Flexible Generic Framework for Evidence Synthesis in Health Technology Assessment

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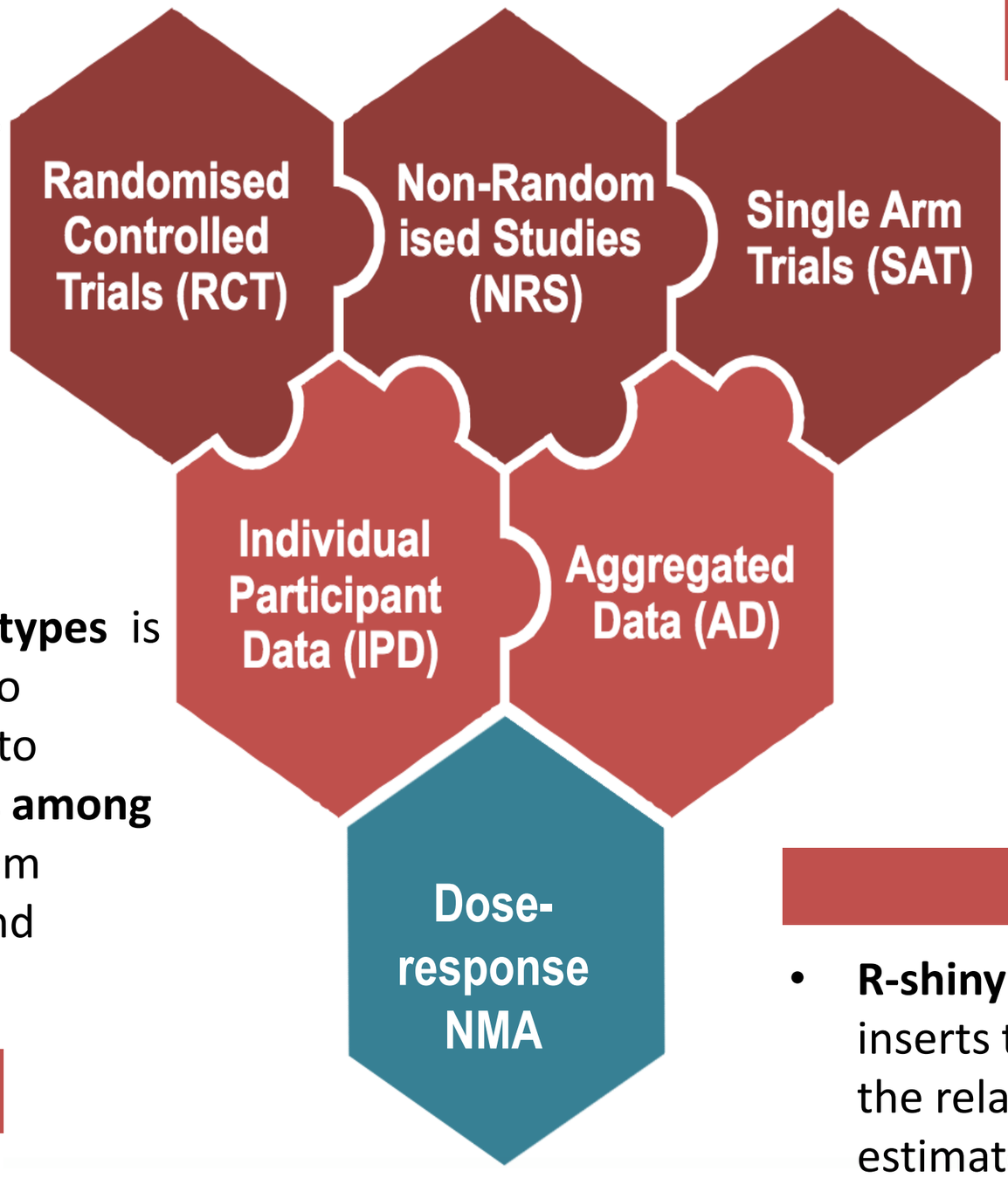
Generic framework for network meta-analysis (NMA)

Background

- **Network Meta-Analysis** (NMA) is the synthesis of evidence from multiple interventions by combining using direct and indirect comparisons across a network of studies.
- Different types of **data types** is available and we need to combine them taking into account **the differences among them** that are raised from various study designs and different data types.



Model

- A **Bayesian hierarchical models** that combines information about multiple treatments from various study designs (RCT, NRS and ST) and different data types (AD and IPD)
- We will extend the model to **network meta-regression**.
- We will adjust for lower credibility of non-randomized evidence.

Data

- Simulated data.
- All types of data about the efficacy of drugs for multiple sclerosis.

Output

- **R-shiny** web application, where the user inserts the patients characteristics and the relative treatment effects are estimated.
- The treatment hierarchy according to the outcome will also be presented.

Dose-response meta-analysis

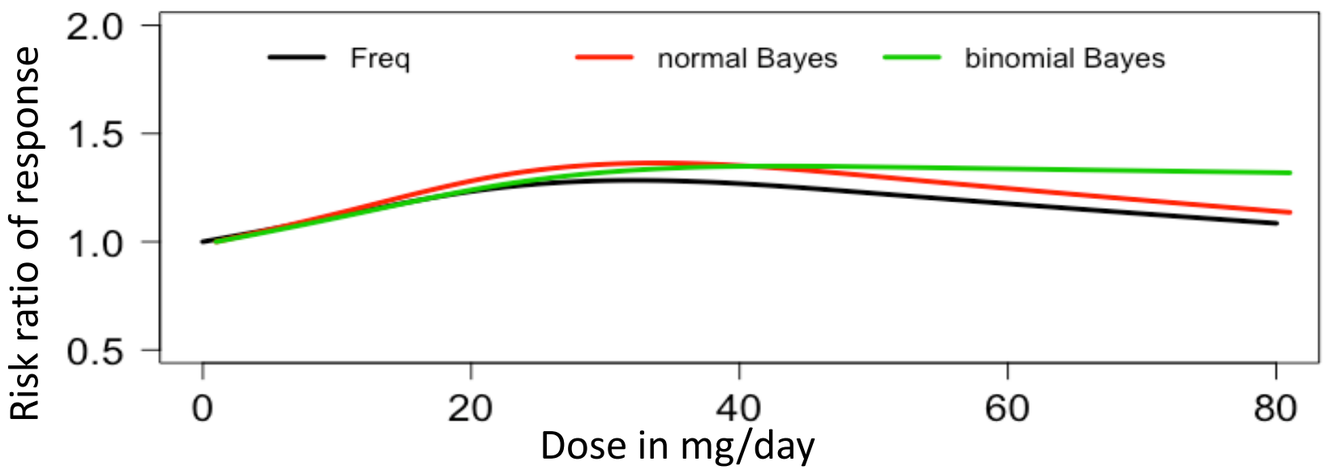
Model

- For dose j in a study i, the dose-response transformation f (e.g. linear) relates the relative effects y_{ij} to $dose_{ij}$. We propose **a hierarchical dose-response meta-analysis -model** with 2 levels:
- **Level 1:** within each study, the dose-response curve is estimated.
- **Level 2:** across studies, all dose-response curves are synthesized using the standard fixed or random-effect model.
- We fit 3 models to the data: two-stage model in frequentist setting, and our hierarchical Bayesian models with normal or binomial likelihood.

Data

- A dataset of 77 RCTs comparing response to antidepressants
- 85 different dose-specific effect are reported

Results



- The three approaches meet remarkably.
- our analyses showed dose dependency in efficacy up to around 20–40 mg fluoxetine equivalents.

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