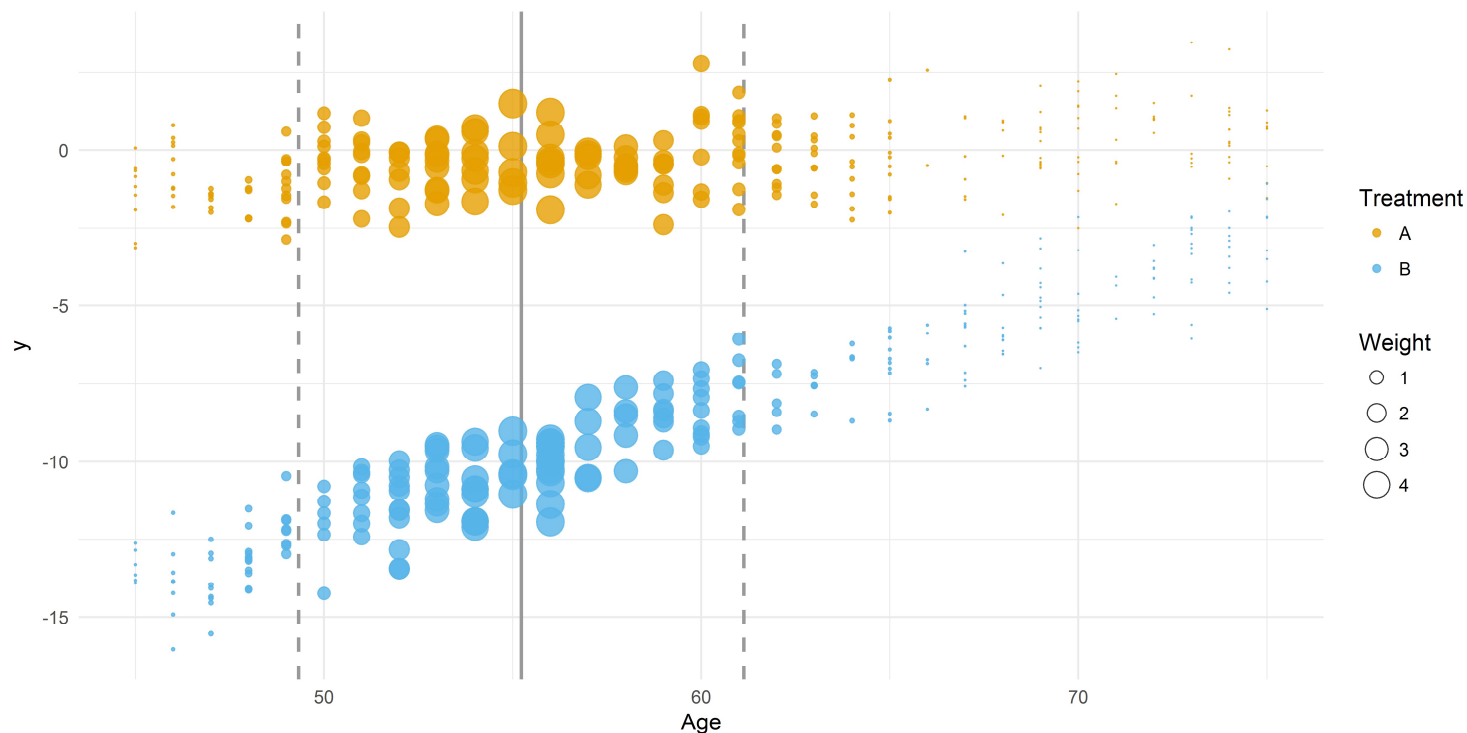
- Population reweighting method (similar to propensity score re-weighting)
- Weight AB individuals to balance covariate distribution with AC trial



Matching-Adjusted Indirect Comparison (MAIC)

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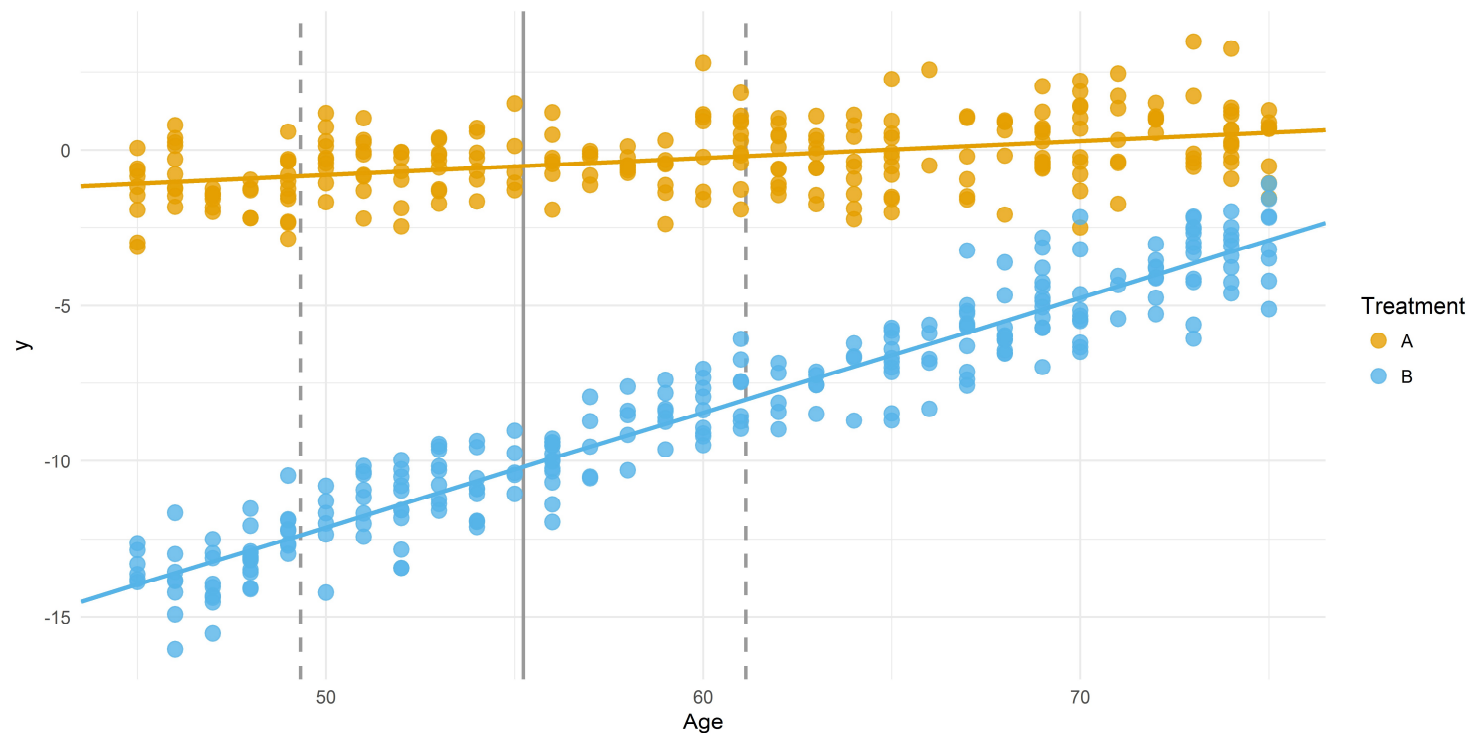
- Population reweighting method (similar to propensity score re-weighting)
- Weight AB individuals to balance covariate distribution with AC trial
- Requires AC population to be contained in the AB population
- Estimates are valid for the AC (Aggregate Data) population
- Cannot be used for networks of evidence



Simulated Treatment Comparisons (STC)

Ishak et al. (2015)

- Create an outcome regression model in the AB trial
- Use this to predict mean outcomes on treatments A and B in the AC trial population
- Can handle some lack of overlap, but relies on extrapolation
- Estimates are valid for the AC (Aggregate Data) population
- Vulnerable to aggregation bias
- Cannot be used for networks of evidence



Multilevel Network Meta-Regression (ML-NMR)

Phillippo et al (2020)

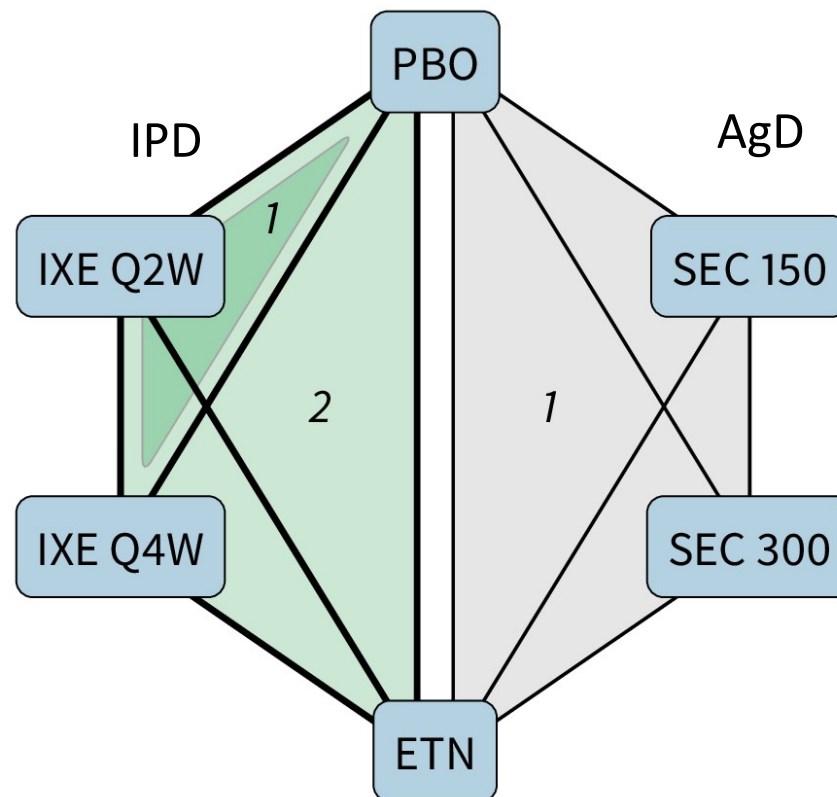
- Combines IPD and Aggregate Data
 - Using an individual-level regression model integrated over covariate distribution
- General framework
 - Builds on previous approaches
 - Jackson et al. (2006, 2008), Jansen (2012)
 - Special cases
 - Standard NMA with no adjustment
 - IPD network meta-regression with full IPD
- Can be used in **networks of all sizes**
- Produces estimates in **any specified target population**

ML-NMR: Assumptions about EM Interactions

- **Common/shared** EM interactions
 - May be justified for treatment classes
- **Independent** EM interactions
 - Requires IPD, or several AgD studies at different covariate values, **on each treatment**
- **Exchangeable** EM interactions
 - Similar data requirements to independent EM interactions
 - Hard to estimate in practice

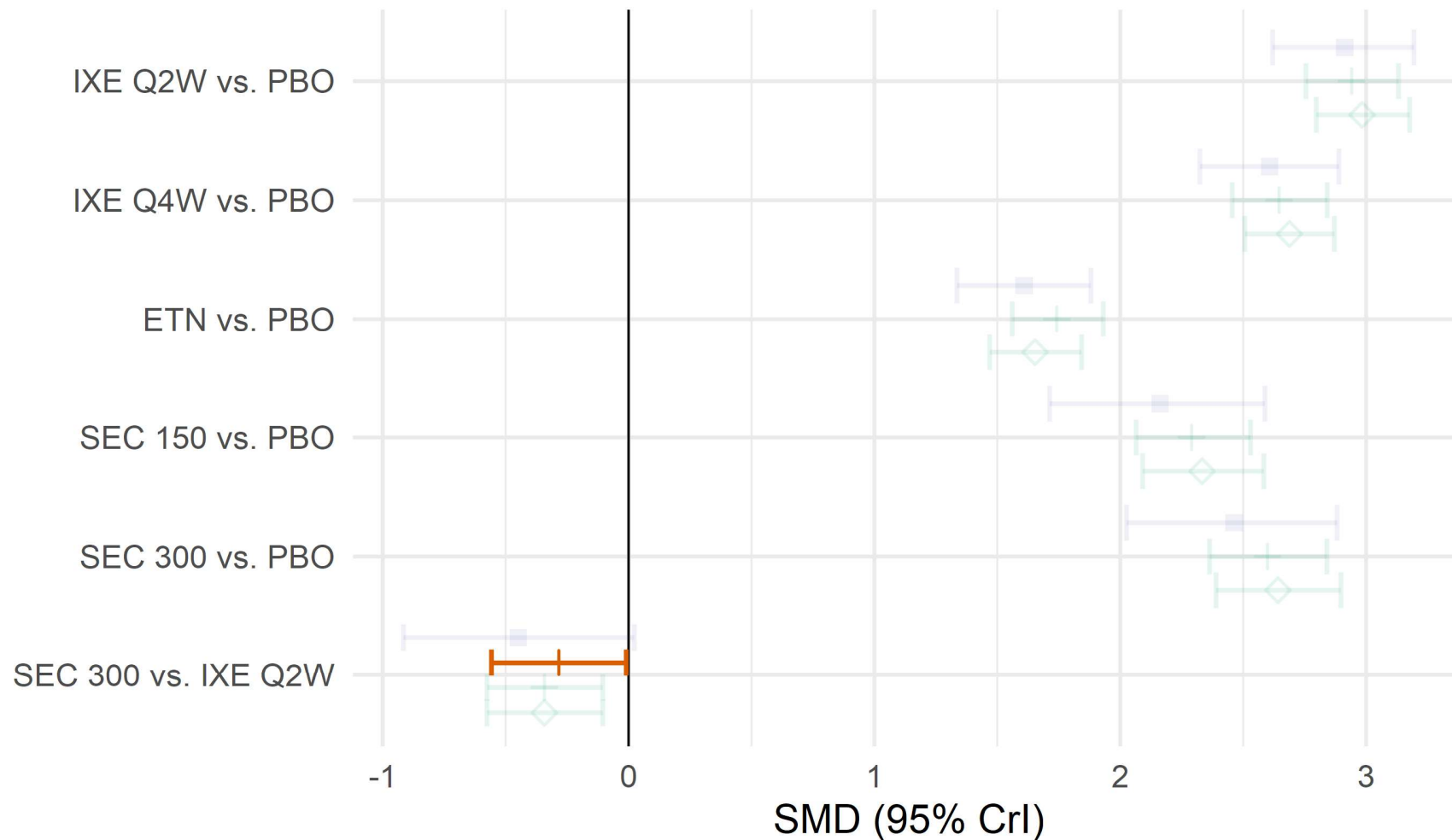
Example: Plaque Psoriasis (ML-NMR)

- Two treatment classes (plus placebo)
 - IL blocker
 - anti-TNFa



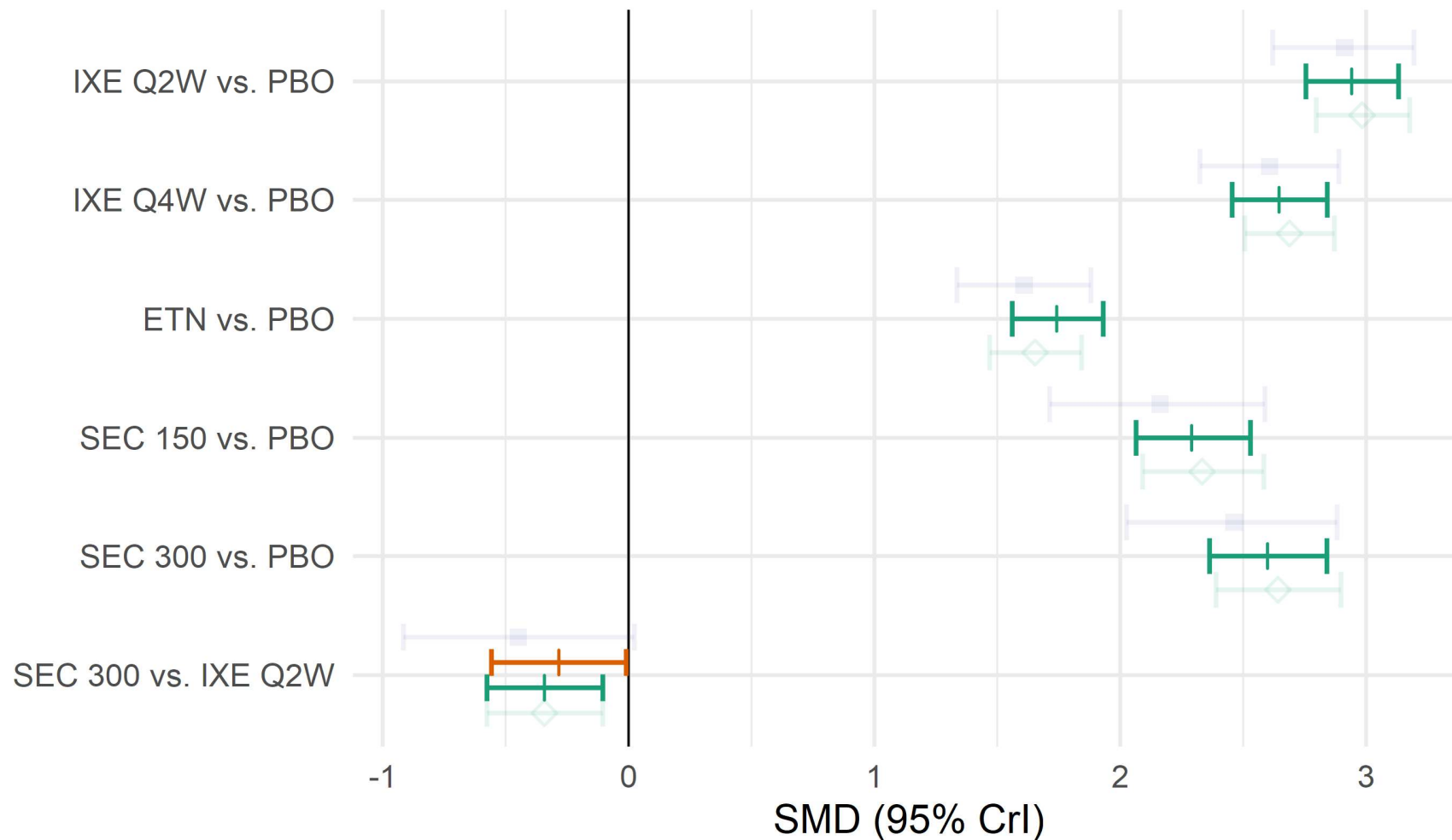
Identifying Important Covariates

- Based on individual patient data
 - Interaction tests / subgroup analyses / regression models ... but lack of power
- Expert clinical opinion / previous studies
- Need to be reported in all studies
 - omit individuals with missing covariates, or use imputation techniques
- Five covariates identified in psoriasis example
 - duration of psoriasis, body surface area, weight, previous systemic treatment, psoriatic arthritis
- Shared effect modifier assumption made for treatments within the same class



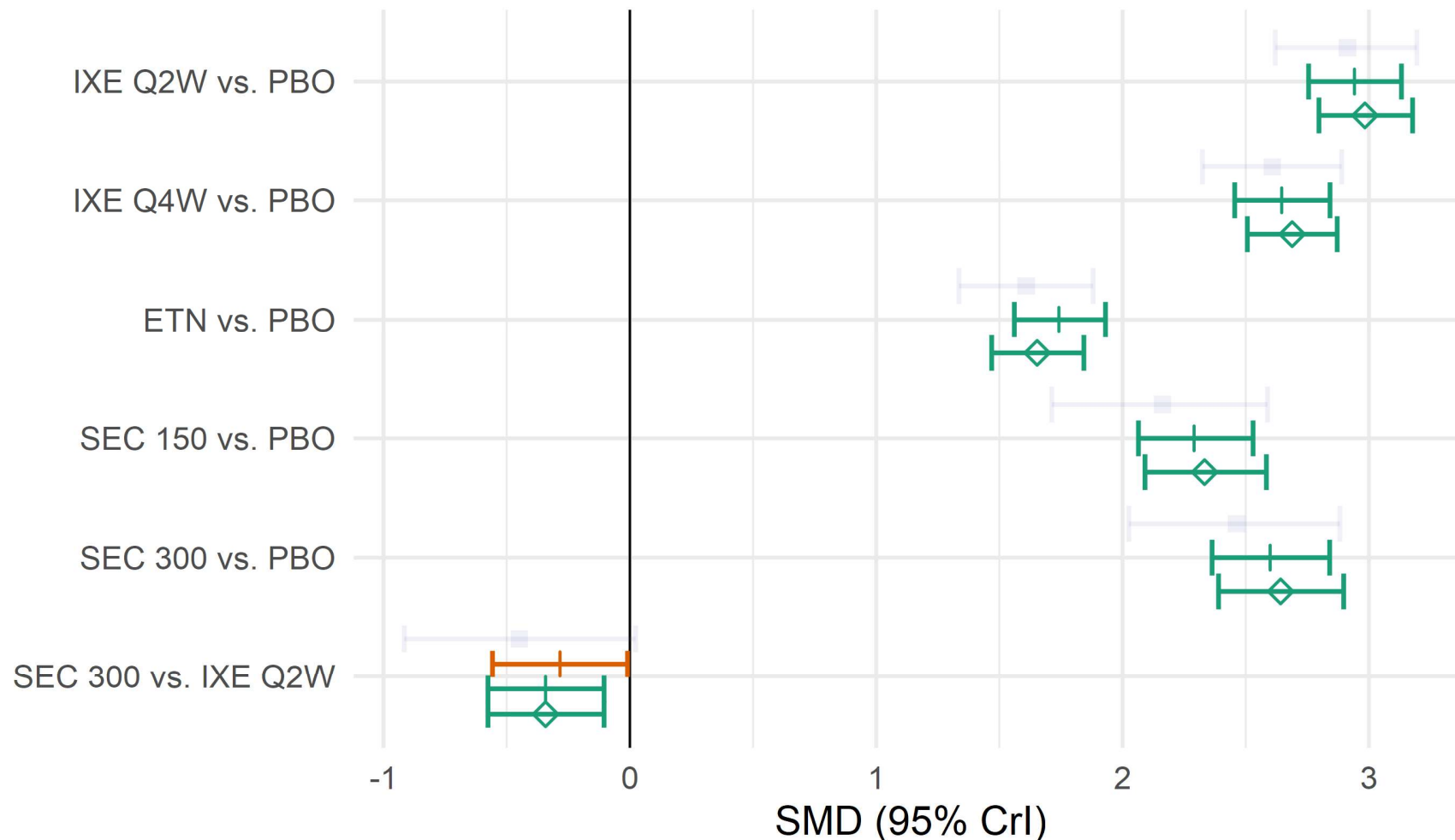
Study population ■ RE NMA + FIXTURE ◇ UNCOVER-1

Method — ML-NMR — MAIC — RE NMA



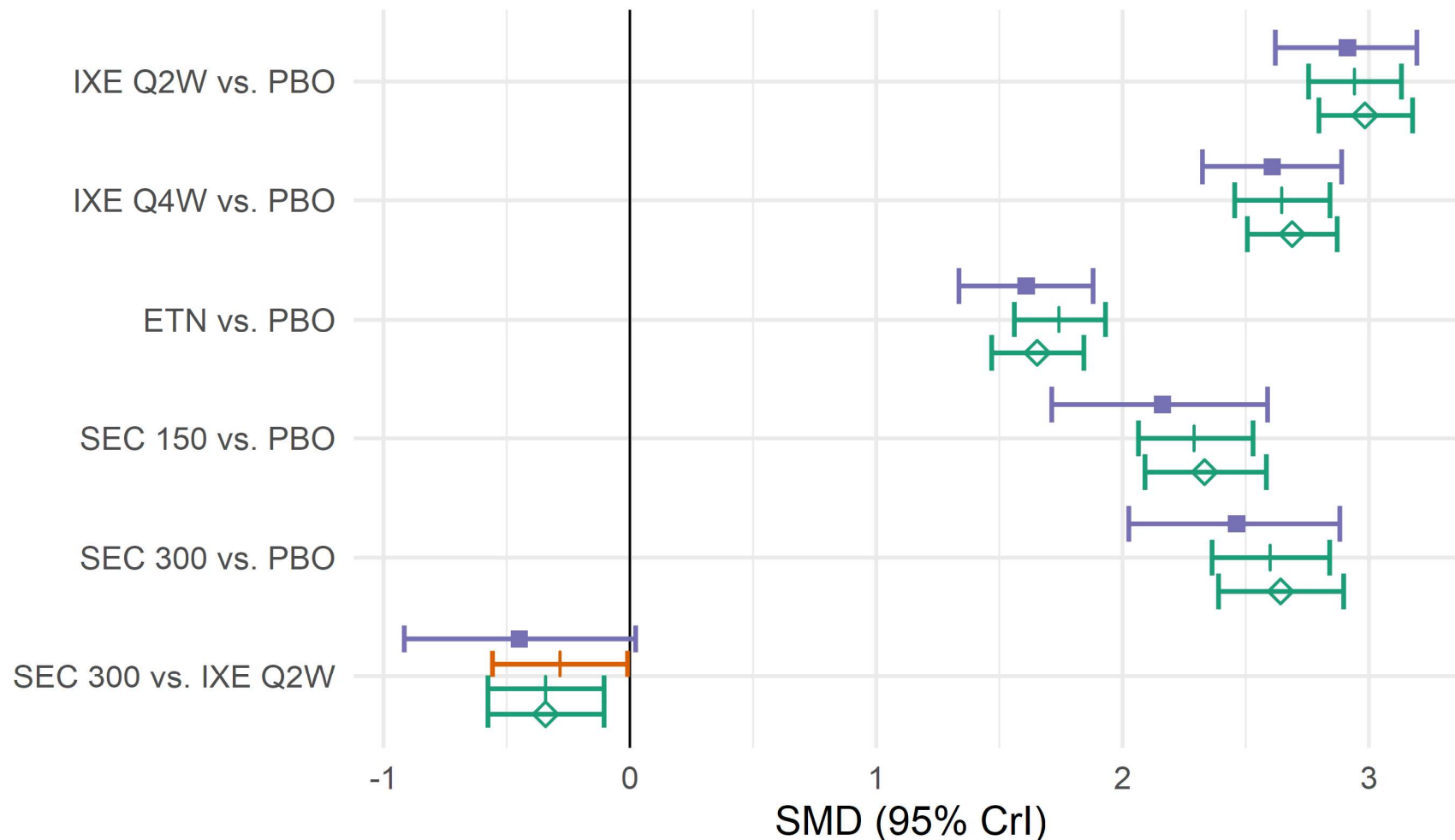
Study population ■ RE NMA + FIXTURE ◇ UNCOVER-1
 Method — ML-NMR — MAIC — RE NMA

- Produce a full set of coherent estimates
- Reduced uncertainty compared to MAIC



Study population ■ RE NMA + FIXTURE ◇ UNCOVER-1
 Method — ML-NMR — MAIC — RE NMA

- Produce a full set of coherent estimates - **in any target population**
- **Reduced uncertainty compared to MAIC**



Study population ■ RE NMA + FIXTURE ◇ UNCOVER-1
 Method — ML-NMR — MAIC — RE NMA

- Produce a full set of coherent estimates - in any target population
- Reduced uncertainty compared to MAIC

ISPOR World 2022 • Substantially reduced uncertainty compared to RE NMA

Findings from a Simulation Study

Phillippo 2020

- ML-NMR and STC both performed similarly well throughout
 - Both incur bias when extrapolation or shared EM assumption invalid
 - ML-NMR not seen to be sensitive to additional assumptions regarding joint covariate distribution in AgD population
- MAIC performed poorly in almost all scenarios, in some cases even increasing bias compared to a standard Bucher IC
 - Especially with small sample sizes
 - Needs full overlap to be unbiased, and for stable estimation of SE
- All methods susceptible to bias (and resulting under-coverage) when missing any EMs
 - Highlights the need for careful, justified variable selection (TSD 18)

Recommendations for Practice

- Use regression methods (ML-NMR, STC) over weighting methods (MAIC) when populations do not fully overlap
 - i.e. when AgD study population not fully contained within IPD population
 - Important to examine covariate distributions, and ESS for MAIC
- Use network meta-analysis based methods (ML-NMR) when presented with more than 2 studies
 - Repeated MAIC/STC will not give coherent or compatible estimates
 - Standard heterogeneity and inconsistency checks can assess assumptions in connected networks

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- Signorovitch, J. E. et al. (2010), 'Comparative Effectiveness Without Head-to-Head Trials A Method for Matching-Adjusted Indirect Comparisons Applied to Psoriasis Treatment with Adalimumab or Etanercept', *Pharmacoeconomics* 28(10), 935--945.
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- Phillippo DM, Dias S, Ades AE, Belger M, Brnabic A, Schacht A, Saure D, Kadziola S, Welton NJ. Multilevel Network Meta-Regression for population-adjusted treatment comparisons. *JRSSA* 2020. 183:1189-1210. <https://doi.org/10.1111/rssa.12579>
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