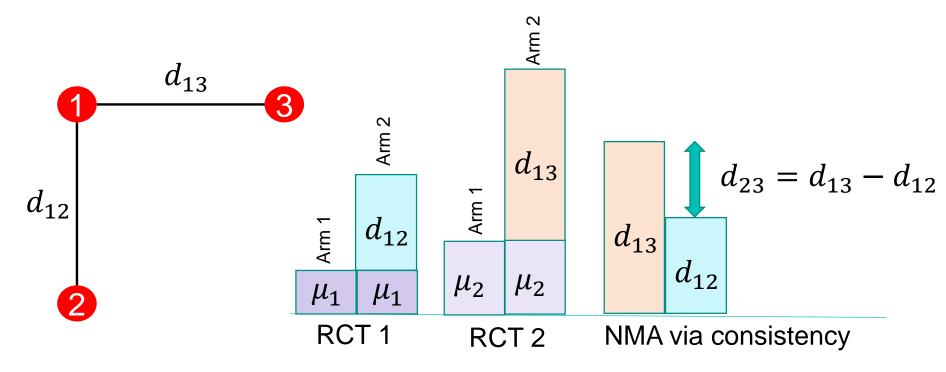


Getting data ready for network meta-analysis

Howard Thom



Network meta-analysis



- A method for indirectly comparing interventions that have not been compared in a head-to-head RCT.
- NMA often conducted in Bayesian framework using OpenBUGS software
- This is linked from R using R2OpenBUGS



The problem

- RCTs going into network meta-analyses are identified by a systematic literature review (SLR).
- Data generated by the SLR is saved in a Data Extraction Sheet (DES).
- DES rarely in the format needed for OpenBUGS NMA code
- We need to write code that converts DES data to OpenBUGS NMA format

The application





Intracavity lavage and wound irrigation for prevention of surgical site infection: systematic review and network meta-analysis

Howard Thoma

with Gill Norman^c, Nicky J Welton ^{a, b}, Emma Crosbie ^d, Jane Blazeby ^{a, b}, and Jo C Dumville ^c

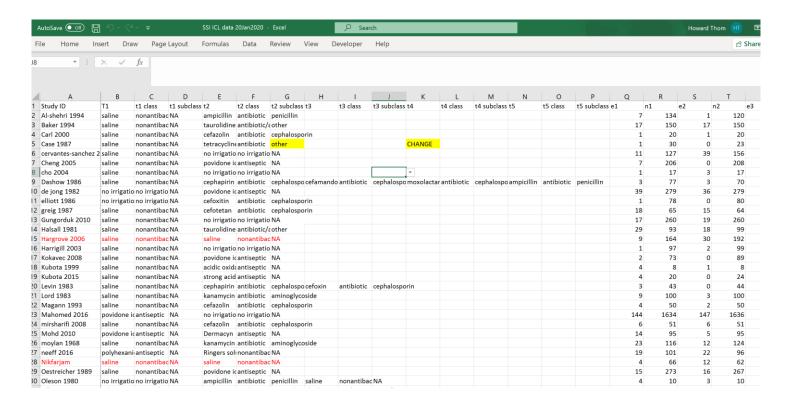
- ^a Surgical Innovation theme of the National Institute for Health Research (NIHR) Bristol Biomedical Research Centre (BRC), Bristol Medical School, University of Bristol, Bristol, UK
- ^b MRC <u>ConDuCT</u>-II Hub for Trials Methodology Research (Collaboration and Innovation for Difficult or Complex Randomised Controlled Trials in Invasive Procedures), Bristol Medical School, University of Bristol, Bristol, UK
- ^c Division of Nursing, Midwifery & Social Work, School of Health Sciences, Faculty of Biology, Medicine & Health, University of Manchester, Manchester Academic Health Science Centre, Manchester, UK
 - ^d Division of Cancer Sciences, Faculty of Biology, Medicine & Health, University of Manchester, Manchester Academic Health Science Centre, Manchester, UK







Raw data format



- Note that this application is cleaner than most!
 - We only need to exclude 'red' studies and the numbers of events and patients don't need to be imputed



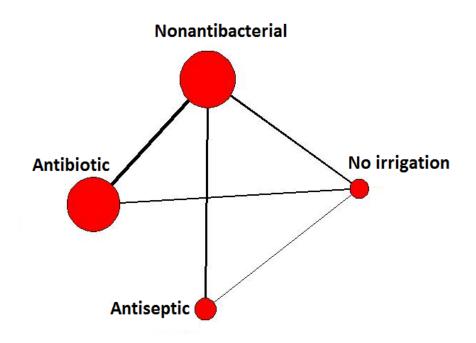
Format needed by ROpenBUGS

- ns is the number of studies
- na[] is a vector of number of arms for each study
- t[,] is a numeric matrix with ns rows and max(na) columns. Each entry is the treatment in that arm
- r[,] is a numeric matrix with ns rows and max(na) columns. Each entry is the number of events in that arm
- n[,] is a numeric matrix with ns rows and max(na) columns. Each entry is the number of patients in that arm
- Ideally need a mapping from numeric t[,] to the actual treatment names

Niggles

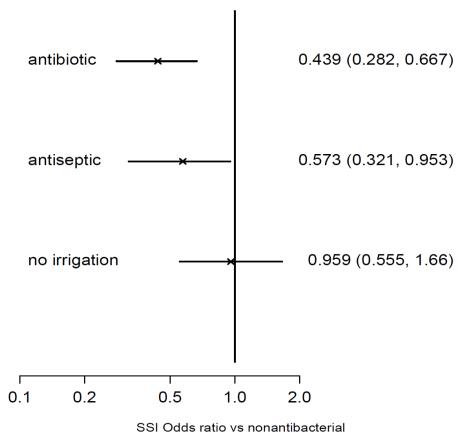
- Treatment numbers need to be in ascending order
- The reference treatment (nonantibacterial irrigation) needs to be 1

Bonus – generate network plot



- Can do this using our formatted data
- Use existing code or write a new function, maybe with ggplot

Super stretch goal – generate forest plot



This first needs the OpenBUGS code to run

What do we want?

Goal

 Increase efficiency of going from systematic literature reviews to network meta-analyses

Output

- A script that is publicly available on GitHub
- Statisticians can adapt to other situations going forward